International Plant Breeding Congress
# ABSTRACT BOOK

IPBC

International Plant Breeding Congress
10-14 November 2013 Antalya, Turkey

# ORGANIZING COMMITTEE, SECRETARIAT AND CONTACT INFORMATION

| ORGANIZING COMMITTEE | |
|---|---|
| Dr. Vehbi ESER | Chair of IPBC |
| Assoc. Prof. Dr. Yalçın KAYA | Vice Chair of IPBC |
| Assoc. Prof. Dr. S. Ahmet BAGCI | President of Plant Breeders Union of Turkey |
| Kamil YILMAZ | President of Plant Breeders Association |
| Dr. Ali Osman SARI | Deputy Director of Agricultural Research and Policy |
| Dr. Eva THORN | Chair of Plant Genetic Resources Section of EUCARPIA |
| Edgar KRIEGER | General Secretary of CIOPORA |
| Prof. Dr. Mehmet CAKIR | Murdoch University, Australia |
| Bayram ÖZDEMİR | Plant Breeders Union of Turkey |

| CONGRESS SECRETARIAT | |
|---|---|
| Mustafa AKIN | Secretary of Congress |
| Osman Barış KILINÇ | Assistant Secretary of Congress |
| Tuğba HELVACIKARA | Assistant Secretary of Congress |

| ORGANIZING INSTITUTIONS |
|---|
| Plant Breeders Union of Turkey (BISAB) |
| Plant Breeders Association (TUBID) |
| Turkish Seed Union (TURKTOB) |
| Economic Cooperation Organization Seed Association (ECOSA) |
| General Directorate of Agricultural Research and Policy (TAGEM) |
| International Maize and Wheat Improvement Center (CIMMYT) |
| International Center for Agricultural Research in the Dry Areas (ICARDA) |
| European Association for Plant Breeding Research (EUCARPIA) |
| International Community of Breeders of Asexually Reproduced Ornamental and Fruit Varieties (CIOPORA) |

| SUPPORTING INSTITUTIONS | |
|---|---|
| Moldova Science Academy | Moldova |
| Serbia Seed Trade and Plant Breeders Association | Serbia |
| Bulgaria Seed Association | Bulgaria |
| The Hellenic Scientific Society for Plant Genetics and Breeding | Greece |
| Murdoch University | Australia |
| Akdeniz University | Turkey |

# ORGANIZING INSTITUTIONS

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T.C.
GIDA TARIM VE HAYVANCILIK
BAKANLIĞI

TÜRKTOB

BİTKİ ISLAHÇILARI DERNEĞİ
TUBID
2003

ecosa

CIMMYT
International Maize and Wheat Improvement Center

ICARDA

EUCARPIA
European Association for Research on Plant Breeding
Europäische Gesellschaft für Züchtungsforschung
Association Européenne pour l'Amélioration des Plantes

CIOPORA

FAO
FIAT PANIS

## SCIENTIFIC COMMITTEE

| NAME | DUTY | COUNTRY | INSTITUTION |
|---|---|---|---|
| Prof. Dr. Kayhan Z. KORKUT | Head of SC | TURKEY | NKU Tekirdag AF |
| Prof. Dr. Bülent UZUN | Deputy Head of SC | TURKEY | AK U Antalya AF |
| Prof. Dr. Cengiz TOKER | Deputy Head of SC | TURKEY | AK U Antalya AF |
| | | | |
| **NAME** | **INSTITUTION** | **COUNTRY** | **FIELD OF INTEREST** |
| Assoc. Prof. Dr. Taner AKAR | EU Kayseri AF | TURKEY | Cereals |
| Dr. Zeynal AKPEROV | Genetic Resources Institute | AZERBAIJAN | Genetic Resources |
| Prof. Dr. Salem S. ALGHAMDI | King Saud University, Riyadh | SAUDI ARABIA | Legumes |
| Prof. Dr. Neset ARSLAN | Ankara University | TURKEY | Tuber and Aromatic Crops |
| Prof. Dr. Halis ARIOĞLU | Çukurova Univ | TURKEY | Oil Crops |
| Prof. Dr. Atanas ATANASSOV | Joint Genomic Center | BULGARIA | Viticulture - Molecular Breeding |
| Prof. Dr. Stephan BAENZIGER | Nebraska State University | USA | Wheat Breeding |
| Assoc. Prof. Dr. S. Ahmet BAGCI | Selcuk Univ., Konya | TURKEY | Cereals |
| Prof. Dr. Ahmet BALKAYA | Ondokuzmayis University | TURKEY | Cucurbit Breeding |
| Prof. Dr. David BALTENSPERGER | President of Crop Science Society US | USA | Alternative Crops |
| Prof Dr. Nilgün BAYRAKTAR | Ankara University | TURKEY | Oilseed Crops |
| Dr Necmi BEŞER | Trakya ARI | TURKEY | Rice |
| Dr. Yılmaz BOZ | YALOVA Agric. Research Institute | TURKEY | Fruits / Viticulture |
| Prof. Dr. Hikmet BUDAK | Sabanci University | TURKEY | Molecular Breeding |
| Prof Dr M. Emin ÇALIŞKAN | Nigde University | TURKEY | Potato |
| Prof. Dr. Mehmet ÇAKIR | Murdoch University | AUSTRALIA | Molecular Genetics Cereals |
| Prof. Dr. Esen ÇELEN | Ege University | TURKEY | Forage Crops |
| Prof. Dr. Anne Frary DOĞANLAR | IYTE | TURKEY | Molecular Genetics |
| Prof. Dr. Jaraslow DOLEZEL | Centre of Plant Structural and Func. Genomics | CHECK REPUBLIC | Wheat and Forage Crops Genomic |

|  |  |  |  |
|---|---|---|---|
| Prof. Dr. Wolfgang FRIEDT | Giessen University | GERMANY | Oilseed Crops |
| Prof. Dr. Bikram GILL | Kansas State University | USA | Resistance Breeding |
| Dr. Danny HUNTER | Bioversity International | ITALY | Agricultural Biodiversity Resistance Breeding |
| Dr. Kshirod K. JENA | IRRI | PHILIPPINNES | Rice |
| Dr. Necdet KAPLAN | TAGEM | TURKEY | Fruits |
| Assoc. Prof. Dr. Yalcin KAYA | Trakya ARI | TURKEY | Sunflower |
| Dr. Davut KELEŞ | ALATA | TURKEY | Solaneacae Breeding |
| Dr. Mesut Keser | ICARDA | TURKEY | Wheat |
| Prof. Dr. Kayhan Z. KORKUT | NKU Tekirdag AF | TURKEY | Cereals |
| Prof. Dr. Yue JIN | USDA, Minnesota | USA | Pathologist |
| Prof. Dr. Muhammed MERGOUM | North Dakota State University | USA | Wheat Breeding |
| Dr. Alex MORGOUNOV | CIMMYT | MEXICO | Wheat |
| Dr. Ali Akbar MOAYEDI | Agricultural Research Center | IRAN | Wheat |
| Prof. Dr. Nikolay DZYUBENKO | Vavilov Institute, St. Petersburg | RUSSIA | Genetic Resources |
| Prof. Dr. Abd El-Aziz ABD EL-NABY | Field Crops Research Institute | EGYPT | Maize |
| Prof. Dr. A. Naci ONUS | Akdeniz University Antalya | TURKEY | Solanacaea Breeding |
| Prof. Dr. Sebahattin ÖZCAN | Ankara University | TURKEY | Molecular Genetics |
| Prof. Dr. Murat ÖZGEN | Ankara University | TURKEY | Molecular Genetics |
| Dr Isa ÖZKAN | TAGEM | TURKEY | Cotton |
| Dr. B. M. PRASANNA | CIMMYT | MEXICO | Maize |
| Prof. Dr. Jaime PROHENS | Politecnica de Valencia | SPAIN | Solanaceae Breeding |
| Assoc. Prof. Dr. Zafer SAĞEL | Turkish Atomic Energy Authority | TURKEY | Legume Breeding-Mutation |
| Prof. Dr. Nebahat SARI | Çukurova University | TURKEY | Cucurbit Breeding |
| Dr. Jay W. SCOTT | University of Florida | USA | Tomato Breeding |
| Prof. Dr. Vladimir SHAMANIN | Omsk State Agric. University | RUSSIA | Cereal Resistance Breeding |
| Prof. Dr. Kadambot H.M. SIDDIQUIE | University of Western Australia | AUSTRALIA | Legumes |

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|---|---|---|---|
| Prof. Dr. Vyacheslav SOKOLOV | Plant Breeding and Genetics Institute Odessa | UKRAINE | Maize |
| Dr. Hussain Rahim SOURUSH | RRIR, Rasht | IRAN | Rice |
| Assoc. Prof. Dr. Ahmet TAMKOÇ | Selçuk University | TURKEY | Forage Crops |
| Dr. Eva THORN | EUCARPIA | SWEEDEN | Genetic Resources |
| Prof. Dr. Ioannis TOKATLIDIS | Democritus University of Thrace | GREECE | Plant Breeding |
| Prof. Dr. Mahmut TOR | University of Worcester | ENGLAND | Arabiodopsis, Pathology Molecular Breeding |
| Prof. Dr. Önder TÜRKMEN | Selçuk University | TURKEY | Cucurbit Breeding |
| Prof. Dr. Metin TUNA | NKU Tekirdag AF | TURKEY | Forage Crops, Cytogenetics |
| Prof. Dr. Cengiz TOKER | Antalya University | TURKEY | Legume Crops |
| Dr. Hari D. UPADHYAYA | ICRISAT | INDIA | Genetic Resources |
| Prof. Dr. Bülent UZUN | AK U Antalya AF | TURKEY | Oilseed Crops |
| Dr. Ali ÜSTÜN | Safgen Seed Ltd. | TURKEY | Soybean |
| Dr. Yong XU | National Engineering Res Cen. Vegetables | CHINA | Cucurbit resistance molecular breeding |
| Prof. Dr. Richard VISSER | Wageningen University | NETHERLAND | Potato |
| Prof. Dr. Ahmet YILDIRIM | Karamanoglu Mehmetbey Univ. | TURKEY | Molecular Genetics |
| Dr Necmettin BOLAT | NBC Seed Co | TURKEY | Cereal Diseases, Breeding |
| Prof Dr Rishi Kumar BEHL | University of Hisar, Haryana, | INDIA | Biotic and Abiotic Stress Resistance |
| Prof Dr Fahri ALTAY | SEU Bilecik NSF | TURKEY | Cereal Diseases, Breeding |

## INVITED SPEAKERS

| NAME | INSTITUTIONS | COUNTRY | SUBJECT AREA |
|---|---|---|---|
| Prof. Dr. David BALTENSPERGER | President of Crop Science Society of US | USA | Alternative Crops |
| Prof. Dr. Wolfgang FRIEDT | Giessen University | GERMANY | Oilseed Crops |
| Prof. Dr. Nikolay DZYUBENKO | Vavilov Institute, St. Petersburg | RUSSIA | Genetic Resources |
| Dr. B. M. PRASANNA | CIMMYT | MEXICO | Maize |
| Dr. Jay W. SCOTT | University of Florida | USA | Tomato Breeding |
| Prof. Dr. Kadambot H.M. SIDDIQUIE | University of Western Australia | AUSTRALIA | Legumes |
| Dr. Hari D. UPADHYAYA | ICRISAT | INDIA | Genetic Resources |
| Prof. Dr. Richard VISSER | Wageningen University | NETHERLAND | Potato |

## INTELLECTUAL PROPERTY RIGHTS IN PLANT BREEDING SESSION

| NAME | POSITION | COUNTRY | INSTITUTION |
|---|---|---|---|
| Peter Button | Vice-Secretary General of the UPOV | SWITZERLAND | UPOV - International Union for the Protection of New Varieties of Plants |
| Marting Ekvad | President of the CPVO | FRANCE | CPVO - Community Plant Variety Office |
| Dr. Gabor Abbas | Lawyer | NETHERLANDS | AOMB Law Firm |
| Dr. Edgar Krieger | Secretary General of CIOPORA | GERMANY | CIOPORA, International Community of Breeders of Assexually Reproduced Onamental Plants and Fruit Varieties |

# 1

# General Session

## SUNDAY, NOVEMBER 10th, 2013

| | |
|---|---|
| $14^{00}$ - $18^{30}$ | **Registration** |
| $17^{00}$ - $18^{30}$ | **Welcome Cocktail** |
| $14^{00}$ - $18^{30}$ | Side Events and Stands |

## MONDAY, NOVEMBER 11TH 2013

| | |
|---|---|
| $08^{00}$ - $09^{00}$ | Registration |
| $09^{00}$ - $10^{30}$ | Opening Ceremony |
| $10^{30}$ – $10^{45}$ | Coffee break |
| $10^{45}$ - $12^{30}$ | **OPENING SESSION:**<br>Session Chair: **Dr. Vedat MIRMAHMUTOĞULLARI,** Undersecretary of Ministry of Food, Agriculture and Livestock of Turkey |
| $10^{45}$ – $11^{15}$ | ***Invited Speaker*** **Prof. Dr. David BALTENSPERGER**<br>**“Plant Breeding for Future”** |
| $11^{15}$ – $11^{45}$ | ***Invited Speaker*** **Prof. Dr. Richard VISSER**<br>**“Potential and future of novel molecular breeding techniques in practical plant breeding”** |
| $11^{45}$ – $12^{15}$ | ***Invited Speaker*** **Prof. Dr. Nikolay DZYUBENKO**<br>**“Genetic Resources for Plant Breeding: Past, Present and Future”** |
| $12^{15}$ – $12^{30}$ | DISCUSSION |
| $12^{30}$ – $13^{30}$ | LUNCH |

# 2

# Kanuni Sultan Süleyman Han Meeting Room

(Field Crop Session - 1)

## MONDAY, NOVEMBER 11$^{TH}$ 2013

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|---|---|
| 13$^{30}$ - 15$^{30}$ | ***1st Session - Session Chair:* DR BEAT BOLLER** |
| 13$^{30}$ - 14$^{00}$ | ***Invited Speaker*** **Prof Wolfgang FRIEDT**<br>**“Breeding Oilseeds for Bioenergy or Food Production”** |
| 14$^{00}$ - 14$^{15}$ | FC-51: Breeding of Peanut (*Arachis Hypogeae* L.) Variety (*Osmaniye-2005*) Tolerant to Iron Deficiency Chlorosis - H.H. Arıoğlu, B. Onat, C. Kurt, L. Güllüoğlu, S. Çalışkan |
| 14$^{15}$ - 14$^{30}$ | FC-224: Agronomic performance of soybean with resistance potential to stink bugs – K. C. Oliveira; F. Rocha; M. C. Ferreira; F. B. Pereira; J. B. Pinheiro |
| 14$^{30}$ - 14$^{45}$ | FC-102: Genetic performance of vegetative traits of MPOB oil palm interspecific hybrids in inland and coastal soils. A. Mohd Din, A. Kushairi, A. Noh, N. Rajanaidu |
| 14$^{45}$ - 15$^{00}$ | Discussion |
| 15$^{00}$ - 15$^{30}$ | Coffee break |
| 15$^{30}$ - 17$^{30}$ | ***2nd Session - Session Chair:* PROF DR MAHMUT TOR** |
| 15$^{30}$ - 15$^{45}$ | Direct Regeneration from Leaf Disc Explants of Peanut: Grafting Improves survival Rate – M. Hassan, Z. Akram, F. Nazir, N. Fatima, Y. F. Zafar |
| 15$^{45}$ - 16$^{00}$ | FC-214: Inheritance of drought resistance, yield and quality parameters in cotton (*Gossypium hirsutum* L..) - B. Akgöl, O. Gençer |
| 16$^{00}$ - 16$^{15}$ | FC.54: Combining Ability through Lines × Tester Analysis and Heritability Studies in Upland Cotton - N. U. Khan, K. Makhdoom, S. Gul |
| 16$^{15}$ - 16$^{30}$ | FC-56: Prospects of Association Mapping in Cotton (*Gossypium hirsutum* L.)<br>M. Saeed, G. Wangzhen, Z. Tianzhen |
| 16$^{30}$ - 16$^{45}$ | FC-285: Determination of heterotic effects of seed cotton weight per boll in F1 hybrids double cross in cotton – R. Ekinci, S. Başbağ, O. Gençer |

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| 16$^{45}$ - 17$^{00}$ | Determination of stability and adaptation ability for some promising cotton (Gossypium hirsutum l.) genotypes in Aegean and Cukurova regions – Y. Akişcan, B Akgöl, H. Güngör, D. Can |
| 17$^{00}$ - 17$^{30}$ | Discussion |
| 17$^{30}$ - 18$^{30}$ | ***Poster Session*** |
| 19$^{00}$ - | **Dinner** |
| 08$^{30}$ - 18$^{30}$ | Side Events and Stands |

## TUESDAY, NOVEMBER 12$^{ND}$ 2013

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|---|---|
| 09$^{00}$ - 10$^{30}$ | ***3rd Session - Session Chair:*** **PROF DR RISHI BEHL** |
| 09$^{00}$ - 09$^{15}$ | FC-53: Breeding wheat (*Triticum aestivum* L.) with enhanced bioactive compunds Bedő, Z., Rakszegi, M., Lafiandra, D., Gebruers, K., Ward, J., Láng, L., Shewry, P. R. |
| 09$^{15}$ - 09$^{30}$ | FC-91: Comparison of chemical composition of two durum wheat (T. durum L.) and bread wheat (*T. aestivum* L.) germ oils – Y. Zarroug, J. Mejri, M. El Felah |
| 09$^{30}$ - 09$^{45}$ | FC-113: Genetic potential of winter wheat grain quality in central Asia - Abugaliyeva A.I., Morgounov A.I. |
| 09$^{45}$ - 10$^{00}$ | The determination of genetic progress for yield and quality traits at winter bread wheat – N. Gummadov, A. Topal, A. Morgounov, M. Keser, S. A. Bağcı, B. Akın |
| 10$^{00}$ - 10$^{15}$ | GR- 67: Molecular genetic analysis of Ukrainian bread wheat gene pool - S. Chebotar |
| 10$^{15}$ - 10$^{30}$ | Discussion |
| 10$^{30}$ - 11$^{00}$ | Coffee break |
| 11$^{00}$ - 12$^{30}$ | ***4th Session - Session Chair:*** **PROF DR AIGUL ABUGALIYEVA** |
| 11$^{00}$ - 11$^{15}$ | FC-6: Genealogical analysis of resistance to pre-harvest sprouting in the north-American spring wheat varieties - S.Martynov, T. Dobrotvorskaya |
| 11$^{15}$ - 11$^{30}$ | FC-8: Method of ecological breeding an example program “ECADA” - V. V. Syukov, V. G. Zakharov, V. G. Krivobochek, V. I. Nikonov, N. Z. Vasilova, V. A. Ganeev, D. V. Kochetkov |
| 11$^{30}$ - 11$^{45}$ | Cryopreservation techniques of cereal genetic resources - H. Yavuz EMEKLİER |
| 11$^{45}$ - 12$^{00}$ | FC-223: Adaptive changes of physiological signs of wheat genotypes under soil drought conditions - T.I. Allahverdiyev, J.M.Talai, I.M.Huseynova, J.A.Aliyev |
| 12$^{00}$ - 12$^{15}$ | FC-32: Identification of differentially expressed genes under low temperature in winter wheat – R. Armonienė, G. Brazauskas |
| 12$^{15}$ - 12$^{30}$ | Discussion |

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| $12^{30}$ - $13^{30}$ | Lunch |
| $13^{30}$ - $15^{30}$ | ***5th Session - Session Chair:* PROF DR ZOLTAN BEDO** |
| $13^{30}$ - $14^{00}$ | ***Invited Speaker* Prof Dr. Kadambot H.M. Siddique**<br>**“Breeding for Stress Tolerance”** |
| $14^{00}$ - $14^{15}$ | FC-5: Functional genomics and transcriptomics of abiotic stresses and their applications on rice breeding – S. Jiang, S. Ramachandran |
| $14^{15}$ - $14^{30}$ | Development of drought-tolerant vegetative (triploid) bermudagrass [Cynodon dactylon] – S. Sever Mutlu, N. Mutlu, C. Selim |
| $14^{30}$ - $14^{45}$ | FC-220: Yield stability of some bread wheat varieties released to dry areas of central Anatolia – E. Dönmez, A. Salantur, S. Yazar, Y. Yıldırım, B. Özdemir |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***6th Session - Session Chair:* ASSOC PROF DR TANER AKAR** |
| $15^{30}$ - $15^{45}$ | Agro-morphologic variation in a large barley germplasm collection under central anatolian highlands -the first year (2005-06) - N. Ergün, T. Akar, A. Karagöz, V. Eser, İ. Sayim, H. Sipahi, K. Özbek, A. Engin, S. Aydoğan |
| $15^{45}$ - $16^{00}$ | FC-31: Genetic and QTL analysis for agronomic traits in a Tunisian doubled-haploid barley population - M. Cherif, S. Rezgui |
| $16^{00}$ - $16^{15}$ | FC-115: Models of new varieties of spring barley – Kudaibergenov, M.S. Kenenbaev SH |
| $16^{15}$ - $16^{30}$ | FC-171: Effects of seed priming on glumed and glumeless barley cultivars - N. E.P. Mokhtari, E. Dönmez, S. A. Bağcı |
| $16^{30}$ - $16^{45}$ | Investigation of some agricultural traits and stability of the barley (*Hordeum vulgare* l.) genotypes İ. Öztürk, R. Avcı |
| $16^{45}$ - $17^{00}$ | FC-134: The results of the directed selection for reducing the height of winter rye - V. Skoryk |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{30}$ | Poster Session |
| $08^{00}$ - $18^{30}$ | **Side Events and Stands** |
| $19^{00}$ - | **Dinner** |

## WEDNESDAY, NOVEMBER 13RD 2013 EXCURSION

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|---|---|
| $08^{30}$ - $19^{00}$ | Perge Antique City, Aspendos Antique Theater, Düden Waterfall, Antalya center, Kaleiçi and City Tour. etc.. |
| $19^{00}$ - | **Dinner and Turkish Night** |

## THURSDAY, NOVEMBER 14TH 2013

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|---|---|
| 09$^{00}$ - 10$^{30}$ | ***7th Session - Session Chair:* DR ALIREZA POURMOHAMMAD** |
| 09$^{00}$ - 09$^{15}$ | Development of somaclones with low ODAP content in grass pea (*L. sativus* L.) – S. Barpete, S. Kumar, H. Nakkaul, P. Gupta, A. Amri, A. Sarker, M. Singh, M. Baum |
| 09$^{15}$ - 09$^{30}$ | FC-195: Research on the possibilities of cultivation of the fodder crops on pasture and meadow areas of Eastern Anatolia – M. Uzun M. M. Özgöz, S. E. Dumlu, P. Uysal, E. Aksakal, Ş. Çakal, K. Terzioğlu, M. Atici, A. Tavlaş, A. Yazici, H. Cebeci |
| 09$^{30}$ - 09$^{45}$ | FC-210: Effects of Salicylic acid and GA3 preconditioning treatments on regeneration from cotyledon explants of cv. Karaelci – M. Mirzapour, K. M. Khawar, H. Kendir |
| 09$^{45}$ - 10$^{00}$ | FC-250: New Sources of Resistance to the Cowpea Weevil (*Callosobruchus maculatus* F.) in Chickpea (*Cicer arietinum* L.) Accessions – C. İkten, İ. Şahin, F. Öncü Ceylan-Baloğlu, S. Bereket, B. Uzun, C. Toker |
| 10$^{00}$ - 10$^{15}$ | FC-119: Selection of promising safflower genotypes under contrasted environmental conditions - L. Zraibi., A. Nabloussi, H. Serghini Caid |
| 10$^{15}$ - 10$^{30}$ | Discussion |
| 10$^{30}$ - 11$^{00}$ | Coffee break |
| 11$^{00}$ - 12$^{30}$ | ***8th Session - Session Chair:* PROF DR IOANNIS TOKATLIDIS** |
| 11$^{00}$ - 11$^{15}$ | FC-36: Inoculation effect of endophytic bacterium (Bacillus sp.) isolated from wild rice Oryza nivara on Sri Lankan traditional rice variety Ma wee. H.W.K.S.L Kumara, N. Ahlgren, E. P. Greenberg, G. Senanayake, S Geekiyanage |
| 11$^{15}$ - 11$^{30}$ | FC-109: Determination of heritability and gene effects on quantitative traits in rice genotypes – H. R. Soroush, A. Ismaili, F. N. Firouzabadi, M. H. Chaleshtari |
| 11$^{30}$ - 11$^{45}$ | FC-205: Yield and yield component performance, morphological and quality characteristics of Aromatik-1 rice variety which is the first aromatic rice registered in Turkey – N. Beser, H. Sürek, R. Kaya |
| 11$^{45}$ - 12$^{00}$ | FC-147: Genotypes x environment interaction effect on nutritional quality of sorghum lines in Indonesia - Trikoesoemaningtyas, D. Wirnas, D. Sopandie, T. Tesso |
| 12$^{00}$ - 12$^{15}$ | FC-255: Determination of yield performances and stability analysis of some rice cultivars grown under the Osmancik conditions – M. Şahin, İ. Sezer, H. Akay, O. Dengiz, A. Sırat, F. Öner |
| 12$^{15}$ - 12$^{30}$ | Discussion |
| 12$^{30}$ - 13$^{30}$ | Lunch |

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|---|---|
| $13^{30}$ - $15^{30}$ | ***9th Session - Session Chair:* PROF DR ISMET BAŞER** |
| $13^{30}$ - $14^{00}$ | ***Invited Speaker* Dr. B.M. PRASANNA**<br>**“Meeting the challenges of global climate change and food security through innovative maize research”** |
| $14^{00}$ - $14^{15}$ | FC-2: Breeding of density-independent cultivars is a viable option to combat climate changes – a case study for maize and wheat – I. S. Tokatlidis |
| $14^{15}$ - $14^{30}$ | FC-7: Mapping Genes for Northern Corn Leaf Blight in Maize – R. Singh, R. P. Srivastava, L. Ram, K. Srivastava |
| $14^{30}$ - $14^{45}$ | FC-224: Maize Breeding studies in Turkey; past, present and future – R. Cengiz. |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***10th Session - Session Chair:* DR. B.M. PRASSANNA** |
| $15^{30}$ - $15^{45}$ | FC-121: Using DNA Technologies for Developing Inbred Lines and Hybrids in Maize - V.M. Sokolov, A.A. Belousov |
| $15^{45}$ - $16^{00}$ | Wheat landraces potential of Turkey: A Swot Analyses - M. Kan, M. Küçükçongar, A. Morguonov, M. Keser, F Özdemir, Hafiz Muminjanov |
| $16^{00}$ - $16^{15}$ | FC-149: Marker-assisted identification and transferring new resistance gene from Aegilops speltoides to bread wheat - Salina E.A., Petrash N.V., Stasyuk A.I., Adonina I.G. |
| $16^{15}$ - $16^{30}$ | FC-174: Estimation of hybrid yield performance by the selection of heterotic groups on dent type maize inbred lines using SSRs – A. Okumus, A. Oz, L. Mercan, H. Kapar |
| $16^{30}$ - $16^{45}$ | FC-55 : Mutant Varieties of Soybean, Tobacco, Chickpeas and Their Developed Characteristics – Z. Sağel, M. İ. Tutluer, H. Peşkircioğlu, B. Kunter, Y. Kantoğlu |
| $16^{45}$ - $17^{00}$ | Improved vegetable varieties for Central Asia and the Caucasus developed from AVRDC – the world vegetable center germplasm - R. F. Mavlyanova |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{00}$ | ***Closing Ceremony*** |
| $19^{00}$ - | Dinner |

**FRIDAY, NOVEMBER 15TH 2013 LEAVING FROM HOTEL**

3

# Fatih Sultan Mehmet Han Meeting Room

## (Field Crop Session - 2)

## MONDAY, NOVEMBER 11TH 2013

| | |
|---|---|
| $13^{30}$ - $15^{30}$ | ***1st Session - Session Chair:* PROF DR TAHSİN KESİCİ** |
| $13^{30}$ - $14^{00}$ | ***Invited Speaker* Dr. Hale Ann TUFAN - Borlaug GRI**<br>**Using Genomic Selection to Accelerate the Rate of Genetic Improvement in Cassava and Wheat Breeding** |
| $14^{00}$ - $14^{15}$ | FC-117: Pathogen guided resistance breeding: benefits and pitfalls – M. Tör, G. Boztaş, E. Fantozzi, A. Woods-Tör |
| $14^{15}$ - $14^{30}$ | FC-75: Powdery mildew resistance in wheat (North – West Region of Russia) - T. V. Lebedeva |
| $14^{30}$ - $14^{45}$ | FC-227: Breeding for wheat rust diseases in Algeria and strategies for pathogenicity reduction - A.Benbelkacem, C. Djenadi |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***2nd Session - Session Chair:* DR ALEX MORGOUNOV** |
| $15^{30}$ - $15^{45}$ | FC-294: Monitoring of cereal pests and diseases and identification of resistant varieties in Tajikistan – M. Otambekova, B. Husenov, A. Morgounov, H. Muminjanov |
| $15^{45}$ - $16^{00}$ | FC-218-Rust occurrence, epidemic development and resistance of wheat cultivars deployed in northwest of Pakistan - G. Farooq, S. J. Shah, M. Ibrahim, S. Hussain |
| $16^{00}$ - $16^{15}$ | GR-70: Trait analysis and diversity in some wheat landraces and advance breeding lines evaluated under drought and heat stress conditions - S. Sareen, B S Tyagi, O P Dhillon, I. Sharma |
| $16^{15}$ - $16^{30}$ | FC-94: Development of Initial Material of Spring and Winter Wheat on the Basis of New Sources of Resistance to Leaf and Stem Rust - N. Gainullin, I. Lapochkina, I. Iordanskaya, O. Baranova, A. Anisimova |

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| $16^{30}$ - $16^{45}$ | FC-201. The development resistant material to yellow rust and stem rust by using anther culture in wheat breeding program - A. Salantur, K. Akan, V. Eser, M. E. Alyamaç |
| $16^{45}$ - $17^{00}$ | FC-33: Identification of wheat breeding material resistant to leaf rust *Puccinia recondita* f. sp. *Tritici* - A. Kokhmetova, Z. Sapakhova, A. Madenova, M. Atishova, G. Yessenbekova, A.Sedlovsky, L. Typina, K. Galymbek, D. Zhanuzak, Zh. Keyshilov |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{30}$ | ***Poster Session*** |
| $19^{00}$ - | **Dinner** |
| $08^{30}$ - $18^{30}$ | Side Events and Stands |

## TUESDAY, NOVEMBER 12$^{ND}$ 2013

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|---|---|
| $09^{00}$ - $10^{30}$ | ***3$^{RD}$ Session - Session Chair:*** **PROF DR HOSSEIN R. SOURUSH** |
| $09^{00}$ - $09^{15}$ | FC-154: Yellow rust resistant, new improved winter wheat genotypes for Central Asia and the Caucasus - R. C. Sharma, Z. Ziyaev, O. Amanov, Z. Khalikulov, Z. Eshonova, D. Bedoshvili, M. Keser, A. Morgounov |
| $09^{15}$ - $09^{30}$ | FC-241: Breeding strategies and progress towards improvement of yellow rust and stem rust resistances in Tajik wheat breeding program - M. Rahmatov, B. Husenov, B. Soliev, M. Otambekova, Z. Eshonova, R. Wanyera, M. Rouse, M. Hovmøller, A. Morgounov, H. Muminjanov |
| $09^{30}$ - $09^{45}$ | FC-112: Enhancing spot blotch resistance in wheat through introgression of QTLs using molecular back cross breeding – N. K. Vasistha, B. Arun, V. K. Mishra, R. Chand, A. K. Joshi |
| $09^{45}$ - $10^{00}$ | FC-269: Importance of photosynthetic signs for the breeding of high-yielding wheat varieties – J. A. Aliyev |
| $10^{00}$ - $10^{15}$ | GR-51: Impact of KASIB project genetic stock into solution of problems of spring bread wheat breeding in Altai territory - N. I. Korobeinikov |
| $10^{15}$ - $10^{30}$ | Discussion |
| $10^{30}$ - $11^{00}$ | Coffee break |
| $11^{00}$ - $12^{30}$ | ***4th Session - Session Chair:*** **DR MESUT KESER** |
| $11^{00}$ - $11^{15}$ | FC-120: The problem of climate warming and the objectives of spring soft wheat breeding in Western Siberia - Shamanin V. P., Morgounov A.I., Petukhovskiy S. L., Likhenko I. E. |
| $11^{15}$ - $11^{30}$ | FC-208: Cross-compatibilities of durum wheat with *Aegilops tauschii* accessions screened under water-deficit stress – M. Inagaki, B. Humeid, S. Tawkaz, A. Amri |

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| $11^{30} - 11^{45}$ | FC-209: Determination of the convenient method to be used in testing cold hardiness in some cereal genotypes - Ü. Küçüközdemir, E. Dorukoğlu, B. Denizer A. Kara |
| $11^{45} - 12^{00}$ | FC-217: Principal Component Analysis (PCA) and Examination of Drought Indices in Durum Wheat Lines – F. Nofouzi, V. Rashidi, A. Tarinejad |
| $12^{00} - 12^{15}$ | FC-230: Cell viability and membrane fluidity in relation to drought tolerance of wheat: genetic options for improvement – S. Singh, R. Munjal |
| $12^{15} - 12^{30}$ | Discussion |
| $12^{30} - 13^{30}$ | Lunch |
| $13^{30} - 15^{30}$ | ***5th Session - Session Chair:* PROF DR GHEORGE DUCA** |
| $13^{30} - 13^{45}$ | Application of RNA silencing: a changing paradigm in crop improvement - V. K. Srivastava, A. P. Singh |
| $13^{45} - 14^{00}$ | FC-212: Genetic resilience in wheat for tolerance to heat stress in relation to climate change - R. K. Behl |
| $14^{00} - 14^{15}$ | FC-221: Effects of salinity stress on wheat grain quality and screening for tolerance by molecular markers – U. Ibrahimova, G. Hasanova, Z. Suleymanova, A. Mammadov |
| $14^{15} - 14^{30}$ | FC-276: Genomic Selection in Wheat Breeding using Diversity Arrays Technology (DArT) - E. Elçi, H. Güngör, F. Löschenberger |
| $14^{30} - 14^{45}$ | FC-125: Physiological Responses and Recovery Potentials of Cultivated and Wild Wheat Seedlings Exposed to Heat Stress - Sezgin, D.E., Eyidoğan, F., Ekmekçi, Y. Terzioğlu, S. |
| $14^{45} - 15^{00}$ | Discussion |
| $15^{00} - 15^{30}$ | Coffee break |
| $15^{30} - 17^{30}$ | ***6th Session - Session Chair:* PROF DR RICHARD VISSER** |
| $15^{30} - 16^{00}$ | ***Invited Speaker* Prof. Dr. Hikmet Budak**<br>**“History and current status of genome sequencing”** |
| $16^{00} - 16^{15}$ | Application of food biotechnology in agriculture: benefits and risks - P. Singh, V. K. Srivastava |
| $16^{15} - 16^{30}$ | *FC-213: In vitro* culture use for durum wheat (*Triticum durum* Desf.) regenerated production under salt stress - Ayed-Slama O., Ayed S., Slim-Amara H. |
| $16^{30} - 16^{45}$ | FC-149: Molecular mapping for grain protein content in a *Triticum aestivum* and *Triticum spelta* cross - S Jayasudha, B Arun, V K Mishra, G P Singh, A K Joshi |
| $16^{45} - 17^{00}$ | FC-127: QTL analysis of grain yield and yield -related traits using recombinant inbred lines in wheat under drought stress - F. Mohammadi, S. A. Bezenjani, G. M. Nejad, A. Karimzade |
| $17^{00} - 17^{30}$ | Discussion |
| $17^{30} - 18^{30}$ | ***Poster Session*** |

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| $08^{00}$ - $18^{30}$ | Side Events and Stands |
| $19^{00}$ - | **Dinner** |

## WEDNESDAY, NOVEMBER 13RD 2013 EXCURSION

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| $08^{30}$ - $19^{00}$ | Perge Antique City, Aspendos Antique Theater, Düden Waterfall, Antalya center, Kaleiçi and City Tour. etc.. |
| $19^{00}$ - | **Dinner and Turkish Night** |

## THURSDAY, NOVEMBER 14TH 2013

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| $09^{00}$ - $10^{30}$ | ***7th Session - Session Chair:* PROF DR LAZSLO LANG** |
| $09^{00}$ - $09^{15}$ | Effects of inbreeding depression in vegetative and reproductive parameters of *Anagyris foetida* (*Leguminosae, Papilionoideae*) in two populations from sw spain<br>F. J. ValtueÑa$^{*}$, J. LÓpez, A. Ortega-Olivencia, T. Rodriguez-RiaÑo |
| $09^{15}$ - $09^{30}$ | The use of relative water content and leaf water potential for the selection of maize inbred lines under drought stress – F. Gekas, I. Mylonas, E. Ninou, C. Pankou, A. Lithourgidis, J. K. Petrevska, F. Papadopoulou, P. Zouliamis, G. Tsaprounis, F. Papathanasiou, I. Tokatlidis, C. Dordas |
| $09^{30}$ - $09^{45}$ | Determination of grain moisture changes in some corn hybrids in Konya ecological conditions – M. Tezel, A. Üstün |
| $09^{45}$ - $10^{00}$ | FC-199: The contribution of ashes of waste of the plants to in vitro regeneration of potato (Solanum tuberosum L.). Belguendouz A. , Sahnoue M., Adda A |
| $10^{00}$ - $10^{15}$ | Variation in fatty acid composition of three Turkish slit flower opium poppy (*Papaver somniferum*L.) lines – N. Valizadeh, A. Rahimi, N. Arslan |
| $10^{15}$ - $10^{30}$ | Discussion |
| $10^{30}$ - $11^{00}$ | Coffee break |
| $11^{00}$ - $11^{30}$ | ***8th Session - Session Chair:* PROF DR FAHRI ALTAY** |
| $11^{00}$ - $11^{30}$ | ***Invited Speaker* Prof. Dr. Mehmet ÇAKIR**<br>**“Molecular tools and technologies for next generation plant breeding”** |
| $11^{45}$ - $12^{00}$ | FC-148: Linkage between *Sr2* and *lm1* and its effect on phenotypic expression of lesion mimic in wheat - S. Singh, P. S. Yadav, R. Chand, V. K. Mishra, R.N. Kharwar |
| $12^{00}$ - $12^{15}$ | FC-128: Relationship between transgressive segregation and genetic distance based on AFLP markers in *Cicer* species - C. Toker, F.O. Ceylan, C. Ikten, E. Bolucek, I. Sahin, B. Uzun |

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| $12^{15}$ - $12^{30}$ | Discussion |
| $12^{30}$ - $13^{30}$ | Lunch |
| $13^{30}$ - $15^{30}$ | ***9th Session - Session Chair:* HARI D. UPADHYAYA** |
| $13^{30}$ - $13^{45}$ | FC-107: Accessing novel genes for chickpea improvement – S. Sharma, HD Upadhyaya, CLL Gowda |
| $13^{45}$ - $14^{00}$ | FC-12: Analysis of diallel cross for some quantitative traits in common bean (*Phaseolus vulgaris* L.) - R. C. Jagadeesha, Gangadhar K., S. Tirakannanavar |
| $14^{00}$ - $14^{15}$ | FC-42: Proteomics analysis in soybean root inoculated with compatible bacteria under flooding stress- Can *Bradyrhizobium japonicum* induce flood tolerance? – A. Khatoon, S. Rehman, M. Jamil, I. Ahmad, S. Komatsu |
| $14^{15}$ - $14^{30}$ | FC-81: Validation and deployment of resistance-linked SCAR molecular markers for marker-assisted breeding of the common bean – A. Namayanja, P. Paparu, A. Namusoke, J. Mukabaranga, A. Male, P. Gepts |
| $14^{30}$ - $14^{45}$ | GR-68: Preliminary studies on the breeding of *Vaccaria hispanica* : a new crop species for Turkey E. Ari**,** A. Topuz, İ. G. Deniz, İ. Genç, F. Kantar, Z. Suludere |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***10th Session - Session Chair:* PROF. DR. SALEM S. ALGHAMDI** |
| $15^{30}$ - $15^{45}$ | FC-292 Implications of common bean centromere structure on breeding efforts. Ahmet L. Tek, A. Iwata, K. Nagaki, S. Jackson |
| $15^{45}$ - $16^{00}$ | FC-144: Developing peanut (*Arachis hypogaea* L.) leafspot resistant cultivars: yield evaluation of advanced generation lines – Y. Wahyu, W. Junaedi, Achmad |
| $16^{00}$ - $16^{15}$ | FC-153: The effects of seed priming on seed yield in chickpea (*Cicer arietinum* L.) - F. Rezaei, S. Ünver İkincikarakaya |
| $16^{15}$ - $16^{30}$ | FC-162: Comparison of Different Leaf Types of Chickpea (*Cicer arietinum* L.) Genotypes for Yield and Yield Components – A. Aydoğan, C. Y. Çiftçi |
| $16^{30}$ - $16^{45}$ | Molecular Analysis of Floral Transition in Soybean – P. L. Bhalla, M. B. Singh |
| $16^{45}$ - $17^{00}$ | FC-159: Canopy Diameter as Selection Criteria for Yield Improvement of Bambara Groundnut (*Vigna subterranea* (L.) Verdc.) – Y. Wahyu, E. Sjamsudin, D. Actaria, L. Juwita |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{00}$ | ***Closing Ceremony*** |
| $19^{00}$ - | Dinner |

**FRIDAY, NOVEMBER $15^{TH}$ 2013 LEAVING FROM HOTEL**

4

# Yavuz Sultan Selim Han Meeting Room

(Horticultural Crops Session)

## MONDAY, NOVEMBER 11TH 2013

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|---|---|
| $13^{30}$ - $15^{30}$ | ***1st Session - Session Chair:* ASSOC PROF DR MASUM BURAK** |
| $13^{30}$ - $13^{45}$ | HC-78: Development of Downy mildew resistant markers for cucumber breeding program - S. Lee, J. Verose, K. Song |
| $13^{45}$ - $14^{00}$ | HC-79: Development of longer pepper lines resistant to potato virus y (pvy) **–** İ. Çelik, R. Özalp, N. Çelik, İ. Polat, A. Ünlü |
| $14^{00}$ - $14^{15}$ | Investigate of some tomato genotypes in breeding of tomato rootstocks – A. Ata, D. Keleş, H. Pınar, A. Özarslandan, H. Yetişir, S. Büyükalaca |
| $14^{15}$ - $14^{30}$ | HC-59: Investigations on the resistance of some processing white head cabbage (*Brassica oleracea* L. var. *capitata subvar. alba*), genotypes to root–knot nematodes [Meloidogyne incognita] M. Özbakır Özer, A. Balkaya, S. Mennan |
| $14^{30}$ - $14^{45}$ | HC-94: The development of *Xanthomonas* and TuMV - resistant doubled haploid lines of Brassica - Zubareva I.A., Goloveshkina E.N., Vinogradova S.V, Ignatov A.N. |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***2nd Session - Session Chair:* PROF DR NEBAHAT SARI** |
| $15^{30}$ - $16^{00}$ | ***Invited Speaker* Dr. Jay W. SCOTT**<br>**"Adventures in breeding fresh market tomatoes for fruit quality"** |
| $16^{00}$ - $16^{15}$ | HC-36: Heterosis and Combining ability Studies for High Temperature Tolerance and yield traits in tomato (*Solanum lycopersicum* L.) – S. Kumar, K. Srivastava, A. Vaishampayan, R. Singh |
| $16^{15}$ - $16^{30}$ | HC-87: Microsatellite assessment of genetic diversity among Jordanian tomato (*Solanum lycopersicum* L.) Landrace – M. Brake, H. M. Migdadi, M. Sadder, L. Gadomi, M. Qaryouti, M. Al-Khatib, A. Ali El-Oqlah |

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| $16^{30}$ - $16^{45}$ | HC-32: Yield and Quality Traits of Developed Tomato Lines by Mutation Breeding - K. Y. Kantoğlu, Z. Sağel, İ. Tutluer, H. Peşkircioğlu, B. Kunter, M. Özçoban, Z. Işık, D. Özmen, E. İç, S. Şekerci, N. Günçağ, E. Seçer, A. Şenay, G. Aydın, H. Şirin |
| $16^{45}$ - $17^{00}$ | HC-42:The estimation of combining ability and heterosis effect for yield and yield components in tomato (*Lycopersicon esculentum* Mill.) at lowland - S. Iis Aisyah, S. Wahyuni, M. Syukur |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{30}$ | ***Poster Session*** |
| $19^{00}$ - $20^{30}$ | **Gala Dinner** |
| $08^{30}$ - $18^{30}$ | Side Events and Stands |

## TUESDAY, NOVEMBER 12$^{ND}$ 2013

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|---|---|
| $09^{00}$ - $10^{30}$ | ***3$^{RD}$ Session - Session Chair:* PROF DR SAMI DOĞANLAR** |
| $09^{00}$ - $09^{15}$ | HC-99: Aegean Agricultural Research Institute Tomato Breeding Studies - S. Mutlu, M. A. Haytaoğlu, S. Binbir, A. Kahraman |
| $09^{15}$ - $09^{30}$ | HC-2: Combining ability and gene action in cherry tomato for yield and quality (*Solanum lycopersicum* l. var. *cerasiforme* Mill) – P. Pujer, R. C. Jagadeesha |
| $09^{30}$ - $09^{45}$ | HC-8: QTL analysis to identify metabolites potentially related to thrips resistance in pepper (*Capsicum*) - A. Maharijaya, B. Vosman, A. Purwito, R. G.F. Visser, R. E. Voorrips |
| $09^{45}$ - $10^{00}$ | HC-91: Studies on improving Cucumber (*Cucumis sativus* L.) lines for chilling tolerance - V. Gözen, A. Tepe, A. Ünlü |
| $10^{00}$ - $10^{15}$ | HC-66: Long Term Onion Breeding Program in Turkey - A. F. Gökçe |
| $10^{15}$ - $10^{30}$ | Discussion |
| $10^{30}$ - $11^{00}$ | Coffee break |
| $11^{00}$ - $12^{30}$ | ***4th Session - Session Chair:* DR JAY W. SCOTT** |
| $11^{00}$ - $11^{30}$ | **Invited Speaker Prof. Dr. Atanas ATANASSOV**<br>**“Future challenges for the breeders struggling the climatic changes”** |
| $11^{30}$ - $11^{45}$ | Development of resistant varieties to tomato spotted wild virus and root knot nematodes in pepper by using molecular markers – A. Kün, A. Atasayar, N. Güneşdoğdu, A. Cansızer, D. Özdemir, H. İlbi |
| $11^{45}$ - $12^{00}$ | HC-125: Determination of High Temperature Tolerance of Some Pepper Genotypes – D. Keles, H. Pınar, Z. Kapircın, U. Rastgeldi, A. Ateş |
| $12^{00}$ - $12^{30}$ | Discussion |
| $12^{30}$ - $13^{30}$ | Lunch |

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| $13^{30}$ - $15^{30}$ | ***5th Session - Session Chair:* PROF DR HÜLYA İLBİ** |
| $13^{30}$ - $13^{45}$ | GR-7: Efficiency of microsatellite markers in the investigation and confirmation of introgression in *Brassica* species – S. Iqbal, Farhatullah, M. A. Rabbani, N. Yousaf, M. Kanwal, L. Fayyaz |
| $13^{45}$ - $14^{00}$ | HC-72: Characterization of some agronomic traits and β-carotene contents of orange fleshed Altınbaş melon dihaploid lines grown in Antalya and Bursa locations - M. Göçmen, E. Aydın, İ. Şimşek, N. Sarı, İ. Solmaz, A. Gökseven |
| $14^{00}$ - $14^{15}$ | High resolution map of eggplant (Solanum melongena) S. Doğanlar |
| $14^{15}$ - $14^{30}$ | Preparing RNAi construct for *fad2* gene fragment of *Brassica nappus* as a step towards gene silencing - S. D. Khabbazi, B. Baghban, A. Gholizadeh |
| $14^{30}$ - $14^{45}$ | HC-60: Strengths and weaknesses traits for *Brassica* vegetable crops production of Turkey – A. Balkaya |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***6th Session - Session Chair:* PROF DR A. NACI ONUS** |
| $15^{30}$ - $15^{45}$ | HC-65: Improvement of F1 Hybrid Vegetable Varieties and Qualified Lines Project in Turkey – A. Ünlü, V. Gözen, A. Kabaş, R. Özalp, F. Boyacı, M. Ünlü, A. Oğuz, İ. Çelik, A. Tepe, S. Zengin, V. Topçu, Y. Köksal, N. Çelik, M. Öten, R. Kurum, L. Keskin, I. Demirtaş, F. Öktüren, İ. Polat, E. Gümrükçü, H. Tokgöz, M. Gölükçü, İ. Tekşam |
| $15^{45}$ - $16^{00}$ | HC-9:Response of shallot cultivar lokos somatic embryo to polyethilene glicol 6000 in vitro culture – A. Ulandari, D. Dinarti |
| $16^{00}$ - $16^{15}$ | Biotechnological Steps in Strawberry Tree (Arbutus unedo L.) Breeding – A. Cavusoglu, M. Sulusoglu, S. Erkal… |
| $16^{15}$ - $16^{30}$ | HC-07: Markers assisted assay of the tea cultivars grown in Pakistan – H. Ahmad, S. Gul Afridi |
| $16^{30}$ - $16^{45}$ | HC-63: Breeding of Pear Cultivars Resistant to Fire Blight Disease (*Erwinia amylovora*): Promising genotypes and Molecular Characterization – G. Öztürk, R. A. Emre, Ö. F. Karamürsel, H. C. Sarısu, E. Kaçal, M. Aksu, H. Basım |
| $16^{45}$ - $17^{00}$ | HC-04: Identification of Tunisian apricot genotypes for future breeding program: Self-compatible with flower and good fruit qualities – A. Lachkar, M. Mars |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{30}$ | ***Poster Session*** |
| $08^{00}$ - $18^{30}$ | Side Events and Stands |
| $19^{00}$ - | **Dinner** |

## WEDNESDAY, NOVEMBER $13^{RD}$ 2013 EXCURSION

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|---|---|
| 08$^{30}$ - 19$^{00}$ | Perge Antique City, Aspendos Antique Theater, Düden Waterfall, Antalya center, Kaleiçi and City Tour. etc.. |
| 19$^{00}$ - | **Dinner and Turkish Night** |

## THURSDAY, NOVEMBER 14$^{TH}$ 2013

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|---|---|
| 09$^{00}$ - 10$^{30}$ | ***7th Session - Session Chair:*** **PROF DR ATANAS ATANASOV** |
| 09$^{00}$ - 09$^{15}$ | HC-35: From field to the genes approach for breeding of *Populus nigra* – K. Yıldırım,E. Zeybek, A. Uluğ, Z. Kaya |
| 09$^{15}$ - 09$^{30}$ | HC-62: Using Different Molecular Markers for Breeding of Some Horticultural Plants – A. Atak, Y. Boz, A. Doğan, E. Cebeci, F. Hancı, M. Baş, E. Kaya |
| 09$^{30}$ - 09$^{45}$ | HC-05: Improvement in transcriptomes analysis of horticultural crops using next generation – P. Majidian, M. Zeinalabedini, Z. Nemati |
| 09$^{45}$ - 10$^{00}$ | HC-54: Development of polymorphic SSR primers in pistachio from enriched ga repeat library in Siirt cultivar - Çoban, N., H. Topçu, S. Kafkas |
| 10$^{00}$ - 10$^{15}$ | HC-46: Development of polymorphic microsatellite primers in walnut (*Juglans regia*) designed from *Juglans nigra* genomic GA enriched library sequences - Topçu, H., N. Aslan, S. Kafkas |
| 10$^{15}$ - 10$^{30}$ | Discussion |
| 10$^{30}$ - 11$^{00}$ | Coffee break |
| 11$^{00}$ - 12$^{30}$ | ***8th Session - Session Chair:*** **DR DAVUT KELEŞ** |
| 11$^{15}$ - 11$^{30}$ | HC-100: Clementine × Blood Orange Crosses – G. Oruç, Z. Dalkılıç |
| 11$^{30}$ - 11$^{45}$ | HC-6: New Satsuma Mandarin Varieties with Thin Peel; BATEM İncisi and BATEM Yıldızı - E. Turgutoğlu, Ş. Kurt, G. Demir |
| 11$^{45}$ - 12$^{00}$ | HC-10: Determination of Suitable GA3 Concentration and Embryo Growing Stages for Culture of Embryos Obtained with Hybridization of Common Sourorange x Carrizocitrange, Common Sourorange x Alanya Dilimli orange and Common Sour orange x Flying Dragon - Ş. Kurt, E. Turgutoğlu, G. Demir |
| 12$^{00}$ - 12$^{15}$ | HC-102: Study of ovule fertility in the mandarin group (*Citrus reticulata*) under manual and open pollination conditions - Benyahia H., Belmehdi I., Beniken L., Omari Fez., Talha A., Benazzouz A., Handaji N., Benaouda H. Tahiri A. |
| 12$^{15}$ - 12$^{30}$ | Discussion |
| 12$^{30}$ - 13$^{30}$ | Lunch |

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| $13^{30}$ - $15^{30}$ | ***9th Session - Session Chair:* PROF DR CHAD FINN** |
| $13^{30}$ - $13^{45}$ | HC-104: An example to the use of genetic resources for improvement the resistance: the development of new powdery mildew tolerant grape varieties – C. Özer, E. Solak, N. Özer, Ü. Eser, L. Öztürk |
| $13^{45}$ - $14^{00}$ | HC-55: Phytosanitary status of *Ficus carica* collection in Crimea and features of figs in vitro micropropagation - I. Mitrofanova, O. Mitrofanova, N. L. Sedoshenko |
| $14^{00}$ - $14^{15}$ | HC-56: Genetic variation and multivariate analysis of fruit traits for improvement of pomegranate (*Punica granatum* L.) cultivars - F. Zaouay, M. Mars |
| $14^{15}$ - $14^{30}$ | HC-127: A Clonal selection in ‘0900 Ziraat’ sweet cherry cultivar and molecular characterization by AFLP analysis - İ. Demirtaş, H. C. Sarısu, Ö. F. Karamürsel, İ. Eryılmaz, S. Kafkas |
| $14^{30}$ - $14^{45}$ | HC-29: Improving new traits by mutation breeding in sweet cherry - B. Kunter, M. Baş, S. Özyiğit, Y. Kantaroğlu, M. Burak |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***10th Session - Session Chair:* PROF DR SEDAT SERÇE** |
| $15^{30}$ - $16^{00}$ | ***Invited Speaker* - Chad FINN**<br>**“Trends in Fruit Breeding for Future”** |
| $16^{00}$ - $16^{15}$ | HC-109: Clonal Selection of Cherry Rootstock Candidates in the Central and Eastern Black Sea Region in Turkey – A. Koc, Z. Celik, M. Akbulut, S. Bilgener, S. Ercisli, R. l. Gercekcioglu, A. Esitken, M. Gunes |
| $16^{15}$ - $16^{30}$ | HC-101: *In vitro* Pollen Viability and Pollen Germination in *Prunus laurocerasus* L. (Cherry Laurel) – M. Sülüşoğlu, A. Çavuşoğlu, |
| $16^{30}$ - $16^{45}$ | HC-68: Selection breeding of wild Prunus cerasus L. clonal rootstocks for sweet and sour cherries - H. C. SARISU, Ö. F. Karamürsel, F. P. Öztürk, İ. Demirtaş, İ. Gür, H. Koçal, M. Aksu, Z. Babalık, Ş. Sekmen, S. Özyiğit |
| $16^{45}$ - $17^{00}$ | HC-98: A New Promising Fruit: Cherry laurel (*Prunus laurocerasus* L.) and steps on breeding – M. Sülüşoğlu, A. Çavuşoğlu, S. Erkal |
| $17^{00}$ - $17^{30}$ | Discussion |
| $17^{30}$ - $18^{00}$ | ***Closing Ceremony*** |
| $19^{00}$ - | Dinner |

## FRIDAY, NOVEMBER 15TH 2013 LEAVING FROM HOTEL

# 5

# Osman Gazi Han Meeting Room

## (Genetic Resources Session)

### MONDAY, NOVEMBER 11TH 2013

| | |
|---|---|
| $13^{30}$ - $15^{30}$ | ***1st Session - Session Chair:*** **DR. ALİ OSMAN SARI** |
| $13^{30}$ - $13^{45}$ | HC-69: The rootstock breeding and selection studies for Cucurbitaceae vegetables in Turkey – O. KARAAĞAÇ, A. BALKAYA |
| $13^{45}$ - $14^{00}$ | Characterization of local okra (*Abelmoschus esculentus*) populations- S. Binbir, A. Kahraman, S. Mutlu, M. Asım Haytaoğlu |
| $14^{00}$ - $14^{15}$ | GR-36: Reactions of some Turkish *Aegilops* and *Triticum* materials to *Pgt* race RTKTC - K. Akan, Z. Mert, L. Çetin, K. Özbek, A. Karagöz |
| $14^{15}$ - $14^{30}$ | GR-33. The Adaptive Capability of Some Cereals from Geographically and Environmentally Different Areas of Azerbaijan – N. A. Nabiyeva |
| $14^{30}$ - $14^{45}$ | Using an “Index of Merit” for multi trait evaluation of winter hardy feed pea lines – A. Homer, R. W. Groose |
| $14^{45}$ - $15^{00}$ | Discussion |
| $15^{00}$ - $15^{30}$ | Coffee break |
| $15^{30}$ - $17^{30}$ | ***2nd Session - Session Chair:*** **PROF DR FILIPPOS A. ARAVANOPOULOS** |
| $15^{30}$ - $16^{00}$ | ***Invited Speaker*** **Ayfer TAN**<br>**“Plant Diversity Conservation in Turkey”** |
| $16^{00}$ - $16^{15}$ | GR-66: Genetic monitoring of crop wild relatives: theory, approach and value for conservation F.A. (Phil) Aravanopoulos |
| $16^{15}$ - $16^{30}$ | GR-54: Plant genetic resources are important for food security in Central Asia and the Caucasus - Z. Khalikulov, J. Turok, R. Sharma |
| $16^{30}$ - $16^{45}$ | Importance of interspecific hybridization in developing 00-type rapeseed – F. Seyis, E. Aydın |
| $16^{45}$ - $17^{00}$ | GR-30: Analysis of genetic diversity of Sri Lankan traditional rice variety *“Honderawala”* E.U.U . Rathnathunga, K.H.W.K.S. Lalith, K.G.P.B. Karunarathne, S. Senaweera, N. Dissanayake, G. Senanayake, S. Geekiyanage |

| | |
|---|---|
| $17^{00}$ - $17^{30}$ | Discussion |
| $19^{00}$ - | Dinner |
| $08^{00}$ - $18^{30}$ | Side Events and Stands |

## TUESDAY, NOVEMBER 12$^{ND}$ 2013

| | |
|---|---|
| $09^{00}$ - $10^{30}$ | ***3rd Session - Session Chair:*** **PROF. DR. HAFIZ MUMINJANOV** |
| $09^{00}$ - $09^{30}$ | ***Invited Speaker*** **Dr. Chikelu MBA "Optimal Harnessing of the Potentials of Plant Genetic Resources for Food and Agriculture"** |
| $09^{30}$ - $09^{45}$ | GR-97: Evaluation of *in vitro* calli induction and regeneration of *Lavandula angustifolia*- A. Mohammadi, N. Sharif, K. Mostafavi |
| $09^{45}$ - $10^{00}$ | GR-81: Genetic diversity analysis in cassava (*Manihot esculenta* crantz) from baixada cuiabana in brazil using SSR markers – N. F. Carrasco, J. R.L.R. Oler, F. F. Marchetti, M. C.D.M. Amorozo, T. L. Valle, M. A. Carniello, E. A. Veasey |
| $10^{00}$ - $10^{15}$ | GR-69: RAD sequencing and SNP detection in a pearl millet germplasm collection for use in genome wide association analysis of agronomic traits in pearl millet.<br>S. Prasad Das, M. Hegarty, G. Slavov, R. Yadav |
| $10^{15}$ - $10^{30}$ | Discussion |
| $10^{30}$ - $11^{00}$ | Coffee break |
| $11^{00}$ - $12^{30}$ | ***4rd Session - Session Chair:*** **PROF DR PREM L. BHALLA** |
| $11^{15}$ - $11^{30}$ | GR-13:The formation and study in the culture of Genetic Resources of forage grasses by the expeditionary collection of wild forms from the natural landscapes of Kazakhstan - G. T. Meirman, S. T. Yerzhanova |
| $11^{30}$ - $11^{45}$ | GR-24: Agronomic evaluation of bambara groundnut (*Vigna subterranea* L) landrace collections in a dry environment - SM Magongwa, J. Ogola, C. Mathews |
| $11^{45}$ - $12^{00}$ | GR-32: Genetic diversity in bottle gourd [*Lagenaria siceraria* (Mol.) Stand.] A. K. M. Quamruzzaman, M.M. Rahaman, M. M. Hossain, M.A. K. Mian, S. Ahmad |
| $12^{00}$ - $12^{15}$ | Genetic diversity study of summer squash landraces (*Cucurbita pepo*) with neutral and gene-based molecular markers - Xanthopoulou A., Ganopoulos I., Kalivas A., Ralli P., Tsaftaris A., Nianiou-Obeidat I., Madesis P. |
| $12^{15}$ - $12^{30}$ | Discussion |
| $12^{30}$ - $13^{30}$ | Lunch |

## WEDNESDAY, NOVEMBER 13$^{RD}$ 2013 EXCURSION

| | |
|---|---|
| $08^{30}$ - $19^{00}$ | Perge Antique City, Aspendos Antique Theater, Düden Waterfall, Antalya center, Kaleiçi and City Tour. etc.. |
| $19^{00}$ - | **Dinner and Turkish Night** |

## THURSDAY, NOVEMBER 14$^{TH}$ 2013

| | |
|---|---|
| $09^{00}$ - $10^{30}$ | ***6th Session - Session Chair:* PROF DR NIKOLAY DZYUBENKO** |
| $09^{00}$ - $09^{30}$ | ***Invited Speaker* Hari D. UPADHYAYA**<br>**“Establishing core collections for enhanced use of germplasm in crop”** |
| $09^{30}$ - $09^{45}$ | GR-8: Evaluation of data from an olive germplasm collection – H. Kaya, F. Sefer, M. Şahin, Ö. Çetin, N. Mete, U. Güloğlu, M. Hakan |
| $09^{45}$ - $10^{00}$ | Collection and evaluation of *Fragaria* genotypes from Turkey – S. Serçe, S. Paydaş, N. Kaşka, K. Gündüz, E. Özdemir, J. F. Hancock, A. Z. Makarnacı |
| $10^{00}$ - $10^{15}$ | GR-109: Form diversity and selection of walnut in Kyrgyzstan - Mamadzhanov DK |
| $10^{15}$ - $10^{30}$ | Discussion |
| $10^{30}$ - $11^{00}$ | Coffee break |
| $11^{00}$ - $12^{30}$ | ***7th Session - Session Chair:* PROF DR MARIA DUCA** |
| $11^{00}$ - $11^{15}$ | GR-1: Exploitation of resistance gene analogs encoding NBS-LRR domains in wide hybridization of cotton – M. T. Azhar |
| $11^{15}$ - $11^{30}$ | GR-62: Molecular and physiological classification of divergent *Camelina* spp. germplasm – S. Lee, J. Verose, J. L. Lee |
| $11^{30}$ - $11^{45}$ | Can we still find landraces in Europe after 2000 Investigations in Lemnos and Lefkada - P. J. Bebeli, K. Thomas, R. Thanopoulos, H. Knüpffer |
| $11^{45}$ - $12^{00}$ | FC-106 Morphological and molecular characterization of faba bean (*Vicia faba* L.) germplasm - S. S. Alghamdi, A. Al-Shameri, H. M. Migdadi, M. H. Ammar |
| $12^{00}$ - $12^{15}$ | Characterization of confectionary sunflower (*Helianthus annuus* L.) land races of Turkey- A. S. TAN, M. Aldemir, A. Altunok, A. Tan |
| $12^{15}$ - $12^{30}$ | Discussion |

## FRIDAY, NOVEMBER 15$^{TH}$ 2013 LEAVING FROM HOTEL

# 6

# Osman Gazi Han Meeting Room

## Intellectual Property Rights in Plant Breeding Session

**TUESDAY, NOVEMBER 12TH 2013**

| | |
|---|---|
| $13^{30}$ - $15^{50}$ | ***1st Session: Session Chair* MR. ANDREA MANSUINO** |
| $13^{30}$ - $13^{40}$ | ***Opening Talk by* Andrea MANSUINO, President of CIOPORA** |
| $13^{40}$ - $14^{00}$ | **Benjamin RIVOIRE, Program Officer at the UPOV** (International Union for the Protection of New Varieties of Plants) The Latest Developments in UPOV |
| $14^{00}$ - $14^{20}$ | **Mr. Francesco MATTINA, Head at CPVO** (Community Plant Variety Office)<br>Community plant variety office: an overview of the European plant variety protection system and co-operation activities outside the EU |
| $14^{20}$ - $14^{40}$ | **Dr. T.H. Wittop KONING -AOMB Law Firm** – The Netherlands<br>Patents – a fruitful alternative for plant breeders' rights? |
| $14^{40}$ - $15^{00}$ | **Dr. Edgar KRIEGER, Secretary General of CIOPORA**<br>Intellectual property protection for plant innovations |
| $15^{00}$ - $15^{30}$ | Discussion |
| $15^{30}$ - $16^{00}$ | Coffee break |
| $16^{00}$ - $18^{00}$ | ***2nd Session: Session Chair* Prof Dr N. Ayşe ODMAN BOZTOSUN** |
| $16^{00}$ - $16^{20}$ | **Kamil YILMAZ – TUBID**<br>Plant Breeders' Rights System and Its Implementation in Turkey |
| $16^{20}$ - $16^{40}$ | **Dr Ayşegül DEMİRCİOĞLU - Turkish Patent Institute**<br>Assessment of the scope of intellectual property rights and patent implementations of biotechnological products in Turkey |
| $16^{40}$ - $17^{00}$ | **Alexei MORGUNOV, Thomas S. PAYNE**<br>Road to the International Treaty for Plant Genetic Resources for Food and Agriculture |

| | |
|---|---|
| $17^{00}$ - $17^{20}$ | **Prof Dr Vladimir SHAMANIN**<br>Plant Breeder’s Right in Russia |
| $17^{20}$ - $18^{00}$ | Discussion |

# 7

# FAO Regional Stakeholder Workshop

## FAO REGIONAL STAKEHOLDER WORKSHOPS: GUIDELINES FOR DEVELOPING NATIONAL PGRFA STRATEGY

WEDNESDAY TO THURSDAY, NOVEMBER 13TH – 15TH 2013

# 8

# Osman Gazi Han Meeting Room

## IWWIP Session

### THURSDAY, NOVEMBER 14TH 2013

| | |
|---|---|
| 13$^{30}$ - 15$^{30}$ | ***1st Session*** |
| 13$^{30}$ - 14$^{00}$ | ***OPENING SESSION*** TAGEM, CIMMYT, ICARDA |
| 13$^{40}$ - 14$^{00}$ | IWWIP: introduction and general presentation - F. Ozdemir |
| 14$^{00}$ - 14$^{15}$ | Climate change and adjustment of winter wheat breeding strategy and methodology - A. Morgounov |
| 14$^{15}$ - 14$^{30}$ | Status of rusts in Turkey and development of resistant germplasm - Z. Mert |
| 14$^{30}$ - 14$^{45}$ | Application of physiological approaches in winter wheat drought breeding (BDIARI) |
| 14$^{45}$ - 15$^{00}$ | Discussion |
| 15$^{00}$ - 15$^{30}$ | Coffee break |
| 15$^{30}$ - 17$^{30}$ | ***2nd Session*** |
| 15$^{30}$ - 15$^{45}$ | Status of wheat landraces in Turkey: what they are, where they are still grown and why? - M. Keser |
| 15$^{45}$ - 16$^{00}$ | Progress towards identifying salinity tolerant improved winter and facultative wheat in Central Asia - R. Sharma |
| 16$^{00}$ - 16$^{15}$ | Genetic gains in winter and spring wheat in Turkey in the last 50 years and directions for the future |
| 16$^{15}$ - 16$^{30}$ | Status of rusts in Central and West Asia and development of new varieties - N. Kumarse |
| 16$^{30}$ - 16$^{45}$ | Winter hardiness and agronomic performance of the historical set of germplasm from Turkey, Ukraine and USA (U. Kucukozdemir) |
| 16$^{45}$ - 17$^{00}$ | Discussion |
| 17$^{00}$ | Closure |

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| | İNCI COLTART | Enza Zaden Tarim / Vegetable Breeding Company | TURKEY |
| | ÖZLEM ÖZKIRMIZI | Enza Zaden Tarim / Vegetable Breeding Company | TURKEY |
| | ONUR OZBAS | Enza Zaden Tarim/ Vegetable Breeding Company | TURKEY |
| | TANER AKAR | Erciyes University  Faculty of Agriculture Kayseri | TURKEY |
| | OSMAN GÜLŞEN | Erciyes University Agriculture Faculty Horticulture Department | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
|  | SATI UZUN | Erciyes University/Faculty of Agriculture/Deparment of Field Crops | TURKEY |
|  | KENAN SONMEZ | Eskisehir Osmangazi University Faculty of Agric. Dept Horticulture | TURKEY |
|  | ENGIN KINACI | Eskisehir Osmangazi University Faculty of Agric. Dept of Field Crops | TURKEY |
|  | GULCAN KINACI | Eskisehir Osmangazi University Faculty of Agric. Dept of Field Crops | TURKEY |
|  | ZEKIYE BUDAK BASCİFTCİ | Eskisehir Osmangazi University Faculty of Agric. Dept of Field Crops | TURKEY |
|  | YASEMIN EVRENOSOGLU | Eskisehir Osmangazi University Faculty of Agric. Dept of Horticulture | TURKEY |
|  | IMREN KUTLU | Eskisehir Osmangazi University Faculty of Agric. Dept. Horticulture | TURKEY |
|  | MEHMET GÜL | Euralis Seed CO | TURKEY |
|  | HILMI KOCATAŞ | Fig Research Station Erbeyli Aydin | TURKEY |
|  | EMEL KAÇAL | Fruit Research Station Isparta | TURKEY |
|  | Ö FARUK KARAMÜRSEL | Fruit Research Station Isparta | TURKEY |
|  | R ALI EMRE | Fruit Research Station Isparta | TURKEY |
|  | H C SARISU | Fruit Research Station 00 Egirdir Isparta | TURKEY |
|  | İ ERYILMAZ | Fruit Research Station 00 Egirdir Isparta | TURKEY |
|  | FATMA PINAR ÖZTÜRK | Fruit Research Station Egirdir Isparta | TURKEY |
|  | HAKKI KOÇAL | Fruit Research Station Egirdir Isparta | TURKEY |
|  | HASAN CUMHUR SARISU | Fruit Research Station Egirdir Isparta | TURKEY |
|  | İBRAHIM GÜR | Fruit Research Station Egirdir Isparta | TURKEY |
|  | MEHMET AKSU | Fruit Research Station Egirdir Isparta | TURKEY |
|  | ŞAFAK SEKMEN | Fruit Research Station Egirdir Isparta | TURKEY |
|  | ZEHRA BABALIK | Fruit Research Station Egirdir Isparta | TURKEY |
|  | GÖKHAN ÖZTÜRK | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | İSMAIL DEMİRTAŞ | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | MELIH AYDINLI | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | ŞERIF ÖZONGUN | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | TURGAY SEYMEN | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | YUSUF ÖZTÜRK | Fruit Research Station Eğirdir Isparta | TURKEY |
|  | FIGEN ERASLAN | Fruit Research Station, Eğirdir Isparta | TURKEY |
|  | M ZEKI KARİPÇİN | GAP Agricultural Research Center Sanliurfa | TURKEY |
|  | ALI İLKHAN | GAP Agricultural Research Institute Şanlıurfa | TURKEY |
|  | İBRAHIM HALIL ÇETINER | GAP Agricultural Research Institute Şanlıurfa | TURKEY |
|  | KADER ERCİK | GAP International Agricultural Research and Training Center | TURKEY |
|  | SULTAN TÜRKOĞLU | GAZİANTEP BÜNİVERSİTESİ | TURKEY |
|  | DEREN AMCA | Genta Agricultural Products CO | TURKEY |
|  | D. SEZGIN | Hacettepe University Faculty of Science Department of Biology | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
| | S. TERZIOĞLUS | Hacettepe University Faculty of Science Department of Biology | TURKEY |
| | YASEMİN EKMEKÇI | Hacettepe University Faculty of Science Department of Biology | TURKEY |
| | EBRU SAKAR | Harran University Agriculture Faculty Horticulture Department | TURKEY |
| | ALI İSLAM | Hazelnut Research Station Giresun | TURKEY |
| | ALI TURAN | Hazelnut Research Station Giresun | TURKEY |
| | ARZU SEZER | Hazelnut Research Station Giresun | TURKEY |
| | ERDAL SIRAY | Hazelnut Research Station Giresun | TURKEY |
| | HASBI ŞEKER | Hazelnut Research Station Giresun | TURKEY |
| | HÜSEYIN İRFAN BALIK | Hazelnut Research Station Giresun | TURKEY |
| | NERIMAN BEYHAN | Hazelnut Research Station Giresun | TURKEY |
| | ÖMÜR DUYAR | Hazelnut Research Station Giresun | TURKEY |
| | ÖZGÜN KALKIŞIM | Hazelnut Research Station Giresun | TURKEY |
| | SELDA KAYALAK BALIK | Hazelnut Research Station Giresun | TURKEY |
| | TURGUT ŞİŞMAN | Hazelnut Research Station Giresun | TURKEY |
| | VELI ERDOĞAN | Hazelnut Research Station Giresun | TURKEY |
| | ÇETIN NACAR | Horticulture Research Station Alata | TURKEY |
| | MESUT KESER | ICARDA – Ankara | TURKEY |
| | NAZARI KUMARSE | ICARDA – Ankara | TURKEY |
| | BEYHAN KIBAR | Iğdır University Agriculture Faculty Horticulture Department | TURKEY |
| | BEYHAN AKIN | International Maize and Wheat Improvement Center (CIMMYT) | TURKEY |
| | ALI TEVFIK UNCU | Izmir Institute of Technology Dept of Molecular Biology and Genetics | TURKEY |
| | ANNE FRARY | Izmir Institute of Technology Dept of Molecular Biology and Genetics | TURKEY |
| | ASENA AKKÖSE | Izmir Institute of Technology Dept of Molecular Biology and Genetics | TURKEY |
| | ÇELIK İBRAHIM | Izmir Institute of Technology Dept of Molecular Biology and Genetics | TURKEY |
| | SAMI DOĞANLAR | Izmir Institute of Technology Dept of Molecular Biology and Genetics | TURKEY |
| | AYDIN AKKAYA | Kahramanmaras Sutcu Imam University Agricultural Faculty Department of Field Crops | TURKEY |
| | HILAL KARAKUZULU | Kahramanmaras Sutcu Imam University Agricultural Faculty Department of Agricultural Biotechnology | TURKEY |
| | MEHMET BARIŞ DEMİRTAŞ | Kahramanmaras Sutcu Imam University Agricultural Faculty Department of Agricultural Biotechnology | TURKEY |
| | AYSUN CAVUSOGLU | Kocaeli University Arslanbey Agricultural Vocational School | TURKEY |
| | MELEKBER SÜLÜŞOĞLU | Kocaeli University Arslanbey Agricultural Vocational School | TURKEY |
| | A GÜNEŞDOĞDU | LİDER Seed Company Antalya | TURKEY |
| | D. CANSIZER | LİDER Seed Company Antalya | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
| | A EŞREF ÖZBEY | Maize Research Station Sakarya | TURKEY |
| | AHMET DUMAN | Maize Research Station Sakarya | TURKEY |
| | LÜTFI DEMIR | Maize Research Station Sakarya | TURKEY |
| | M CAVIT SEZER | Maize Research Station Sakarya | TURKEY |
| | MESUT ESMERAY | Maize Research Station Sakarya | TURKEY |
| | NIYAZI AKARKEN | Maize Research Station Sakarya | TURKEY |
| | RAHIME CENGIZ | Maize Research Station Sakarya | TURKEY |
| | YAVUZ AĞI | Maize Research Station Sakarya | TURKEY |
| | İBRAHIM MANCAK | Manier Tohumculuk Ltd.Şti | TURKEY |
| | AYSEN YUMURTACI | Marmara Univ Faculty of Science and Arts Department of Biology | TURKEY |
| | GEOFFREY L THOMAS | MAY Seed CO | TURKEY |
| | ASIYE ULUĞ | Middle East Technical University Biological Sciences Department | TURKEY |
| | EVRIM ZEYBEK | Middle East Technical University Biological Sciences Department | TURKEY |
| | KUBILAY YILDIRIM | Middle East Technical University Biological Sciences Department | TURKEY |
| | ZEKI KAYA | Middle East Technical University Biological Sciences Department | TURKEY |
| | GÖKHAN ORUÇ | Ministry of Food Agriculture and Animal Husbandary Babadağ District | TURKEY |
| | VEHBI ESER | Ministry of Food Agriculture and Livestock | TURKEY |
| | ZUMRUT CELIK | Ministry of Food Agriculture and Livestock Ataturk Orman Ciftligi | TURKEY |
| | FULYA ARSLAN | MONSANTO | TURKEY |
| | ÖZGÜR IŞLER | Monsanto Ltd. | TURKEY |
| | ERDEM KAHVECI | Multi Seed | TURKEY |
| | ERKAN EREN | Mushroom Cultivation Program Bergama Vocational School Ege Univ. | TURKEY |
| | YAŞAR AKIŞCAN | Mustafa Kemal University Agricultural Faculty Field Crops Dep | TURKEY |
| | EMINE ÖZDEMİR | Mustafa Kemal University Agriculture Faculty Horticulture Dept | TURKEY |
| | KAZIM GÜNDÜZ | Mustafa Kemal University Agriculture Faculty Horticulture Dept | TURKEY |
| | AYHAN EKICI | Namdhari Seeds / Turkey | TURKEY |
| | NURAY ÖZER | Namık Kemal University Agriculture Faculty | TURKEY |
| | İSMET BAŞER | Namık Kemal University Agriculture Faculty Field Crops Department | TURKEY |
| | GÜLSEMIN SAVAŞ TUNA | Namık Kemal University Dept of Field Crops Faculty of Agriculture | TURKEY |
| | KAYIHAN Z KORKUT | Namık Kemal University Dept of Field Crops Faculty of Agriculture | TURKEY |
| | METIN TUNA | Namık Kemal University Faculty of Agriculture Dept of Field Crops | TURKEY |
| | FEYZA ÇAY | Namık Kemal University Graduate College | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
|  | ERTAN ATEŞ | Namik Kemal University Tekirdag | TURKEY |
|  | OĞUZ BILGIN | Namik Kemal University Tekirdag | TURKEY |
|  | BURHAN ARSLAN | Namık Kemal University Tekirdağ Agriculture Faculty Field Crops Dept | TURKEY |
|  | VOLKAN SEZENER | Nazilli Cotton Research Institute Nazilli Aydın | TURKEY |
|  | NECMETTIN BOLAT | NBC Seed C0 – Eskişehir | TURKEY |
|  | MEHMET E. ÇALIŞKAN | Niğde University Agriculture and Technology Faculty NİĞDE | TURKEY |
|  | SEDAT SERÇE | Niğde University Agriculture and Technology Faculty NİĞDE | TURKEY |
|  | SEVGI ÇALIŞKAN | Niğde University Agriculture and Technology Faculty NİĞDE | TURKEY |
|  | MURAT OLGUN | OLGUNLAR TOHUMCULUK | TURKEY |
|  | FILIZ SEFER | Olive Research Institute Bornova Izmir | TURKEY |
|  | HÜLYA KAYA | Olive Research Institute Bornova Izmir | TURKEY |
|  | MEHMET HAKAN | Olive Research Institute Bornova Izmir | TURKEY |
|  | MUSTAFA ŞAHİN | Olive Research Institute Bornova Izmir | TURKEY |
|  | NURENGIN METE | Olive Research Institute Bornova Izmir | TURKEY |
|  | ÖZNUR ÇETİN | Olive Research Institute Bornova Izmir | TURKEY |
|  | UĞUR GÜLOĞLU | Olive Research Institute Bornova Izmir | TURKEY |
|  | ŞENAY DAĞIDIR | Ondokuz Mayıs Univ Agric. Biotechnology Dept Agriculture Faculty | TURKEY |
|  | AHMET OKUMUS | Ondokuz Mayıs Univ Agricultural Biotechnology Dept of Agric Faculty | TURKEY |
|  | LEVENT MERCAN | Ondokuz Mayıs Univ Agricultural Biotechnology Dept of Agric. Faculty | TURKEY |
|  | İSMAIL ERPER | Ondokuz Mayıs Univ Faculty of Agriculture Plant Protection Dept | TURKEY |
|  | GÜLAY KILIÇ | Ondokuz Mayıs Univ. Faculty of Agriculture Plant Protection Dept | TURKEY |
|  | AHMET BALKAYA | Ondokuz Mayıs University Faculty of Agriculture Horticulture Dept. | TURKEY |
|  | FERDA ALTAY | Ondokuz Mayıs University Field Crops Dept Faculty of Agronomy | TURKEY |
|  | MEHMET CAN | Ondokuz Mayıs University Field Crops Dept Faculty of Agronomy | TURKEY |
|  | KASIM KÜLEK ÖZ | Özaltın Seed CO Koçarlı Aydın | TURKEY |
|  | PEYNIRCIOĞLU CENG | Özaltın Seed CO Koçarlı Aydın | TURKEY |
|  | SÜLEYMAN KARAHAN | PANKOBİRLİK | TURKEY |
|  | MUSTAFA AKBULUT | Pazar Vocational School Recep Tayyip Erdogan University | TURKEY |
|  | BÜŞRA YAPICI | PETEKTAR SEED CO | TURKEY |
|  | ESRA OLDAÇ | PETEKTAR SEED CO | TURKEY |
|  | MURAT GÜNEY | Pistachio Research Station | TURKEY |
|  | SALIH KAFKAS | Pistachio Research Station | TURKEY |
|  | H TOPÇU | Pistachio Research Station Gaziantep | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
|  | NERGİZ ÇOBAN | Pistachio Research Station Gaziantep | TURKEY |
|  | N ASLAN | Pistachio Research Stiuation Gaziantep | TURKEY |
|  | ABDULLAH ÜNLENEN | Potato Research Station Niğde | TURKEY |
|  | HÜSEYIN ONARAN | Potato Research Station Niğde | TURKEY |
|  | MURAT NAM | Potato Research Station Niğde | TURKEY |
|  | DENIZ CAN | ProGen Seed CO Antakya | TURKEY |
|  | HÜSEYIN GÜNGÖR | ProGen Seed CO Antakya | TURKEY |
|  | BATUHAN AKGÖL | ProGen Seed CO Antakya | TURKEY |
|  | CELILE DEĞIRMENCI | Progen Tohum A.Ş. | TURKEY |
|  | EMINUR ELÇI | Progen Tohum A.Ş. | TURKEY |
|  | CANSERİ BOZKUŞ | PROTO TOHUM-SÜRDETARIM | TURKEY |
|  | ARZU GÜNDÜZ | Research Station of Soil Water and Combating Desertification Konya | TURKEY |
|  | SIKKE VAN DER SCHAAR | Rijk Zwaan Seed CO | TURKEY |
|  | WIJBE HIELKE | Rijk Zwaan Seed CO | TURKEY |
|  | EMINE AYDIN | RTE University Field Crops Dept Faculty of Agronomy and Natural Sci | TURKEY |
|  | FATIH SEYIS | RTE University Field Crops Dept Faculty of Agronomy and Natural Sci | TURKEY |
|  | ISMAIL CAKMAKI | Sabanchi University | TURKEY |
|  | MERAL YUCE | Sabanci University Nanotechnology Research and Application Center | TURKEY |
|  | ALI ÜSTÜN | SAFGEN Tohumculuk Konya | TURKEY |
|  | ALI TOPAL | Selçuk University Agriculture Faculty Field Crops Department | TURKEY |
|  | ÖNDER TÜRKMEN | Selçuk University Agriculture Faculty Horticulture Department | TURKEY |
|  | SEYDI AHMET BAĞCI | Selçuk University Sarayönü Vocational High School | TURKEY |
|  | DURSUN BABAOĞLU | Selçuk University Sarayönü Vocational High School Konya | TURKEY |
|  | İRFAN ÖZER | Selcuk University Vocational School of Sarayönü | TURKEY |
|  | HULYA SIPAHI | Sinop University Faculty of Science and Art Department of Biology | TURKEY |
|  | HÜSNÜ AKTAŞ | South Eastern Anatolia Agricultural Research Institute Diyarbakır | TURKEY |
|  | ŞEVKET TEKIN | South Eastern Anatolia Agricultural Research Institute Diyarbakır | TURKEY |
|  | MUSTAFA CÖLKESEN | Sütçü İmam Univ Agric. Faculty Field Crops Dept Kahramanmaraş | TURKEY |
|  | ÜMIT GİRGEL | Sütçü İmam Univ Agric. Faculty Field Crops Dept Kahramanmaraş | TURKEY |
|  | MÜZEYYEN UĞURER | Sutcu Imam Univ Agricultural Faculty Dept of Agricultural Biotech | TURKEY |
|  | TEVRICAN DOKUYUCU | Sutcu Imam Univ Agricultural Faculty Dept of Agricultural Biotech | TURKEY |
|  | ZIYA DUMLUPINAR | Sutcu Imam Univ Agricultural Faculty Dept of Agricultural Biotech | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
| | HAYDAR KURT | TAGEM - ANKARA | TURKEY |
| | İSA ÖZKAN | TAGEM Field Crops Department Ankara | TURKEY |
| | VICDAN ACAR | TAGEM Field Crops Department Ankara | TURKEY |
| | MASUM BURAK | TAGEM General Directorate of Agricultural Research and Policy | TURKEY |
| | AYTEKIN AKSOY | Tasaco SEED CO | TURKEY |
| | CENGIZ ÖZER | Tekirdağ Viticultural Research Station | TURKEY |
| | ERHAN SOLAK | Tekirdağ Viticultural Research Station | TURKEY |
| | LERZAN ÖZTÜRK | Tekirdağ Viticultural Research Station | TURKEY |
| | ÜMIT ESER | Tekirdağ Viticultural Research Station | TURKEY |
| | ONUR ERGÖNÜL | Tekirdağ Viticulture Research Station | TURKEY |
| | ZELIHA ORHAN ÖZALP | Tekirdağ Viticulture Research Station | TURKEY |
| | HAKAN ÖZTÜRK | TİTİZAGRO GRUP A.Ş. | TURKEY |
| | İBRAHİM EMRE KÖSE | TİTİZAGRO GRUP A.Ş. | TURKEY |
| | KAMİL SAVAŞ TİTİZ | TİTİZAGRO GRUP A.Ş. | TURKEY |
| | ADNAN TÜLEK | Trakya Agricultural Research Institute Edirne | TURKEY |
| | GOKSEL EVCI | Trakya Agricultural Research Institute Edirne | TURKEY |
| | IBRAHIM M YILMAZ | Trakya Agricultural Research Institute Edirne | TURKEY |
| | İRFAN ÖZTÜRK | Trakya Agricultural Research Institute Edirne | TURKEY |
| | MERVE GUZEL | Trakya Agricultural Research Institute Edirne | TURKEY |
| | NECMI BESER | Trakya Agricultural Research Institute Edirne | TURKEY |
| | VELI PEKCAN | Trakya Agricultural Research Institute Edirne | TURKEY |
| | YALCIN KAYA | Trakya Agricultural Research Institute Edirne | TURKEY |
| | ALTUĞ PILASLI | Trakya Oilseeds Grower Cooperatives Edirne | TURKEY |
| | NESRIN CITAK | Trakya Oilseeds Grower Cooperatives Edirne | TURKEY |
| | NILÜFER TUNA | Trakya Oilseeds Grower Cooperatives Edirne | TURKEY |
| | ONUR AY | Trakya Oilseeds Grower Cooperatives Edirne | TURKEY |
| | YILMAZ YILDIRIM | Transitional Zone Agricultural Research Institute | TURKEY |
| | ARZU KÖSE | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | ERDINÇ SAVAŞLI | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | FERDA Ç KOŞAR | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | MUSTAFA ÇAKMAK | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | ÖZLEM BİLİR | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | SABRI ÇAKIR | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | SAVAŞ BELEN | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |
| | YAŞAR KARADUMAN | Transitional Zone Agricultural Research Institute – Eskişehir | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
| | AYSEL YORGANCILAR | Transitional Zone of Agricultural Research Institute Eskisehir | TURKEY |
| | OZCAN YORGANCILAR | Transitional Zone of Agricultural Research Institute Eskisehir | TURKEY |
| | NURTEN LÖKOĞLU | Transitional Zone Research Institute | TURKEY |
| | SALI FIDAN | Transitional Zone Research Institute | TURKEY |
| | ŞULE MYIĞITOĞLU | Transitional Zone Research Institute | TURKEY |
| | ŞULE SARICAM | Transitional Zone Research Institute | TURKEY |
| | HACI YILMAZ | Troya SEED CO | TURKEY |
| | NURI ERDEM ŞIRIN | Troya SEED CO | TURKEY |
| | HANDAN AYDIN | TÜMAŞ AGRICULTURE-BAYRAM SEED | TURKEY |
| | ALI ŞENAY | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | BURAK KUNTER | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | DILAN ÖZMEN | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | EMINE SEÇER | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | ERHAN İÇ | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | GÜLIZAR AYDIN | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | HAYRETTIN PEŞKİRCİOĞLU | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | HAZMA ŞİRİN | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | İHSAN TUTLUER | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | K YAPRAK KANTOĞLU | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | M İHSAN TUTLUER | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | MUSTAFA ÖZÇOBAN | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | NÜKET GÜNÇAĞ | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | SELMA ÖZYİĞİT | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | SÜREYA ŞEKERCİ | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | YAPRAK KANTOĞLU | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | ZAFER IŞIK | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | ZAFER SAĞEL | Turkish Atomic Energy Sarayköy Nuclear Research & Training Center | TURKEY |
| | FATIH LEBLEBİCİ | Turkish Grain Board Opium Alkaloid Factory Afyon | TURKEY |
| | MÜFIT ENGIZ | Turkish Seed Industry Association (TÜRKTED) | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
| | AYHAN HORUZ | Univ of Ondokuz Mayis Faculty of Agriculture Dept of Horticulture | TURKEY |
| | ÖMER SÖZEN | University of Ahi Evran Faculty of Agricultural Kırşehir | TURKEY |
| | ALPTEKIN KARAGÖZ | University of Aksaray Faculty of Arts and Science | TURKEY |
| | SABER D. KHABBAZI | University of Ankara | TURKEY |
| | RUHSAR YANMAZ | University of Ankara Faculty of Agriculture Horticulture Department | TURKEY |
| | SEMA BAŞBAĞ | University of Dicle Agricultural Faculty Dept of Field CropsDiyarbakir | TURKEY |
| | SULTAN BAY TÜRKOĞLU | University of Gaziantep Science and Arts Faculty | TURKEY |
| | CANAN CAN | University of Gaziantep Science and Arts Faculty | TURKEY |
| | HALIT SEYFETTIN ATLI | University of Gaziantep Science and Arts Faculty | TURKEY |
| | SEVILHAN MENNAN | University of Ondokuz Mayıs Faculty of Agric. Plant Protection Dept | TURKEY |
| | HÜLYA SIPAHI | University of Sinop Faculty of Arts and Science | TURKEY |
| | ERHAN KOÇAK | University of Suleyman Demirel Isparta | TURKEY |
| | YILDIRIM S. OZDEN | Variety Registration and Seed Certification Centre | TURKEY |
| | IRMAK GÜRSOY | Vilmorin/Anadolu | TURKEY |
| | ABDULLAH ÜNLÜ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | AHU ÇINAR | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | AKIN TEPE | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | ASU OĞUZ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | AYLIN KABAŞ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | EMINE GÜMRÜKÇÜ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | ERTUĞRUL TURGUTOĞLU | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | FILIZ BOYACI | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | FILIZ ÖKTÜREN | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | GÜLAY DEMİR | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | HALUK TOKGÖZ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | HFILIZ BOYACI | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | İBRAHIM ÇELIK | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | İLKNUR POLAT | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
| | İLYAS TEKŞAM | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |

| # | NAME | INSTITUTION | COUNTRY |
|---|---|---|---|
|  | IŞIL DEMİRTAŞ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | LEVENT KESKİN | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | MEHMET ÖTEN | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | MEHMET PAMUKÇU | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | MENSURE ÖZGÜVEN | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | MINE ÜNLÜ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | MUHARREM GÖLÜKÇÜ | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | NAZIM ŞEKEROĞLU | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | NEJLA ÇELİK | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | RAMAZAN ÖZALP | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | RANA KURUM | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | SAADET TUGRUL AY | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | ŞEKIP ERDAL | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | ŞENAY KURT | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
|  | SINAN ZENGİN | Western Mediterranean Agricultural Research Institute Antalya | TURKEY |
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1. GENETIC RESOURCES FOR PLANT BREEDING PAST, PRESENT AND FUTURE

2. INTELLECTUAL PROPERTY PROTECTION FOR PLANT INNOVATIONS

3. THE LATEST DEVELOPMENTS IN UPOV

4. MOLECULAR TOOLS AND TECHNOLOGIES FOR NEXT GENERATION PLANT BREEDING

5. USING GENOMIC SELECTION TO ACCELERATE THE RATE OF GENETIC IMPROVEMENT IN CASSAVA AND WHEAT BREEDING

6. HISTORY AND CURRENT STATUS OF GENOME SEQUENCING

7. PATENTS – A FRUITFUL ALTERNATIVE FOR PLANT BREEDERS’ RIGHTS

8. PLANT BREEDING FOR THE FUTURE

9. COMMUNITY PLANT VARİETY OFFİCE AN OVERVİEW OF THE EUROPEAN PLANT VARİETY PROTECTİON SYSTEM AND CO-OPERATİON ACTİVİTİES OUTSİDE THE EU

10. POTENTIAL AND FUTURE OF NOVEL MOLECULAR BREEDING TECHNIQUES IN PRACTICAL PLANT BREEDING

11. BREEDING OILSEEDS FOR BIOENERGY OR FOOD PRODUCTION

12. MEETING THE CHALLENGES OF GLOBAL CLIMATE CHANGE AND FOOD SECURITY THROUGH INNOVATIVE MAIZE RESEARCH

13. PLANT DIVERSITY CONSERVATION IN TURKEY

14. FUTURE CHALLENGES FOR THE BREEDERS STRUGLING THE CLIMATIC CHANGES

15. ESTABLISHING CORE COLLETIONS FOR ENHANCED USE OF GERMPLASM

16. ADVENTURES IN BREEDING FRESH MARKET TOMATOES FOR FRUIT QUALITY

17. BREEDING FOR ABIOTIC STRESSES TOLERANCE IN COOL SEASON GRAIN LEGUMES

18. OPTIMAL HARNESSING OF THE POTENTIALS OF PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

# PLANT BREEDING FOR THE FUTURE

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Transformational change in our food and fiber production capacity has occurred over the last 100 years, with the development and marketing of crop hybrids, semi-dwarf wheat and rice (green revolution), and more recently the incorporation of traits for herbicide resistance, insect resistance and disease resistance. Crop yields per unit of land have increased dramatically over this period of time and while much can be attributed to improved nutrient management and cultural practices, these were all made possible by new varieties with increased responsiveness to this management. As we look at the drivers of this change in food and fiber production (which is greater than in the previous 2,000 years) it can be broken into major factors. The first I will discuss is a group of breakthroughs in fundamental knowledge, including statistical approaches to plant breeding, technology to produce hybrids of crops, elucidation of DNA form and function, development of the plant transformation system, development of high-throughput sequencing systems and develop of markers and management of large data sets. The second area I will discuss is education. Prior to 1920 there were very few plant breeders and even less that were applying more than mass selection. Plant breeders and those working on fundamental genetics in support of plant breeding have increased many fold. Today we have more people working in this area at Texas A&M than there were in the whole world 100 years ago and this has occurred through a massive educational effort. The third area I want to discuss is the area of intellectual property. Recent advances in intellectual property rights throughout the world have led to investments by major companies in plant breeding research with the top three companies investing as much as 5 million dollars per day in plant breeding research. The final area I want to discuss is public investment in plant breeding. The role of our International Centers such as CIMMIT, IRRI and ICARDA along with major Universities around the world and individual country investments such as EMBRAPA and ARS were the primary drivers of the historical change – what will be there role going forward? Future plant breeding gains will largely be driven by these same fundamentals. Encouragement of investment in plant breeding through protection of intellectual property developed through it, development of new fundamental technology and ongoing investment in education to feed and clothe 9 billion people over the next 40 years while improving our environment.

## BREEDING FOR ABIOTIC STRESSES TOLERANCE IN COOL SEASON GRAIN LEGUMES

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The role of grain legumes in human and animal nutrition, improving soil fertility and in mitigating greenhouse gases is well documented. However priorities for cultivation and research in grain legumes remain secondary to those for cereals in most cropping systems. Grain legumes are relatively sensitive to several abiotic stresses such as drought, heat, cold, frost, salinity, transient waterlogging and nutrient disorders. Genetic improvements together with agronomic packages can significantly contribute to overcome various abiotic stresses in grain legumes. Most of the breeding programs for improved yield of grain legumes rely on empirical selection for superior seed yield and quality across a wide range of target environments. While direct selection for seed yield can be effective, the approach is difficult and costly, and gains from selection are often low, especially under various abiotic stresses. Breeders currently invest little effort in understanding the physiological basis of genotype X environment interaction, which could potentially increase yields in specific environments by better exploitation of appropriately adapted genotypes. The physiologist can assist the breeder in three ways: (i) identification of suitable environments in which to conduct selection trails, (ii) identification of selection criteria for focussed introgression programs, and (iii) identification of traits as indirect selection criteria in core breeding programs.  In recent years there has been some progress in grain legumes to screen germplasm for tolerance to specific abiotic traits despite they are highly complex and site specific. Conventional breeding programs have made significant progress in improving the adaptation of grain legumes to a range of environments. The rapidly developing area of genomics and molecular biology may aid in both identifying the important biochemical and physiological processes affected by abiotic stresses and in screening for complex traits. To date the use of genomic technologies for grain legume improvement has been minimal. Understanding what alleles are available for key traits and the development of cost-effective genomic tools and molecular markers would facilitate the more rapid introgression of many important traits.

# ADVENTURES IN BREEDING FRESH MARKET TOMATOES FOR FRUIT QUALITY

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One's view of which tomato (*Solanum lycopersicum* L.) fruit quality attributes are important may be different depending on if you are a grower, packer/shipper, seller, or consumer. In numerous countries of the world many consumers are dissatisfied with commercially grown tomatoes and think tomato breeders focus only on traits other than flavor such as yield, shipping ability, and disease resistance. Combining flavor with the other characteristics listed is indeed difficult, but breeding for flavor alone is challenging in and of itself. Tomato flavor involves a complex interaction of sugars, acids, and numerous aromatic volatiles that are strongly influenced by environmental growing conditions. This talk provides some insight relating to the intricacies and realities involved in the development and marketing of tomato varieties with improved flavor. The Tasti-Lee$^{TM}$ variety is used to illustrate some major characteristics that are required for commercial production of a labeled tomato variety with improved flavor. Recent work on making further flavor improvements will be discussed. Availability of sufficient and affordable labor for hand-harvesting of tomatoes and many other horticultural crops in the United States is a major concern. Developing once-over mechanically harvested fresh market tomato varieties that don't require staking and tying is an approach to produce tomatoes with less labor. Our program to develop such varieties that are called compact growth habit (CGH) tomatoes combines the use of the brychytic (*br*) gene to remove apical dominance, jointless pedicels to allow stem-free harvesting, and concentrated fruit setting of large, firm defect free fruit. The present status of this project will be discussed.

# ESTABLISHING CORE COLLECTIONS FOR ENHANCED USE OF GERMPLASM IN CROP IMPROVEMENT

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Plant genetic resources are the basic raw materials and their use in crop improvement is the most sustainable way to conserve biodiversity. Low use of germplasm in crop improvement programs has resulted in large gap between the number of germplasm preserved in genebanks and the number of germplasm or their derivatives used in crop breeding programs across the globe. Breeders are reluctant to use exotic germplasm largely either due to linkage drag or due to breakdown of co-adapted gene complexes, which may prolong cultivar development time. The reduced subsets such as core or mini core collection, representing diversity of a species are the ideal genetic resources for discovering new sources of variations for use in crop improvement programs. Two decades of research at ICRISAT has led to the establishment of core and mini core collections and their subsequent evaluations at ICRISAT and elsewhere have resulted in identification of new diverse sources of variations, for example, resistance to abiotic and/or biotic stresses in chickpea, groundnut, pigeonpea, sorghum, and finger millet. Likewise, a number of diverse and nutritionally dense (high protein, Ca, Fe and Zn) germplasm have been identified in finger millet, foxtail millet, groundnut, pearl millet, and sorghum. A few groundnut germplasm with improved oil quality, as determined by variation in oleic and linoleic fatty acids, were also identified. Many of these germplasm were agronomically at par or superior over controls and showed specific and/or wide adaptation. The identified sources may be used in genomics and breeding to broaden the cultigen's gene pool in these crops.

# FUTURE CHALLENGES FOR THE BREEDERS STRUGLING THE CLIMATIC CHANGES

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The predictions now put that in 2050 the world's population at 9 billion should be fed with three times less arable land, water and rural population. Additionally to that the impact of climate change make the challenge of increasing agricultural yields worldwide even greater. Crop production methods will need to sustain the environment, preserve natural resources and support the lively hood of farmers and population. This presentation outlines not only the current problems and limitations of the global economy in term of population and food demand, environmental issues as a global warming but also the way forward. Special attention is given to the future options in term of adaption to climatic changes, diminishing the factors limited the crop productivity, Emphasis is given to the new modern approaches like biotechnology and genomics and how they could help the breeders to find out solutions for building a proper global food, feed, fiber, bioenergy, bioplastics and phytopharmaceutical strategy.

# OPTIMAL HARNESSING OF THE POTENTIALS OF PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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Farmers require a diverse spectrum of well-adapted crop varieties which, suited to target agroecologies and cropping systems, underpin productive and resilient farming systems. This is imperative for producing significantly more food with fewer inputs, the paradigm for feeding an ever increasing human population with minimal environmental footprints, as climate change and myriad socioeconomic drivers imperil agriculture especially in the most vulnerable regions of the world. To attain this goal of improved crop productivities, appropriate scientific and technological methods, enabled by nurturing policy regimens, can be deployed to unleash the potentials of plant genetic resources for food and agriculture. We highlight some aspects of the work of the Food and Agriculture Organization of the United Nations in this regard. Of particular significance is the International Treaty on Plant Genetic Resources for Food and Agriculture that is devoted to supporting the conservation and use of these resources. We also highlight the work of the multi-stakeholder platform, the Global Partnership Initiative for Plant Breeding Capacity Building, which adopts a multiplicity of approaches in enhancing capacities for translating the potentials of plant genetic resources into improved productivities on farmers' fields. We discuss on-going activities aimed at increasing the use of non-adapted genetic materials in crop improvement through pre-breeding especially the newly launched global platform for promoting public-private partnerships in this new discipline. Perspectives on future activities are also shared.

# PLANT DIVERSITY CONSERVATION IN TURKEY

**Ayfer TAN**

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Turkey is one of the richest countries in terms of plant diversity with over 11000 species and 33% of which are endemic to the country. Being meeting place of three phytogeographical regions; center of origin and center of diversity of many crop/plant species; domestication center for many crops; having high species endemism; being a bridge between Europe and Asia, and has apparently served as a migration route for the penetration of other elements are the potential and the reasons for this richness. The 305 Key Biodiversity Areas of which thirteen sites are important on a regional scale and a total of 144 Important Plant Areas have been identified so far to provide a framework for assessing the effectiveness of conservation activities for plants. Turkey is also a significant country for the agricultural diversity and plant genetic resources. Two of the Vavilov's Center of Origin, The Near Eastern and Mediterranean Centers, extend into Turkey. This, of course, indicates that Turkey is the one of the Center of Origin and/or Center of Diversity of several crop plants. As being micro gene center of several crop species increase the Turkey's importance incrementally. Concerns about the genetic erosion of crop genetic resources become an important part of national policies and international treaties for the immediate conservation and protection of plant diversity. Turkey is one of the pioneer country take action for the protection and conservation of plant and crop diversity *in situ* and *ex situ*. Since 1964 survey, collection, conservation, evaluation and utilization of plant genetic resources (landraces, the wild relatives of these varieties and wild species with economically important plant species) of Turkey were conducted with coordination of Aegean Agricultural Research Institute within the framework of National Plant Diversity and Genetic Resources Program. The National Program involves the researches on *ex situ, in situ* and on-farm conservation and sustainable utilization of plant genetic resources and related aspects of socio-economy, ethno-botany with various projects.

# BREEDING OILSEEDS FOR BIOENERGY OR FOOD PRODUCTION

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The vegetable oil derived from oil plants, incl. oilseeds such as oilseed rape (OSR) or sunflower, is used for different purposes: for human and animal nutrition, for the manufacture of oleochemicals and lubricants, and for the production of fuels such as biodiesel (plant methyl esters). Furthermore, the by-products of oil processing can be used as a valuable feedstuff and component of compound feed for farm animals such as cattle, pigs and poultry. Major components of the feed are derived from cereals and maize as well as oil and protein crops such soybean and OSR. The harvest yield and product quality of major crop plants has been greatly enhanced by genetic amelioration (e.g. using heterosis), targeted breeding (e.g developing F1 hybrids) and optimized cultivation practices. The meal obtained from soybean or oilseed rape fabricated after oil extraction, contains a high-quality protein for livestock feeding. However, in comparison to soybean the meal from OSR includes higher amounts of anti-nutritive compounds, such as glucosinolates, phenolic acids and indigestible fibres. Breeding efforts with respect to meal quality therefore aim at reducing such components, while increasing the content of valuable ingredients such as protein and essential amino acids. It has been shown that OSR genotypes show a large variation for the contents of valuable and anti-nutritive compounds which can be exploited for improving the feeding value of meal and cake by breeding.

Continuous selection for high performance, incl. disease and stress resistance, superior quality and high yield, tends to limit the genetic diversity. However, advances in biotechnology and molecular breeding allow the identification and transfer of genomic sequences and genes from related species into crops to broaden the genetic variation and create new genotypes with improved traits. While traditional breeding mainly relied on phenotypic data from evaluation in several environments plus pedigree information as a basis for selection and recombination, marker assisted selection (MAS) uses molecular markers linked to genes or quantitative trait loci (QTL). In addition, genomic selection (GS) is a new approach for improving quantitative traits in large breeding populations that uses whole-genome molecular markers (high density, high-through-put). Beyond that, genomic prediction combines marker data with phenotypic and pedigree data to increase the accuracy of predicting genotypic values for breeding. This review presents an overview on the state of breeding and production of major oil crops with a focus on Europe. Examples from OSR and other oilseeds will be used to illustrate key breeding aims for the production of high-quality vegetable oil and feedstuffs. Emphasis will be placed on i) approaches to enhance seed yield, e.g. by exploiting heterosis, ii) improving the value of oil and meal (protein), and iii) combining conflictive goals such as outstanding yield and quality with better disease or pest resistance. It is demonstrated that both the amount and composition of valuable seed components from major crop plants can be substantially improved by knowledge-based breeding.

# POTENTIAL AND FUTURE OF NOVEL MOLECULAR BREEDING TECHNIQUES IN PRACTICAL PLANT BREEDING

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Plant breeding is a very innovative profession. New varieties are released at an increasing pace and new technologies are used to improve the efficiency and speed by which outstanding varieties can be made. Genetic modification is one of the most powerful techniques but raises concerns in many parts of the world. Nevertheless the technology is deployed in a number of major agricultural crops like maize, soybean and cotton. Because of the required testing and legislation to be allowed to grow GM crops the technique seems not really an option for many vegetable and horticultural crops. The last few years new technologies have emerged which by definition should be considered as GM techniques but where it is difficult to show in the final product that indeed recombinant DNA techniques have been used. These techniques are in different parts of the world under investigation to see whether they should fall under existing GM rules, whether they could be exempted or whether new rules should be designed. Among these techniques are grafting of GM plants on non-GM plants, VIGS, directed mutagenesis and cisgenesis to name just a few. In potato we are working extensively on cisgenesis as a much faster technique to introgress resistance genes against *Phytophthora infestans* from wild Solanum species into cultivated potato. The power of cisgenesis is that *R*-genes which can be introgressed from wild species by crossing, sometimes taking over 50 years, now can be introgressed in only two to five years thus increasing the speed by which resistant varieties can be developed. Progress in this field will be reported.

# MEETING THE CHALLENGES OF GLOBAL CLIMATE CHANGE AND FOOD SECURITY THROUGH INNOVATIVE MAIZE RESEARCH

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Developing and deploying climate resilient maize germplasm is one of the topmost priorities for international agricultural research-for-development. Since 1975, CIMMYT has been intensively engaged in breeding for drought and low nitrogen stress tolerance, optimizing procedures for undertaking managed stress trials, and developing and disseminating high-yielding and stress tolerant maize varieties, especially for the tropical and subtropical regions, in partnerships with an array of public and private organizations. Mainstreaming heat stress tolerance in elite maize germplasm has emerged as an important breeding objective. Recent studies by CIMMYT Global Maize Program, in collaboration with partners worldwide, indicated that current tropical/subtropical maize germplasm developed for drought tolerance may not perform well under drought stress at elevated temperatures. Nevertheless, a few inbred lines with high levels of tolerance to drought as well as combined drought and heat stress, most notably La Posta Sequia C7-F64-2-6-2-2 and DTPYC9-F46-1-2-1-2, were identified and are presently being utilized in developing elite germplasm with tolerance to combined drought and heat stress in sub-Saharan Africa and Asia. Recent findings by CIMMYT that tolerance to combined drought and heat stress in maize was genetically distinct from tolerance to individual stresses, and tolerance to either stress alone did not confer tolerance to combined drought and heat stress, has major implications in breeding heat stress resilient maize cultivars. New plant breeding strategies that utilize high-density genotyping based on next-generation DNA sequencing technology, coupled with precision phenotyping, genomic selection (GS) and doubled haploid (DH) technology, could significantly accelerate the development of stress-resilient maize varieties. Genome-wide association studies (GWAS), implemented through high throughput genotyping and precision phenotyping, has emerged as a powerful strategy for dissecting complex traits and identifying superior alleles contributing to improved phenotypes in maize. CIMMYT-GMP is intensively engaged in identification of genomic regions associated with an array of important adaptive traits, especially abiotic stress tolerance and disease resistance. In summary, accelerated development and deployment of climate resilient maize varieties requires: (a) carefully undertaken field-based phenotyping in several relevant sites as well as under technically demanding managed-stress screens; (b) better understanding of the genetic architecture of heat stress tolerance as well as tolerance to combined drought and heat stresses; (c) utilization of modern breeding tools/strategies, including genome-wide association studies, genomic selection, and doubled haploid (DH) technology for rapid development of improved products; and (e) intensive multi-institutional efforts to ensure that the products (climate resilient varieties) are effectively scaled-up and reach the climate change vulnerable farming communities.

# HISTORY AND CURRENT STATUS OF GENOME SEQUENCING

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The field of genome sequencing began with the Human Genome Project back in 1990 with a of sequencing the 3 billion base pairs. However this task seemed almost insurmountable, especially at a very high level of accuracy. The goal was to achieve an error rate of less than one mistake in every 10,000 bases. Scientists realised that the immensity of the task would require the development of new technologies. Probably the most important among these technologies were machines able to perform DNA sequencing in a fully automated fashion. In addition to automated sequencing, this also spawned a whole range of high-throughput technologies, including colony pickers, microarray spotters, and other equipment etc.. The sequencing of smaller genomes such as those of baker's yeast and the roundworm were seen as a warm-up to the much larger task. These efforts also laid the foundation for the field of comparative genomics. In this presentation we will discuss the plant genome sequencing and current applications with the emphasis of wheat.

# USING GENOMIC SELECTION TO ACCELERATE THE RATE OF GENETIC IMPROVEMENT IN CASSAVA AND WHEAT BREEDING

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Selectingfor complex traits, such as yield or multigenic disease resistance, often requires resource intensive field based phenotypic selection. This talk will present Genomic Selection (GS) as a plant breeding method that uses statistical modeling to predict plant performance, before it is field-tested. Case studies to illustrate the application of GS to crop improvement will focus on cassava, and also wheat. GS uses genome widemolecular markersto capture the effect multiple loci simultaneously. Novel statistical methods are then used to create a prediction modelthat can predict plant performance on genotypic data alone. Although phenotypic data is essential to “train” and update GS prediction models to accurately predict field performance, GS removes the need for field-testingrequired for selection, instead relying on Genomic Estimated Breeding Values as selection criteria.This dramatic reduction in breeding cycles has potential to significantly reduce the time and cost associated with improvement of long generation crops such as cassava and wheat, especially for quantitative traits. Though still a newcomer to the plant breeding toolbox, GS has potential to revolutionize crop improvement, ushering in dramatic increases in efficiency and genetic gain.

# GENETIC RESOURCES FOR PLANT BREEDING: PAST, PRESENT AND FUTURE

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Nikolai Vavilov was the first scientist to recognize the utmost importance for the humanity and potential value of world-wide collecting of crop seed, including crop wild relatives, and their conservation in viable conditions. Later his views were shaped into an international scientific concept, while his activities in building up seed collections served as a model.It was Vavilov who showed to the world's scientific community that the vast diversity of genes in populations of wild and weedy species, landraces and improved cultivars is a treasury of promising breeding sources. By 1901, the collection of cultivated plants in Russia consisted of 301 accessions; in 2012, it has grown to more than 324,000. In the past 90 years, the Vavilov Institute organized and implemented 1558 collecting missions over the ex-USSR territories and 282 to foreign countries.  At present, there are 1750 plant genebanks over the world. Their holdings amount to 7.3 million plant accessions (FAO, 2010), with more than 1.84 million (24.7%) in the five leading national genebanks (USA, China, India, Russia and Japan). The modern algorithm of crop collecting management comprises the following key components: analysis and assessment of the global plant genetic diversity in nature and in genebanks; systematic inventorying (revision) and assessment of the collected genetic diversity in a national genebank; identification of "gaps" in the genebank's holdings; systematic analysis of national breeding programmes, identification and prognostication of their demands for genetic sources; evaluation of genetic erosion and genetic vulnerability of the accessions for economically important crops and their wild relatives. The ongoing globalization and international integration processes, rapid development of science and technology, introduction of novel technologies, acceleration of genetic erosion, climate change, and escalation of inter-country competition on the world market call for the need to solve common global problems by cooperative and most effective efforts. The main strategic task for the future is to work out governmental and non-governmental measures aimed at abating negative tendencies and securing the most optimal conditions for safe *ex situ* and *in situ* conservation of plant genetic resources, promotion of fundamental and applied research in the sphere of agricultural biodiversity, avoidance of duplication in such activities, increasing the capacity in collecting valuable genetic diversity, and enrichment of national germplasm holdings through targeted collecting missions all over the world.

# MOLECULAR TOOLS AND TECHNOLOGIES FOR NEXT GENERATION PLANT BREEDING

Mehmet Cakir

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Pre-breeding research is the essential driver of crop productivity and genetic gain in breeding programs. Especially private breeding companies are investing into trait-based genetic improvement programs substantially, through the application of advanced technologies. With the discovery of new methodologies and technologies, coupled with the use of SNP markers, genomic assisted-breeding is now possible with the use of approaches such as MARS, MABS, NAM, and GWAS. Plant breeders are developing whole genome-based breeding schemes through marker-based haplotype selection and genomic selection of the target traits. The availability of genomic concepts and tools coupled with the next generation sequencing (NGS) technologies are providing new opportunities to breeders to re-design their breeding strategies. Advances in the NGS has driven the cost down low enough that direct sequencing approaches are being used to generate high density genetic maps with SNP markers, which allows the detection of both major and minor genes controlling the monogenic and multigenic traits. Therefore it is possible to apply whole genome targeted breeding for a number of traits thorugh HTP multiplexing of multiple traits for achieving higher genetic gains in the breeding programs. The potential bottleneck is expected to be the data analysis and processing, including interpretation of the data. The presentation will also outline the strategies and applications for marker-assisted breeding for multiple biotic and abiotic traits in our pre-breeding program.

# PATENTS – A FRUITFUL ALTERNATIVE FOR PLANT BREEDERS' RIGHTS?

Tom Wittop Koning

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Plant Breeders' Rights give protection for a single plant variety. Breeders have to allow others to use their precious traits for further breeding (the breeders' exemption) with the risk that others develop an even better variety. Patents however do not have this drawback. Further, patents are not limited to a single variety but may encompass several varieties or even a plurality of species. Although this could sound like breeders heaven, the way to  a patent is not a paved road, in particular not for plant breeders. It is for example not possible to obtain a patent for biological methods like classical breeding. At present, a very hot topic at the European Patent Office is whether a plant, obtained by such classical breeding is patentable. If yes, the patent system would give breeders enormous possibilities to protect their crown jewels without having to allow others to touch them.  In the presentation, a short introduction in the patent system is given, and the question what is patentable in the plant world will be discussed. Recent case law of the European Patent Office will be presented to discuss the latest developments of European patent law interpretation on plants and breeding, as well as the impact it will have on the breeder's profession.

# COMMUNITY PLANT VARIETY OFFICE: AN OVERVIEW OF THE EUROPEAN PLANT VARIETY PROTECTION SYSTEM AND CO-OPERATION ACTIVITIES OUTSIDE THE EU

Francesco Mattina

Head of the Legal Unit of the CPVO

In 1994 the EU decided to create a regional system for the intellectual protection of new plant varieties. By one application by a breeder to the Community Plant Variety Office protection can be granted throughout the European Union now consisting of 28 Member States. The system is based on the 1991 UPOV Convention and has become the biggest system in the world in terms of numbers of applications received per year. In parallel to the EU system national plant variety protection systems exist. The co-existence of national and a regional system works very well and the Member States and the Community plant variety offices co-operate on technical level, denominations and IT to give some examples. The first part of the presentation is devoted to explain how the regional system of plant variety rights is set up and applied, including the basics on how rights can be enforced. Statistics, such as the number of applications received and titles granted will be shown. The second part of the presentation will highlight some aspects on how the CPVO works with countries outside the European Union. For instance, the CPVO is involved in a project together with candidate countries, such as Turkey, for the purpose of preparing for the time when the countries will join the EU.

# THE LATEST DEVELOPMENTS IN UPOV

Benjamin Rivoire

Senior Program Officer, UPOV (International Union for the Protection of New Varieties of Plants)

The International Union for the Protection of New Varieties of Plants (UPOV) currently has 71 members, the most recent being Serbia, which became a member on January 5, 2013. An update on the status UPOV will be provided. A seminar on essentially derived varieties (EDVs), has been held in Geneva on October 22, 2013, to consider technical and legal views on EDVs and the possible impact on breeding and agriculture, existing experience in relation to EDVs, and the possible role of future UPOV guidance on EDVs in cases before the courts. A report of the outcome of that meeting will be made. UPOV has published the “Trilogy”, which combines the proceedings of the “UPOV Seminar on Plant Variety Protection and Technology Transfer: the Benefits of Public-Private Partnership”, the “Symposium on Plant Breeding for the Future” and the “Symposium on the benefits of plant variety protection for farmers and growers” (see http://www.upov.int/meetings/en/topic.jsp?group_id=73). A number of improvements have been made to the Plant Variety Database (PLUTO database), including new features for searching variety denominations and the development of an online tutorial (https://www3.wipo.int/pluto/user/video/index.html). UPOV is currently developing a prototype electronic form that will contain all the items required for an application with the participating members of the Union. The prototype electronic form will be initially developed for lettuce, potato, rose and apple. Information will be provided on the forthcoming launch of the advanced distance learning course DL-305 “Examination of Applications for Plant Breeders’ Rights”.

# INTELLECTUAL PROPERTY PROTECTION FOR PLANT INNOVATIONS

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In the past 25 years there has been a major shift in production and trade in the sector of horticulture. As a result of globalization and industrialization, a range of new countries have established themselves as important players on the horticultural market, increasingly replacing the traditional producers of the ornamentals and fruits. Furthermore, the latest groundbreaking developments in biotechnology and breeding techniques have strongly contributed to a continuous acceleration of innovation in the sector. In regard to these facts, the systems of Intellectual Property Protection for plant innovation are facing major challenges and are forced to keep pace with the developments of the market. The synchronization of national laws, the accession of all the UPOV members at least to the Convention of 1991, the elimination of the major weaknesses and the expansion of the scope of protection under UPOV 1991 are only some of the necessary steps which have to be undertaken towards the establishment of a strong IP Protection for ornamental and fruit varieties. This speech presents a comprehensive yet brief overview of the existing systems of IP Protection for plant innovation, such systems as Plant Variety Rights, Patents and Plant Patents, followed by a more detailed analysis of the UPOV PBR system. Topics like *minimum distance* between varieties and *Essentially Derived Varieties* are explained as well as the terms *propagation material* and *harvested material* and the necessity of their firm definition in the wording of the acting laws is emphasized.

**Keywords:** Plant Variety Rights, Patents, Plant Patents, Plant Breeder Rights

## FIELD CROPS PAPER LIST

1---ADAPTIVE SELECTIONS OF SPRING-SOWN WHEAT IN THE CONDITIONS OF THE WEST SIBERIAN REGION ON THE BASIS OF USE EXPERIMENTA

2----BREEDING OF DENSITY-INDEPENDENT CULTIVARS IS A VIABLE OPTION TO COMBAT CLIMATE CHANGES – A CASE STUDY FOR MAIZE AND WH

3----DIRECT REGENERATION FROM LEAF DISC EXPLANTS OF PEANUT GRAFTING IMPROVES SURVIVAL RATE

4---- FREEZING TOLERANCE IN CEREALS BREEDING, AGRONOMICAL, PHENOLOGICAL, PHYSIOLOGICAL AND PROTEOME ANALYSIS

5---- FUNCTIONAL GENOMICS AND TRANSCRIPTOMICS OF ABIOTIC STRESSES AND THEIR APPLICATIONS ON RICE BREEDING

6----GENEALOGICAL ANALYSIS OF RESISTANCE TO PRE-HARVEST SPROUTING IN THE NORTH-AMERICAN SPRING WHEAT VARIETIES

7---- MAPPING GENES FOR NORTHERN CORN LEAF BLIGHT IN MAIZE

8---- METHOD OF ECOLOGICAL BREEDING AN EXAMPLE PROGRAMM “ECADA”

9---OCCURRENCE OF SEPTORIA LEAF BLOTCH IN ALGERIA AND ASSES OF WHEAT RESISTANCE

10---SELECTION OF SPRING WHEAT HARD ON THE QUALITY AND SALT TOLERANCE

11----STUDY OF THE FUNCTIONAL STATE OF THE CELL GENOME OF AGRICULTURAL CROPS AS RELATED WITH HETEROSIS

12----ANALYSIS OF DIALLEL CROSS FOR SOME QUANTITATIVE TRAITS IN COMMON BEAN (PHASEOLUS VULGARIS L.)

13---ASSESSING THE SUITABILITY OF SPECTRAL REFLECTANCE INDICES TO SCREEN CONTRASTING WHEAT GENOTYPES FOR DROUGHT TOLERANCE

14---ASSESSING THE SUITABILITY OF VARIOUS MORPHO-PHYSIOLOGICAL TRAITS TO SCREEN WHEAT GENOTYPES FOR DROUGHT TOLERANCE

15---ASSESSMENT OF GENETIC DIVERSITY AMONG POPULATIONS OF ONOBRYCHIS. CORNUTA USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS

16---THE DETERMINATION OF MORPHOLOGICAL AND AGRONOMIC PROPERTIES OF SOME CULTURE AND WILD PEA GENOTYPES IN K.MARAŞ CONDITIONS

17---A NEW APPROACH FOR PLANT BREEDERS PROTEOMIC STUDIES

18---CHICKPEA (CICER ARIETINUM L.) IN VITRO MICROPROPAGATION

19---CLASSIFICATION OF WHEAT VARIETIES WITH BIOCHEMICAL PARAMETERS AND RAPD MARKERS

20---CORRELATION AND PATH COEFFICIENT ANALYSIS FOR PROTEIN YIELD IN CONFECTIONARY

SUNFLOWER

21---CREATING INITIAL FORMS OF SPRING WHEAT IN RELATION TO CLIMATE CHANGE

22---CREATION OF NEW VARIETIES OF PERENNIAL GRASSES ON THE BASIS OF COMPLEX HYBRID POPULATIONS IN NORTHERN KAZAKHSTAN

23---DEVELOPMENT OF NEW VARIETIES OF SAINFOIN WITH HIGH NITROGEN-FIXING POTENTIAL

24---ENCAPSULATED SOMATIC EMBRYOS AND SHOOT TIPS OF RAPESEED

25----EVALUATION OF DROUGHT TOLERANCE IN BREAD WHEAT GENOTYPES USING MORPHO-PHYSIOLOGICAL TRAITS

26---EVALUATION OF DROUGHT TOLERANCEIN CUMIN(CUMINUMCYMINUML.)ECOTYPESIN FIELD CONDITION

27----EXPLOITATION OF HETEROSIS - AN APPROACH FOR ENHANCING DROUGHT TOLERANCE AND YIELD IN POSTRAINY SEASON SORGHUM

28---FEATURES OF GAS EXCHANGE DAILY DYNAMICS IN VARIOUS WHEAT VARIETIES UNDER DROUGHT CONDITIONS

29----FLAG LEAF REFLECTANCE EFFICIENCY AS INDICATOR FOR DROUGHT TOLERANCE IN DURUM WHEAT

30---FLAG LEAF SENESCENCE IN DURUM WHEAT AS SELECTION INDEX FOR GRAIN YIELD UNDER DROUGHT CONDITIONS

31----GENETIC AND QTL ANALYSIS FOR AGRONOMIC TRAITS IN A TUNISIAN DOUBLED

32----IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES UNDER LOW TEMPERATURE IN WINTER WHEAT

33---IDENTIFICATION OF WHEAT BREEDING MATERIAL RESISTANT TO LEAF RUST PUCCINIA RECONDITA F. SP. TRITICI

34---IMPACT ENVIRONMENTAL OF GROWING ON VIABILITY OF SEEDS

35---INFLUENCE OF ENVIRONMENTS ON THE AMOUNT AND STABILITY OF GRAIN YIELD IN THE MODERN WINTER WHEAT CULTIVARS -

36----INOCULATION EFFECT OF ENDOPHYTIC BACTERIUM (BACILLUS SP.) ISOLATED FROM WILD RICE

37---MAJOR CHANGES IN PEROXIDASES SYSTEM UNDER COLD ACCLIMATION IN MEDICAGO

38---MOLECULAR CHARACTERIZATION OF FINGER MILLET (ELESUINE CORACANA L.) GENOTYPES USING INTER SIMPLE SEQUENCE REPEAT (ISSR) MARKERS

39---OBTAINING MAIZE (ZEA MAYS L.) LINES UTILIZING BY DOUBLED HAPLOID TECHNOLOGY AGRONOMIC AND MOLECULAR CHARACTERIZATION.

40---PARTICIPATORY DEVELOPMENT AND SELECTION OF A NEW SET OF CLIMBING BEAN GENOTYPES WITH MORE ACCEPTABLE SEED TYPES AND RESISTANCE T

41---PARTICIPATORY EVOLUTIONARY CEREAL BREEDING UNDER RAINFED AND IRRIGATED CONDITIONS OF IRAN

42----PROTEOMICS ANALYSIS IN SOYBEAN ROOT INOCULATED WITH COMPATIBLE BACTERIA UNDER

43---RELATIONSHIP OF MORPHOLOGICAL TRAITS WITH RAPD AND ISSR MARKERS IN SUGAR BEET

44---RESEARCH AND ESTIMATION OF MORPH PHYSIOLOGICAL TRAITS IN SELECTION OF WHEAT

45---SCREENING OF TWO RICE GENOTYPES (AMBER33 AND AMBER BAGHDAD) FOR DROUGHT TOLERANCE USING CELL SUSPENSION CULTURES AND PLATING TECHN

46---SOYBEAN YIELD AND SEED GERMINATION OF POTENCIAL GENOTYPES FOR RESISTANCE TO STINK BUG COMPLEX

47---THE ASSESSMENT OF PLANT PROPERTIES IN IRANIAN FENNELS FROM PERSPECTIVE OF CLIMATE EFFECTS

48---THE EFFECT OF SALINITY ON SEED GERMINATION AND SEEDLING GROWTH IN CUMIN(CUMINUMCYMINUML.)

49----USE OF PHYTOPATHOGENIC FUNGI TO PROTECT CEREALS AGAINST WEEDS

50-VARIABILITY, HERITABILITY AND ASSOCIATION ANALYSIS FOR YIELD, YIELD COMPONENTS AND KERNEL QUALITY IN SWEET CORN

51----BREEDING OF PEANUT (ARACHIS HYPOGEAE L.) VARIETY (OSMANIYE-2005) TOLERANT TO IRON DEFICIENCY CHLOROSIS

52---BREEDING PROGRESS OF SPRING WHEAT IN WESTERN SIBERIA AND THE PROTECTION OF BREEDING IN RUSSIA

53----BREEDING WHEAT TO ENHANCE BIOACTIVE COMPOUNDS

54----COMBINING ABILITY THROUGH LINES × TESTER ANALYSIS AND HERITABILITY STUDIES IN UPLAND COTTON PRESENTATION

55---MUTANT VARIETIES OF SOYBEAN, TOBACCO, CHICKPEAS AND THEIR DEVELOPED CHARACTERISTICS

56----PROSPECTS OF ASSOCIATION MAPPING IN COTTON

57---CEREAL CROPS BREEDING FOR APHIDS RESISTANCE

58---CLASSIFICATION OF WHEAT VARIETIES WITH BIOCHEMICAL PARAMETERS AND RAPD MARKERS

59---DETECTION OF POLYMORPHISMS AMONG NAKED BARLEY USING AGRO-MORPHOLOGI

HORDEIN RAPD AND ISSR MARKERS

60---ESTIMATION OF NATURE AND MAGNITUDE OF HETEROSIS AND COMBINING ABILITY OF IMPORTANT TRAITS IN MAIZE (ZEA MAYS L.)

61---EVALUATION OF RISE, MAIZE, MILLET AND SORGHUM BY GRAIN AMYLOSE CONTENT FOR BREEDING PROGRAM

62---FACULTATIVE BREAD WHEAT VARIETIES AND INTERNATIONAL COOPERATION IN KYRGYZSTAN

63---FREE PROLINE FOR CEREALS BREEDING ON THE GENERAL ADAPTABILITY

64---GENETIC CONTROL OF SCALD RESISTANCE IN BARLEY LOCAL SAMPLES

65---GENETIC DIVERGENCE ANALYSIS ON SOME BREAD WHEAT GENOTYPES GROWN IN ETHIOPIA

66---GENETIC STRUCTURE OF DURUM WHEAT POPULATIONS BY ISSR MARKERS

67----GENETIC VARIATION OF MINERAL ELEMENT CONTENTS IN GRAIN OF MOROCCAN DURUM WHEAT GENOTYPES

68---GENETICAL DETERMINATION ON OF THE SPRING TYPE OF DEVELOPMENT IN WHEAT TRITICUM AESTIVUM L.

69---GREENBUG RESISTANCE IN BARLEY ACCESSIONS FROM ASIA

70---HETEROSIS STUDIES FOR SOME AGRONOMICAL TRAITS IN OATS

71---IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES UNDER LOW TEMPERATURE IN WINTER WHEAT

72---LENTIL SINGLE-PLANT PROGENIES SELECTED IN THE ABSENCE OF COMPETITION EXHIBIT QUANTITATIVE RATHER THAN QUALITATIVE G×E INTER

73---MEASURE OF STABILITY AND JOINT REGRESSION ANALYSIS FOR YIELD AND YIELD COMPONENTS IN 22 GENOTYPES OF GROUNDNUT

74---POSTULATION FOR ADULT PLANT RESISTANCE GENES IN WHEAT CULTIVARS TO LEAF RUST

75----POWDERY MILDEW RESISTANCE IN WHEAT (NORTH – WEST REGION OF RUSSIA)

76---SELECTION OF INITIAL MATERIAL OF CEREALS RESISTANT TO FUSARIUM FUNGI

77---SELECTION OF INITIAL MATERIAL OF WHEATS RESISTANT TO THE MOST HARMFUL DISEASES

78---SELECTION OF INITIAL WHEAT MATERIAL FOR RESIST TO S NODORUM AND S TRITICI FROM DIFFE GENET COLLECTI

79---SPACE-PLANTED RATHER THAN DENSELY SEEDED CONDITION PREDICTS BETTER CROP YIELD OF GENETICALLY HOMOGENEOUS MAIZE LINES

80---BIOLOGICAL POTENTIAL OF FACULTATIVE WHEAT IN KAZAKHSTAN CONDITIONS (BIOMASS

PRODUCTIVITY, IRON AND ZINC CONTENT IN THE GRAIN)

81----VALIDATION AND DEPLOYMENT OF RESISTANCE-LINKED SCAR MOLEC MA FOR MA BREEDING OF THE COMMON BEAN

82---DEVELOPMENT OF SUNFLOWER PARENTAL LINES WITH BROOMRAPE (OROBANCHE SPP.) RESISTANT AND HIGH OLEIC ACID CONT

83---AMYLOSE CONTENT IN WHEAT, BARLEY AND TRITICALE BREEDING ON THE GRAIN QUALITY

84---APPLICATION OF EMBRYO CULTURE METHOD IN COMBINATION WITH GAMMA IRRADIATION IN SUNFLOWER

85---ASSESSMENT GENOTYPE ENVIRONMENT INTERACTION IN BARLEY CULTIVARS WITH REGRESSION METHOD

86---BIO-PHYSIOCHEMICAL AND PHENOLOGICAL RESPONSES OF FABA BEAN (VICIA FABA L.) TO INDUCED WATER DEFICIT CONDITIONS

87---BREEDING OF MAIZE HYBRIDS ON THE PRODUCTIVITY AND QUALITY OF GRAIN IN THE SOUTH-EAST OF KAZAKHSTAN

88---CALLOGENESIS AND STRAINS SELECTION IN VITRO IN POTENTILLA RECTA L. SUBSP. LACINIOSA (WALDST. ET KIT. EX NESTLER) NYMAN

89---CHLOROPHYLL CONTENT OF THE CULTIVATED LENTIL (LENS CULINARIS MEDIK.) IN COMPARISON TO WILD SPECIES

90---COMBINING ABILITY AND HETEROSIS OF ZP MAIZE INBRED LINES FOR GRAIN YIELD

91----COMPARISON OF CHEMICAL COMPOSITION OF TWO DURUM WHEAT (TRITICUM DURUM L.) AND BREAD WHEAT (TRITICUM AESTIVUM L.) GERM OILS

92---DENSITY AND PLANT ARRANGEMENT ON CALENDULA OFFICINALIS L. YIELD

93---DETERMINATION OF STAY GREEN WITH NDVI IN THE WINTER WHEAT GENOTYPES UNDER STRESS CONDITIONS

94----DEVELOPMENT OF INITIAL MATERIAL OF SPRING AND WINTER WHEAT ON THE BASIS OF NEW SOURCES OF RESISTANCE TO LEAF AND STEM RUST

95---DIRECTIONS AND METHODS OF WHEAT AND TRITICALE BREEDING

96---DONOR OF COARSE-GRAINED WINTER RYE (SECALE CEREALE L.) LARGE-GRAINED

97---ECOLOGICAL VARIETY TRIALS OF CHICKPEA (CICER ARIETINUM L.)IN THE REGION OF ARID STEPPES IN AKMOLA OBLAST, NORTH KAZAKHSTAN

98---EVALUATION OF HYBRID MATERIAL, ORIGINATED FROM WILD ANNUAL SUNFLOWER SPECIES FOR RESISTANCE TO THE LEAVES PATHOGENS CAUSE GREY

99---EVALUATION OF THE SAFFLOWER (CARTHAMUS TINCTORIUS L.) CORE COLLECTION UNDER ECOLOGICAL CONDITIONS OF SAMSUN

100---GENETIC ANALYSIS OF FABE BEAN (VICIA FABA L.) INTER-VARIETAL CROSSES

101---GENETIC DIVERSITY ANALYSIS USING SSR MARKERS AS A TOOL FOR MORE EFFICIENT UTILIZATION OF MAIZE INBRED LINES

102----GENETIC PERFORMANCE OF VEGETATIVE TRAITS OF MPOB OIL PALM INTERSPECIFIC HYBRIDS

103---GLUTENIN SUBUNITS AND GLIADIN IN “KASIB” SPRING WHEAT IDENTIFICATION

104----IDENTIFICATION OF QTLS RELATED OF AGRONOMIC TRAITS IN RECOMBINANT INBRED LINES OF WHEAT (TRITICUM AESTIVUM L.)

105--- PRODUCTION OF PURPLE CONEFLOWER (ECHINACEA PURPUREA L.) THROUGH CELL SUSPENSION CULTURES

106----MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF FABA BEAN (VICIA FABA L.) GERMPLASM

107----ACCESSING NOVEL GENES FOR CHICKPEA IMPROVEMENT

108---ASSESSMENT OF GROAT NUTRITIONAL ASPECT OF NEW DEVELOPED OAT HEXAPLOID LINES THROUGH INTERSPECIFIC CROSS WITH TETRAPLOID OAT A. MURPHYI

109----DETERMINATION OF HERITABILITY AND GENE EFFECTS ON QUANTITATIVE TRAITS IN RICE GENOTYPES

110---DEVELOPMENT OF DOUBLE HAPLOID LINES BY IN VIVO HAPLOID TECHNIQUE IN HYBRID MAIZE BREEDING

111----DEVELOPMENT OF DROUGHT-TOLERANT VEGETATIVE (TRIPLOID) BERMUDAGRASS [CYNODON DACTYLON]

112----ENHANCING SPOT BLOTCH RESISTANCE IN WHEAT THROUGH INTROGRESSION OF QTLS USING MOLECULAR BACK CROSS BREEDING

113---GENETIC POTENTIAL OF WINTER WHEAT GRAIN QUALITY IN CENTRAL ASIA

114---WHEAT BREEDING PROGRAM IN SELGEN INC., PLANT BREEDING STATION UHRETICE

115----MODELS OF NEW VARIETIES OF SPRING BARLEY

116---MORPHOLOGICAL AND ELECTROPHORETICAL CHARACTERIZATION OF INBRED MAIZE LINES

117----PATHOGEN GUIDED RESISTANCE BREEDING BENEFITS AND PITFALLS

118----PROSPECTS OF ASSOCIATION MAPPING IN COTTON (GOSSYPIUMHIRSUTUM L.)

119----SELECTION OF PROMISING SAFFLOWER GENOTYPES UNDER CONTRASTED ENVIRONMENTAL CONDITIONS

120----THE PROBLEM OF CLIMATE WARMING AND THE OBJECTIVES OF SPRING SOFT WHEAT BREEDING IN WESTERN SIBERIA

121----USING DNA TECHNOLOGIES FOR DEVELOPING INBRED LINES AND HYBRIDS IN MAIZE

122---PARAMETRIC STABILITY ANALYSES FOR GRAIN YIELD OF BARLEY

123---PERFORMANCE OF MPOB NIGERIAN HIGH KERNEL OIL PALM GERMPLASM X AVROS PISIFERAS PROGENIES1

124---PHYSIOLOGICAL AND BIOCHEMICAL PARAMETERS AT SEEDLING STAGE AND GRAIN YIELD IN MAIZE UNDER WATER DEFICIT

125----PHYSIOLOGICAL RESPONSES AND RECOVERY POTENTIALS OF CULTIVATED AND WILD WHEAT SEEDLINGS EXPOSED TO HEAT STRESS

126---PREDICTION OF TRANSGRESSIVE SEGREGATION IN RECIPROCAL CROSSES OF THE CULTIVATED CHICKPEA

127----QTL ANALYSIS OF GRAIN YIELD AND YIELD -RELATED TRAITS USING RECOMBINANT INBRED LINES IN WHEAT UNDER DROUGHT STRESS

128----RELATIONSHIP BETWEEN TRANSGRESSIVE SEGREGATION AND GENETIC DISTANCE BASED ON AFLP MARKERS IN CICER SPECIES

129----SCREENING OF KENYA COMMERCIAL WHEAT VARIETIES FOR RESISTANCE TO THE EMERGING STRAINS OF STEM RUST RACE UG99

130---STUDY OF GXE INTERACTION OF TEN MOROCCAN GENOTYPE OF OAT

131---THE GRAIN ZN ACCUMULATION FOR SPRING WHEAT CULTIVARS AND REGIONS

132---THE POTENTIAL FOR RESISTANCE BREEDING IN THE GENUS HELIANTHUS AGAINST OROBANCHE CUMANA, FROM THE BIOCHEMICAL STANDPOINT

133---THE RESULTS OF COOPERATION OF CHELYABINSK SCIENTIFIC RESEARCH INSTITUTE AND CIMMYT ON SOFT SPRING WHEAT

134----THE RESULTS OF THE DIRECTED SELECTION FOR REDUCING THE HEIGHT OF WINTER RYE

135---THE SELECTION OF WINTER RYE (SECALE CEREALE L.) ON PLANT-BREEDING SELECTION AND EXPERIMENTAL STATION OF NOSIVKA

136---THE SHUTTLE BREEDING OUTCOMES OF KURGAN SCIENTIFIC AND RESEARCH INSTITUTE OF AGRICULTURE (KSRIA)

137---THE STUDY OF HEREDITY OF PHOTOSYNTHESIS AND DROUGHT RESISTANCE CHARACTERS OF WHEATS AND DETERMINATION OF THEIR DONOR CAPABLE GENOTYPES

138---THE STUDY OF RHIZOBIA SYMBIOSIS WITH BEAN AND ALFALFA GROWN UNDER SALT STRESS

139---THE UNIQUE MUTANTS OF BARLEY PRODUCED IN CONDITIONS OF PAMIR

140---TOWARDS AN UNDERSTANDING THE MOLECULAR NATURE OF SUNFLOWER FERTILITY RESTORATION GENES

141---UNDERSTANDING G×E INTERACTION AND ITS IMPACT ON OBTAINING BREEDING OBJECTIVE IN WHEAT GENOTYPES

142---UTILIZATION OF WEEDY RICE AS BREEDING MATERIALS TO IMPROVE CULTIVATED RICE YIELDS IN SRI LANKA

143---DETERMINATION OF STABILITY AND ADAPTATION ABILITY FOR SOME PROMISING COTTON GENOTYPES

144---DEVELOPING PEANUT (ARACHIS HYPOGAEA L.) LEAFSPOT RESISTANT CULTIVARS

145---DEVELOPMENT OF SOMACLONES WITH LOW ODAP CONTENT IN GRASSPEA (LATHYRUS SATIVUS L.)

146---DEVELOPMENTAL ACCUMULATION OF ODAP AT DIFFERENT GROWTH STAGES IN GRASSPEA (LATHYRUS SATIVUS L.)

147----GENOTYPES X ENVIRONMENT INTERACTION EFFECT ON  NUTRITIONAL QUALITY OF SORGHUM LINES IN INDONESIA

148----LINKAGE BETWEEN SR2 AND LM1 AND ITS EFFECT ON PHENOTYPIC EXPRESSION OF LESION MIMIC IN WHEAT

149----MARKER-ASSISTED IDENTIFICATION AND TRANSFERRING NEW RESISTANCE GENE FROM AEGILOPS SPELTOIDES TO BREAD WHEAT  OR

150----MOLECULAR MAPPING FOR GRAIN PROTEIN CONTENT IN A TRITICUM AESTIVUM AND TRITICUM SPELTA CROSS

151----OPTIMIZATION OF IN-VITRO CULTURE CONDITION FOR GENETIC TRANSFORMATION OF COTTON (GOSSYPIUM HIRSUTUM L)

152---PHENOTYPIC AND GENETIC IDENTITIES OF FINGER MILLET (ELEUSINE CORACANA (L.) GAERTN) LANDRACES IN NIGERIA

153----THE EFFECTS OF SEED PRIMING ON SEED YIELD İN CHICKPEA

154----YELLOW RUST RESISTANT, NEW IMPROVED WINTER WHEAT GENOTYPES FOR CENTRAL ASIA AND THE CAUCASUS

155-ASSOCIATION MAPPING FOR FIBER TRAITS AND DROUGHT TOLERANCE IN TURKISH COTTON GERMPLASM

156-BREEDING AND PERFORMANCE OF BATEM TATLI (SU) SWEET CORN HYBRID

157-BREEDING VALUE OF AN INITIAL MATERIAL OF WINTER WHEAT IN AZERBAIJAN

158---EFFICIENT SELECTION ON QUALITY TRAITS IN ALGERIAN DURUM WHEAT CULTIVARS

159----CANOPY DIAMETER AS SELECTION CRITERIA FOR YIELD IMPROVEMENT OF BAMBARA GROUNDNUT

160-CEREAL MIXTURES — SOURCE OF PROTEIN IN ANIMAL FODDER

161-COMPARATIVELY DETERMINATION OF AGRONOMIC PERFORMANCES OF STRAIN MEDICAGO

162----COMPARISON OF DIFFERENT LEAF TYPES OF CHICKPEA GENOTYPESFOR YIELD AND YIELD COMPONENTS

163-CURRENT STATUS OF DISEASES AND PEST MONITORING AND CEREAL GRAINS

164-CYTOLOGICAL STUDY OF THE EFFECTIVENESS OF SEEDLING LEAF NUMBER IN RAPESEED

165-DETERMINATION OF DURUM WHEAT GENOTYPES HAVING SUITABLE QUALITY TRAITS

166-DETERMINATION OF GRAIN MOISTURE CHANGES IN SOME CORN HYBRIDS IN KONYA ECOLOGICAL CONDITIONS

167-DETERMINATION OF INFECTION RATES OF EUROPEAN WHEAT STEM SAWFLY BREAD WHEAT CULTIVARS

168-DETERMINATION OF RELIABLE SELECTION CRITERIA FOR EARLY GENERATIONS IN POTATO BREEDING

169-DETERMINATION OF THERMOTOLERANCE IN TWO WHEAT VARIETIES BY PHOTOSYNTHETIC RESPONSES

170-EFFECTIVE SELECTION CRITERIA FOR ASSESSING DROUGHT STRESS TOLERANCE IN WINTER WHEAT (TRITICUM AESTIVUM L.)

171----EFFECTS OF SEED PRIMING ON GLUMED AND GLUMELESS BARLEY CULTIVARS

172-EFFECTS OF SEED PRIMING ON TURKISH COTTON CULTIVARS

173-ELABORATION OF MONITORING TOOLS FOR SUNFLOWER BREEDING

174-ESTIMATION OF HYBRID YIELD PERFORMANCE BY THE SELECTION OF HETEROTIC GROUPS ON DENT TYPE MAIZE INBRED LINES USING SSRS VEYA

175----AGRO-MORPHOLOGIC VARIATION IN A LARGE BARLEY GERMPLASM COLLECTION UNDER CENTRAL ANATOLIAN HIGHLANDS -THE FIRST YEAR (2005-06)

176-EVALUATION OF GRAIN YIELD AND SOME AGRICULTURAL CHARACTERS OF SOME BARLEY (HORDEUM VULGARE L.) GENOTYPES

177----EVALUATION OF GRAIN YIELD AND SOME PHYSIOLOGICAL AND AGRICULTURAL CHARACTERS IN BREAD WHEAT GENOTYPES

178-EVALUATION OF PROMISING SPRING BREAD WHEAT BREEDING LINES UNDER IRRIGATED MULTI-ENVIRONMENT CONDITIONS

179----FORAGE OAT BREEDING IN MOROCCO MOST ACHIEVEMENTS AND FUTURE CHALLENGES

180-GENES EXPRESSION ON SUNFLOWER MICROSPOREGENESIS

181-GENETIC ANALYSIS OF AGRONOMIC CHARACTERS OF SORGHUM UNDER ACID SOIL

CONDITION

182-GENETIC INTRASPECIFIC POLYMORPHISM ANALYSIS FOR THE ELABORATION OF MOLECULAR MARKERS AROMATIC PLANTS

183-GRAIN PROTEIN QUANTITY AND STABILITY FOR LATVIAN BARLEY VARIETIES

184----IDENTIFICATION OF NEW RUST RESISTANT SOURCES OF WHEAT BY MOLECULAR TOOLS AND FIELD EVALUATION

185-IMPACT OF OROBANCHE CUMANA WALLR. ON SUNFLOWER CULTIVARS DOC

186-INTROGRESSION OF RESISTANCE TO POWDERY MILDEW FROM T. TIMOPHEEVII INTO THE GENOME OF T. DURUM

187-INVESTIGATION OF SOME AGRICULTURAL TRAITS AND STABILITY OF THE BARLEY (HORDEUM VULGARE L.) GENOTYPES

188-MINING AND FUNCTIONAL CHARACTERIZATION OF SIMPLE SEQUENCE REPEATS IN GENES OF PUCCINIA TRITICINA

189-MONITORING OF DISTRIBUTION OF THE BASIC DISEASES AND BREEDING ON RESISTANCE TO THEM IN NORTHERN KAZAKHSTAN

190-MORPHOLOGICAL AND SEED YIELD CHARACTERISTICS OF ORCHARDGRASS ECOTYPES OF EASTERN ANATOLIA REGION

191-PARTICULARITIES OF SUNFLOWER – DOWNY MILDEW INTERACTION

192-PHONOLOGICAL, NUTRITIONAL AND MOLECULAR DIVERSITY INTRODUCED LENTIL GENOTYPES GROWN IN SAUDI ARABIA

193-QTL ANALYSIS OF GRAIN YIELD AND YIELD -RELATED TRAITS USING RECOMBINANT INBRED LINES IN WHEAT UNDER DROUGHT STRESS

194-RANDOM AMPLIFIED POLYMORPHIC DNA ANALYSIS OF PLANT GENETIC POLYMORPHISM

195----RESEARCH ON THE POSSIBILITIES OF CULTIVATION OF THE FODDER CROPS ON PASTURE AND MEADOW AREAS OF EASTERN ANATOLIA

196-SCREENING SUNFLOWER HYBRIDS FOR RESISTANCE TO BROOMRAPE (OROBANCHE CUMANA WALLR.) AND IMIDAZOLINONES (IMAZAMOX)

196---THE ALLELIC STATE IDENTIFICATION OF THE NON-RACE SPECIFIC DISEASE RESISTANCE LOCUS IN POLISSIA WINTER WHEAT

197-THE ANALYSIS OF YIELD STABILITY OF MAIZE HYBRIDS

198-THE COMPARISON OF ADAPTIVE CAPABILITY OF TWO WILD SPECIES OF ONOBRYCHIS PLANTS

199----E CONTRIBUTION OF ASHES OF WASTE OF THE PLANTS TO IN VITRO REGENERATION OF POTATO (SOLANUM TUBEROSUM L.)

200-THE DETERMINATION OF SOYBEAN GENOTYPES  ON KONYA ECOLOGICAL CONDITIONS FOR YIELD AND QUALITY

201----THE DEVELOPMENT RESISTANT MATERIAL TO YELLOW RUST AND STEM RUST BY USING ANTHER CULTURE IN WHEAT BREEDING PROGRAM

202-THE EFFECT OF DIFFERENT POLLEN DEVELOPMENT STAGES AND MEDIUM ON ANTHER CULTURE IN WHEAT HYBRID POPULATIONS

203----THE PROCESS WILD CROSSING ANALYSIS OF RYE WITH MAIZE BASED ON THE OBSERVATION OF CYTOLOGICAL POLLEN TUBES BEHAVIOR

204-THE SEARCH FOR MARKERS CONNECTED WITH GENES OF RESISTANCE TO POWDERY MILDEW IN WHEAT

205----YIELD AND YIELD COMPONENT PERFORMANCE, MORPHOLOGICAL AND QUALITY OF AROMATIK-1 RICE

206----ASSESSMENT OF PROTEIC POTENTIAL OF IMPROVED OAT HEXAPLOID LINES DERIVATIVE OF INTERSPECIFIC CROSSES WITH THE TETRAPLOID OAT SPECIES

207----MOLECULAR ANALYSIS OF FL TRANSITION IN SOYBEAN

208----CROSS-COMPATIBILITIES OF DURUM WHEAT WITH AEGILOPS TAUSCHII ACCESSIONS SCREENED UNDER WATER-DEFICIT STRESS

209----DETERMINATION OF THE CONVENIENT METHOD TO BE USED IN TESTING COLD HARDINESS IN SOME CEREAL GENOTYPES

210---EFFECTS OF SALICYLIC ACID AND GA3 PRECONDITIONING TREATMENTS ON REGENERATION FROM COTYLEDON EXPLANT OF CV. KARAELCI

211----GENETIC ANALYSIS AND RESPONSE TO SELECTION OF SOME PHYSIOLOGICAL CHARACTERS IN RELATION TO PRODUCTIVITY IN BREAD WHEAT UNDER SANDY SOIL CONDITIONS

212----GENETIC RESILIENCE IN WHEAT FOR TOLERANCE TO HEAT STRESS IN RELATION TO CLIMATE CHANGE

213- ---IN VITRO CULTURE USE FOR DURUM WHEAT (TRITICUM DURUM DESF.) REGENERANT PRODUCTION UNDER SALT STRESS

214---INHERITANCE OF DROUGHT RESISTANCE, YIELD AND QUALITY PARAMETERS IN COTTON

215---MAIZE RESEARCHES IN TURKEY, YESTERDAY, TODAY AND TOMORROW

216---PEDIGREE AND SSR DATA ANALYSIS REVEAL DOMINANT PREVALENCE OF FEW PARENTS IN PEDIGREES OF PAKISTANI WHEAT VARIETIES

217----PRINCIPAL COMPONENT ANALYSIS (PCA) AND THE EXAMINATION DROUGHT INDICES OF DURUM WHEAT LINES

218----RUST OCCURRENCE, EPIDEMIC DEVELOPMENT AND RESISTANCE OF WHEAT CULTIVARS DEPLOYED IN NORTHWEST OF PAKISTAN

219----THE DETERMINATION OF GENETIC PROGRESS FOR YIELD AND QUALITY TRAITS AT WINTER BREAD WHEAT

220----YIELD STABILITY OF SOME BREAD WHEAT VARIETIES WHICH RELEASED DRY AREAS OF CENTRAL ANATOLIA

221----EFFECTS OF SALINITY STRESS ON WHEAT GRAIN QUALITY AND SCREENING FOR TOLERANCE BY MOLECULAR MARKERS

222---EFFECTS OF SALT STRESS (NACL) ON PLANT GROWTH AND YIELD OF RICE (ORYZA SATIVA L.) VARIETIES

223---ADAPTIVE CHANGES OF PHYSIOLOGICAL SIGNS OF WHEAT GENOTYPES UNDER SOIL DROUGHT CONDITIONS

224----AGRONOMIC PERFORMANCE OF SOYBEAN WITH RESISTANCE POTENTIAL TO STINK BUGS

225---AGRONOMY AND BREEDING OF RAPESEED (BRASSICA NAPUS L.) IN TURKEY

226---AN OUTLOOK TO A PRIVATE POTATO BREEDING PROGRAM IN TURKEY

227----BREEDING FOR WHEAT RUST DISEASES IN ALGERIA AND STRATEGIES FOR PATHOGENICITY REDUCTION

228----BREEDING STRATEGIES AND PROGRESS TOWARDS IMPROVEMENT OF YELLOW RUST AND STEM RUST RESISTANCES IN TAJIK WHEAT BREEDING PROGRAM

229---CAMELINA (CAMELINA SATIVA (L.) CRANTZ) BREEDING OPPORTUNITY IN TURKEY

230----CELL VIABILITY AND MEMBRANE FLUIDITY IN RELATION TO DROUGHT TOLERANCE OF WHEAT GENETIC OPTIONS FOR IMPROVEMENT

231---COMPUTATIONAL EXTRACTION AND COMPREHENSIVE MOTIF ANALYSIS OF EST BASED SSRS IN THREE DIFFERENT PUCCINIA SPECIES

232---DETERMINATION OF AGRICULTURAL CHARACTERS OF SOME SOYBEAN GENOTIPS AS A SECOND CROP UNDER CUKUROVA CONDITIONS

233---WINTER BARLEY BREEDING HISTORY OF TURKEY

234----MAPPING OF QUANTITATIVE TRAIT LOCI FOR GRAIN ZN CONCENTRATION IN WHEAT IN EASTERN GANGETIC PLAINS OF INDIA

235---OVER-EXPRESSION OF A SPECIFIC SOYBEAN GMGSTU4 ISOENZYME IMPROVES

236---MORPHOLOGICAL, PHYSIOLOGICAL AND METABOLOMIC RESPONSE OF TRANSGENIC TOBACCO PLANTS (N. TABACCUM L.) OVEREXPRESSING GMGSTU4 UNDER DROUGHT STRESS

237---MOLECULAR PATHOGENICITY OF WHEAT – FUSARIUM GRAMINEARUM INTERACTION

238---THE USE OF RELATIVE WATER CONTENT AND LEAF WATER POTENTIAL FOR THE SELECTION OF MAIZE INBRED LINES UNDER DROUGHT STRESS

239---SOLATION OF GST ISOENZYMES  FROM PHASEOLUS VULGARIS L. AND CHARACTERIZATION OF DETOXIFYING MECHANISM  UNDER BIOTIC AND ABIOTIC STRESS MADESIS

240---POTATO BREEDING IN THE CZECH REPUBLIC

241---BREEDING FOR GRAIN ZINC DENSITY IN TALL AND SEMI-DWARF INDIAN BREAD WHEAT VARIETIES

242---PLANT REGENERATION AND MICRO PROPAGATION STUDIES USING  TWO TURKISH BROAD BEAN CULTIVARS FOR BREEDING

243---OBTAINING NEW MAINTAINER LINES FROM CMS PLANTS WITH TRADITIONAL BREEDING METHODS IN SUNFLOWER

244---NEW WAY TO DEVELOP AN ECONOMIC HEALTHY FOOD BASED ON OATS EXPLOITATION IN MOROCCO

245---DETERMINATION OF YIELD AND AGRICULTURAL CHARACTERS OF SOME F6 SOYBEAN LINES AS A MAIN CROP UNDER  CUKUROVA REGION CONDITIONS

246---DETERMINATION OF HETEROTIC EFFECTS FOR SIGNIFICANT AGRONOMICAL AND TECHNOLOGICAL PLANT CHARACTERS IN ST 468 X DP 388 COTTON CROSS COMBINATION

247---S1 RECURRENT SELECTION METHOD IN THE POPULATION OF ADAPOP 11 SILAGE CORN

248---SAFFLOWER (CARTHAMUS TINCTORIUS L.) BREEDING ACTIVITIES AT TRAKYA AGRICULTURAL RESEARCH INSTITUTE

249---FAST AND EASILY APPLICABLE QUALITY PARAMETERS FOR SOFT WHEAT BREEDING

250----NEW SOURCES OF RESISTANCE TO THE COWPEA WEEVIL  CHICKPEA ACCESSIONS

251---POLYMORPHISM STUDY IN RILS CREATED BY TOSUNBEY X TAHIROVA 2000 CROSS

252---DEVELOPMENT OF COTTON LINES WITH SUPERIOR YIELD AND FIBER PROPERTIES THROUGH CROSSING OF PARTIAL INTERSPECIFIC LINES WITH COMMERCIAL CULTIVARS

253---RELATION OF COMPONENT CONTENT OF GLIADIN WITH BAKING QUALITY OF WHEAT GRAIN

254---EARLY SELECTION FOR HIGH SPIKE FERTILITY IN BREAD WHEAT

255---DETERMINATION OF YIELD PERFORMANCES AND STABILITY ANALYSIS OF SOME RICE CULTIVARS GROWN UNDER THE OSMANCIK CONDITIONS

256---MICROARRAY ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES UNDER WATER DEFICIT STRESS IN UPLAND COTTON

257---DETERMINATION OF GRAIN YIELD POTENIAL OF SINGLE, THREE-WAY AND DOUBLE CROSSES CORN

258---DETERMINATION OF CORRELATIONS BETWEEN GRAİN YİELD AND YIELD COMPONENTS OF SİNGLE, THREE WAY AND DOUBLE CROSSES CORN

259---VARIATION IN MORPHINE OF SIX TURKISH OPIUM POPPY (PAPAVER SOMNIFERUM L.) LINES

260---DETERMINATION OF HETEROSIS AND HETEROBELTIOSIS VALUES FOR YIELD AND YIELD COMPONENTS OF HOMOZYGOUS MAIZE INBRED LINES

261---DETERMINATION OF RESISTANCE OF SOME ADVANCE BREAD WHEAT LINES GENOTYPES TO COMMON BUNT (TILLETIA SPP.) DISEASES

262----DETERMINATION OF RESISTANCE OF SOME TURKISH BREAD WHEAT GENOTYPES TO YELLOW RUST AND STEM RUST

263---EFFECT OF GROWTH REGULATORS ON TISSUE CULTURE PARAMETERS IN RİCE

264---EFFECT OF HIGH SALT CONCENTRATIONS ON PUMPS IN ROOT SYSTEM AND NADP-MALATE DEHYDROGENASE ACTIVITY IN LEAVES OF DIFFERENT WHEAT GENOTYPES

265---YIELD PERFORMANCE EVALUATION OF DIFFERENT DURUM WHEAT VARIERIES IN MENEMEN CONDITIONS

266---INDUCTION OF HAPLOID EMBRYOS AND PLANTS THROUGH IRRADIATED POLLEN TECHNIQUE IN COTTON

267---DETERMINING YIELD AND SOME FIBER TECHNOLOGICAL PROPERTIES OF F6 GENERATION LINES OBTAINED BY HYBRYDIZATION OF COTTON

268---STUDY AND USE OF WHEAT INTRODUCED FROM INTERNATIONAL NURSERIES IN AZERBAIJAN

269---IMPORTANCE OF PHOTOSYNTHETIC SIGNS FOR THE BREEDING OF HIGH-YIELDING WHEAT VARIETIES

270---MICROPROPAGATION OF ASTRAGALUS VULNERARIAE DC – A POTENTIAL PLANT FOR USE IN ARID LAND SCAPING

271---EVALUATION OF WINTER WHEAT VARIETIES FOR RESISTANCE TO YELLOW RUST IN AZERBAIJAN

272---GENOTYPIC VARIATION FOR DROUGHT TOLERANCE IN WHEAT PLANTS

273---DROUGHT-INDUCED CHANGES IN ISOZYME PROFILES OF ANTIOXIDANT ENZYMES IN WHEAT CULTIVARS

274---EFFECT OF WATER STRESS ON ACTIVITIES OF SUCROSE-METABOLIZING ENZYMES IN GRAINS OF WHEAT (TRITICUM AESTIVUM L.) DURING GRAIN FILLING

275---EVALUATION SPAD METER READING AT DURUM WHEAT POPULATIONS UNDER DIFFERENT NITROGEN CONDITIONS

276----GENOMIC SELECTION IN WHEAT BREEDING USING DIVERSITY ARRAYS TECHNOLOGY (DART)

277----RESISTANCE TO BARLEY YELLOW DWARF VIRUS IN COMMERCIAL WHEAT VARIETIES OF PAKISTAN

278---SAFFLOWER BREEDING RESEARCH AND THE VARIETIES DEVELOPED BY TRANSITIONAL ZONE AGRICULTURAL RESEARCH INSTITUTE

279---POTATO BREEDING IN EASTERN ANATOLIA REGION

280---INFLUENCE OF EPICUTICULAR WAX ON HEAT AND DROUGHT TOLERANCE IN WINTER WHEAT

281---PLEIOTROPIC EFFECTS OF DWARFING GENES ON GENOTYPES OF WINTER BREAD WHEAT ANALOGUE-LINES

282---USING POLYMORPHISM OF GRAIN STORAGE PROTEINS FOR IDENTIFICATION OF MALTING BARLEY VARIETIES

283---WINTER BARLEY AND OAT BREEDING PROGRESS IN BULGARIA

284---EFFECT OF GENOTYPES AND PLANT GROWTH HORMONES ON SOMATIC EMBRYOGENESIS IN PEANUT USING EPICOTYL EXPLANTS

285---DETERMINATION OF HETEROTIC EFFECTS OF SEED COTTON WEIGHT PER BOLL IN F1 HYBRIDS DOUBLE CROSS IN COTTON

286---OCCURRENCE OF SEPTORIA LEAF BLOTCH IN ALGERIA AND ASSES OF WHEAT RESISTANCE

287---VARIATION IN FATTY ACID COMPOSITION OF THREE TURKISH SLIT FLOWER OPIUM POPPY (PAPAVER SOMNIFERUM L.) LINES

288---WHEAT CROP IMPROVEMENT AND BREEDING GOALS IN SUDAN

289---APPLICATION OF RNA SILENCING A CHANGING PARADIGM IN CROP IMPROVEMENT

290---EFFECT OF DIFFERENT NACL CONCENTRATION ON IN VITRO REGENERATION IN ONOBRYCHIS

291---EVALUATION OF SELECTION CRITERIA FOR ASSESSING DROUGHT STRESS TOLERANCE OF THIRTY MAIZE INBRED LINES

292---IMPLICATIONS OF COMMON BEAN CENTROMERE STRUCTURE ON BREEDING EFFORTS

293---IMPROVEMENT OF SALINITY TOLERANCE IN BARLEY CONTRIBUTION OF IN VITRO TECHNIQUES

294----MONITORING OF CEREAL PESTS AND DISEASES AND IDENTIFICATION OF RESISTANT VARIETIES

295---OPIUM POPPY (PAPAVER SOMNIFERUM L.) PRODUCTION AND BREEDING GOALS IN TURKEY

296---WHEAT LANDRACES INVENTORY IN TAJIKISTAN

297---THE DETERMINING OF THE EFFECTS OF SOME GROWTH REGULATOR PRODUCTS ON MALE STERILITY IN SUNFLOWER

298---DEVELOPING CONFECTIONERY SUNFLOWER HYBRIDS AND DETERMINATION OF THEIR YIELD PERFORMANCES IN DIFFERENT ENVIRONMENTAL CONDITIONS

299---DETERMINATION OF YIELD PERFORMANCES OF OLEIC TYPE SUNFLOWER HYBRIDS RESISTANT TO BROOMRAPE AND DOWNY MILDEW

300---YIELD AND QUALITY CHARACTERISTICS OF SOME İZMIR TYPE TOBACCO GENOTYPES

301---AROMATIC BASMATI AND NON-BASMATI RICE VARIETIES GROWN IN HARYANA, INDIA FOR EXPORT

302---INNOVATIVE TRANSGENIC APPROACH TO IMPROVE DROUGHT TOLERANCE OF MAIZE IN SYRIA

303---MEIOSIS OF FERTILE AND STERILE SUNFLOWER AT THE CYTOLOGICAL AND MOLECULAR LEVEL

304----APPLICATION OF FOOD BIOTECHNOLOGY IN AGRICULTURE

305---USING SUNFLOWER GENETIC RESOURCES, TO IMPROVE RESISTANCE TO THE MAIN DISEASES AS WELL AS TO THE BROOMRAPE PARASITE

306----CHARACTERIZATION OF CONFECTIONARY SUNFLOWER (HELIANTHUS ANNUUS L.) LAND RACES OF TURKEY

307---SCENTED VERITIES OF RICE CULTIVATED IN UTTAR PRADESH, INDIA FOR EXPORT

308---INBREEDING IN THE BREEDING OF WINTER RAPESEED IN UKRAINE

309----CRYOPRESERVATION TECHNIQUES OF CEREAL GENETIC RESOURCES

310----EFFECTS OF INBREEDING DEPRESSION IN VEGETATIVE AND REPRODUCTIVE PARAMETERS OF ANAGYRIS FOETIDA SPAIN

311----WHEAT LANDRACES POTENTIAL OF TURKEY A SWOT ANALYSES

312---THE MODEL OF THE STUDY DETERMINATION OF DROUGHT TOLERANCE IN LOCAL DURUM WHEAT CULTIVARS

313---DEVELOPMENT OF SYNTHETIC CULTIVAR OF ALFALFA ON THE BASIS OF POLYCROSS PROGENY PERFORMANCE IN THE SOUTHERN ANATOLIA

314---COMPARISON OF NEAR-ISOGENIC LEAFED AND SEMI LEAFLESS PEA GENOTYPES IN SEED YIELD COMPONENTS

315---NON-HOST RESISTANCE TO WHEAT STRIPE RUST IN BARLEY

316---A NEW SEMIDWARF CULTIVAR URUQ WAS DEVELOPED BY IRRADIATED STORAGE SEEDS OF INIA-66 CULTIVAR

317---RESEARCHING RESULTS OF ECOLOGICALLY CLEAN SOYBEAN CULTIVARS OF DOMESTIC AND FOREIGN BREEDING

318---THE CONTENT AND QUALITY OF FAT IN THE RAPESEED, SOYBEAN AND SAFFLOWER BREEDING

# ADAPTIVE SELECTIONS OF SPRING-SOWN WHEAT IN THE CONDITIONS OF THE WEST SIBERIAN REGION ON THE BASIS OF USE EXPERIMENTAL MUTAGENESIS AND HYBRIDIZATIONS

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Mutations and recombinations at floweringplants play an important role in formation of their adaptive potential. In this regard along with other methods using experimental mutagenesisand mutant varietalhybridization are very actually for management of genetic variability in selection. In particularly, increase of stability and efficiency of agro-ecosystems are important always at a big variety of soil climatic conditions of Russia and the West Siberian region. However, in the twenty-firstcentury this problem becomes priority when negative impact of abiotic and biotic stresses on crops more and more increases. The Omsk region is presented by four soil and climatic zones. The major limiting factors are the general deficiency of moisture during vegetation, frequently excessive loss of a precipitation during grain formation and harvesting, high average daily air temperatures. In these conditions createdvarietiesof a spring-sown wheat have to be drought-resistant, as much as possible use moistening, and at the same time to be steady against drowning and defeat by a rust. Begun by us since 1980 researches on use experimental mutagenesis in the selections allowed not only to specify methodical and theoretical questions of mutational selection of soft wheat, but also to create adaptive varieties to conditions of the West Siberian region. Varieties of a mutant origin are Rosinka, Rosinka2, Slavyankaof Siberia. The varieties received on the basis of mutant and varietal crossings are Katyusha, Lavrusha and Serebristaya. All of them form steadily high productivity of grain, are drought-resistant and steady against diseases, on quality of grain belongto strong and valuable wheat.

# BREEDING OF DENSITY-INDEPENDENT CULTIVARS IS A VIABLE OPTION TO COMBAT CLIMATE CHANGES – A CASE STUDY FOR MAIZE AND WHEAT

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Agriculture in the days ahead will be faced with a double contrasting challenge. On the one hand the climate change that creates tremendous seasonal variability and affects productivity adversely. On the other hand the demand for more food to sustain an ever increasing global population. As maize and wheat are major crops the impact of seasonal variability on their stability is of particular concern. In both crops the harvested grain yield usually lags behind the potential yield leading to a considerable yield gap. A particular cause is density-dependence implying that the optimum density is either very high for some seasons or substantially variable across seasons. The problem is an almost universality in maize, while becomes evident in rain-fed wheat. Indicatively, for dry seasons low density is a prudent option but for propitious seasons only high densities could accomplish the potential yield. Consequently, failure to obtain the most appropriate density ends up to a considerable yield loss. The so far consistent insistence on crowding to raise potential yield and neglect of the single-plant performance is a root cause. Henceforth breeding should prioritize single-plant yield potential targeting on density-independent cultivars (i.e. of wide and low threshold range of optimum density). Improved plant yield potential enables effective resource use at low densities under both marginal and prosperous environments. Density-independent cultivars are imperative to combat the implications of the contemporary climate change on seasonal variability and serve the needs of a flexible agriculture able to farm and produce food into the future as well.

# DIRECT REGENERATION FROM LEAF DISC EXPLANTS OF PEANUT: GRAFTING IMPROVES SURVIVAL RATE

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Leaf discs of 0.5 cm diameter from 10 days old seedlings of four peanut cultivars were cultured on Murashige and Skoog (MS) medium supplemented with twelve different combinations of Thidiazuron (TDZ) and Naphthaleneacetic acid (NAA). Highest number of responding explants (52.67%) with highest (5.65) number of shoot buds per responding explant was achieved at a combination of 0.5 mg/l NAA and 0.5 mg/l TDZ. The explants were then shifted to fresh MS medium containing 8 mg/l Benzylaminopurine (BAP) and 0.5 mg Indole Acetic Acid (IAA) for shoot elongation. Root induction was highest (56.07%) at half strength MS medium supplemented with 1.5 mg/l NAA. Grafting of *in vitro* regenerated shoots on 10 days old seedling root stock showed highest (61.30%) success rate. Survival rate of plants obtained from grafting was almost double (45.76%) than those achieved by rooting of shoots (22.41%). There was significant variation among four varieties regarding number of responding explant, number of shoots per explant, rooting or grafting percentage and survival rate. Grafting of *in vitro* regenerated shoots showed very promising (61.30%) success rate. Survival rate of plants obtained from grafting was almost double (45.76%) than those achieved by rooting of shoots (22.41%).

**Keywords:** Peanut, Leaf disc, In vitro regeneration, Thidiazuron, Naphthaleneacetic acid, grafting

# FREEZING TOLERANCE IN CEREALS: BREEDING, AGRONOMICAL, PHENOLOGICAL, PHYSIOLOGICAL AND PROTEOME ANALYSIS

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Understanding of Agronomical, phenological, physiological and molecular mechanisms of freezing tolerance (FT) in cereals will be useful in the design of plant breeding and production systems for cold regions of the world. This paper focuses on the agronomical, physiological and developmental regulation of freezing tolerance of wheat and barlet genotypes acclimated in both non-freezing and sub-zero temperatures in controlled and field conditions of cold and temperate regions of Iran. Low but non-freezing and sub-zero temperatures associated proteins were identified in proteome analysis of spring, facultative and winter wheat genotypes during the vegetative/ reproductive transition. Also, vernalization response, trend of FT and accumulation pattern of proline, total soluble carbohydrates, sucrose, glucose, fructose, fructan, $H_2O_2$, and MDA and agronomical traits were studied in both parental and isogenic/ recombinant lines during different phenological development of plants. Close link was found between the vegetative/reproductive transition, metabolites accumulations and up-regulation of both low (non-freezing) and sub zero temperature-associated proteins. Based on the results of agronomical, morpho-physiological measurements and proteome analysis, selection criteria for FT in cereals breeding strategies are suggested for improvement of FT in cereals for cold and temperate climates with freezing stress.

**Key words:** Cereals breeding, cold tolerance, cold-induced proteins, metabolites, plant development

# FUNCTIONAL GENOMICS AND TRANSCRIPTOMICS OF ABIOTIC STRESSES AND THEIR APPLICATIONS ON RICE BREEDING

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Abiotic stresses such as high salinity and drought severely diminish rice productivity. To better understand the stress mechanism and to further improve rice varieties in their tolerance by genetic modification, we have carried out studies on functional genomics and transcriptomics of these abiotic stresses. We have developed an efficient two-element maize *Ac/Ds* gene trapped system and have generated around 15,000 *Ds* insertion rice lines. We subjected these lines to drought (PEG), high salinity (NaCl) and cold stress screens and evaluated these lines and functionally annotated their tagged genes. Our data show that random *Ds* insertions into the rice genome have led to various genetic variations in response to these stresses. Although hundreds of genes might contribute to abiotic stress tolerance, knock-out of single gene could significantly increase or decrease rice tolerance. Thus, rice has the genetic potential to survive under abiotic stresses by silencing or suppressing appropriate endogenous genes. The *Ds* insertion lines that exhibit higher tolerance to abiotic stresses may be used for rice breeding by conventional backcrossing combining with molecular marker-assisted selection. On the other hand, we have genome-widely identified genes with differential expression under drought and high salinity stresses between tolerant and sensitive rice lines. These differentially expressed genes encode various proteins functioning as transcription factor, kinase and phosphatase as well as in detoxification, iron homeostasis, and hormone biosynthesis. Some of these regulated genes have been employed to improve rice tolerance to these abiotic stresses by over- or down-expression of these genes through transgenic technology.

# GENEALOGICAL ANALYSIS OF RESISTANCE TO PRE-HARVEST SPROUTING IN THE NORTH-AMERICAN SPRING WHEAT VARIETIES

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For identifying sources of resistance to pre-harvest sprouting (PHS) conducted a genealogical analysis of 148 red-grained and 63 white-grained North-American spring wheat varieties with full pedigrees and PHS estimates. Analysis of variance revealed significant differences in the landrace contributions between the groups of resistant and susceptible varieties. We have identified 8 landraces (Crimean, Hard-Red-Calcutta, Iumillo, Button, Kenya-9M1A3, Kenya-BF4-3B-10V1, Kenya-U, Red-Egyptian) in red-grained, and 13 (Crimean, Hard-Red -Calcutta, Ostka-Galicyjska, Iumillo, Yaroslav-Emmer, Gehun, Hybrid-English, Red-King, Rough-Chaff-White, Ladoga, Polyssu, Rieti, Turco) in white-grained, whose contributions were significantly higher in the resistant varieties. It can be assumed that among these landraces are donors of resistance to PHS. Tracking pedigrees showed that these landraces hit the pedigrees of the modern red-grained varieties through Thatcher, Hope, Kenya-58 and Kenya-Farmer, and white-grained - via Thatcher, Frontana, Redman and RL-2265. As is known, the most important donor of resistance to PHS for North-American spring wheat varieties is the line RL-4137. Its genealogical profile contains 28 landraces, 16 of which are identified by us as sources of resistance to PHS. In the studied groups RL-4137 is included in the pedigrees of resistant varieties majority, whereas in susceptible varieties frequency of occurrence of this line is very low. Pedigree analysis confirmed the value of RL-4137 for North-American spring wheat breeding programs. This line is in the pedigrees of 365 accessions, including 58 released cultivars and 203 advanced lines from Canada, and 22 released cultivars and 53 lines from the United States.

# MAPPING GENES FOR NORTHERN CORN LEAF BLIGHT IN MAIZE

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Northern Corn Leaf Blight “NCLB” is the most common and widespread foliar wilt disease of maize in many tropical and temperate environments. It is caused by the ascomycete fungus *Setosphaeria turcica* (Luttrell) Leonard and Suggs with its conidial state *Exserohilum turcicum* (Passerini) Leonard and Suggs. Symptoms can range from small cigar shaped lesions to complete destruction of the foliage. Mid altitude regions of the tropics about 900-1600 m above sea level has a particularly favorable climate for the disease as dew periods are long and temperatures moderate. Such conditions prevail on millions of hectares of crop land in eastern and southern Africa, Latin America, China and India. The yield losses due to this disease can easily exceed 50% if it appears before flowering. NCLB is mainly controlled by resistant cultivars. The resistance is either qualitative or quantitative. Qualitative resistance is typically race specific and inherited by single genes whereas quantitative resistance is race non specific and oligogenic or polygenic. One cannot equate qualitative with complete and quantitative with partial resistance. Depending on the environment qualitative resistance of maize to *S. turcica* may have a partial effect while quantitative resistance may have a complete effect. In the present study attempt has been made to study quantitative time of resistance with the help of molecular marker. The use of Molecular markers is an efficient alternative to the tedious work of phenotype evaluation for NCLB resistance and allows for efficient selection of NCLB resistance genes. Among the different kind of DNA markers, Simple Sequence Repeat markers have been successfully used to identify Quantitative Trait Loci “QTLs” responsible for resistance for Northern Corn Leaf Blight. In the present study a set of 360 SSR markers were received from Applied Biotechnology Centre, CIMMYT in addition to about 140 SSR primers from Asian Maize Biotechnology Network, AMBIONET. Initial 40 maize lines were screened to select eight inbred of early maturity group to study the presence of “QTLs” for NCLB in maize. In present investigation out of eight inbred; five resistances (CM 104, CM105, CM118, CM145, and V336) and three susceptible (CM212, CM126, V338) were used in the present Study. Parental polymorphism studies have revealed that 103 primers exhibiting polymorphism between CM212 and CM145 followed 101 primers between CM112 and V336 and 100 primers for CM105 and V338, CM126 and CM212 in both the cases. The mapping population (F2-3) of CM212 x CM 145 were raised and phenotypic data related to AUPDC Curve and Incubation Period were raised in two environment viz, BHU Varanasi and Regional Research Station and hot spot for NCLB at Nagenhelly were raised. The genotypic data of all the genotypes of F2-3 population in two environments were generated and the Genotypic and Phenotypic data is subjected to software Map Makers to locate and Map the QTLs for NCLB in Maize.

# METHOD OF ECOLOGICAL BREEDING AN EXAMPLE PROGRAM “ECADA”

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The method of selection of ecologically plastic genotypes (breeding on homeoadaptibility) which consists in connection of three basic elements is submitted. First, formed an artificial ecological gradient (environmental vector “ECAD”) with a different range of pressure limiting environmental factors in the ontogeny across ecological points. Revealed that within the environmental vector genotypic variability contributes to 1,61-4,89 times smaller contribution to the formation of the phenotype by variables than the inherited genotype-environment interactions. Total share paratypic variability ranged from 38.2% (density of productive stalks) to 58.9% (yield). Environmental point at which the most concentrated limiting plant growth and development factors of the environment, is Bezenchuk. Points, the most revealing potential productivity are Ulyanovsk and Kazan. Stable center vector is Karabalik high differentiating parameters of the medium, but not typical vectors in general. Environmental point of Kazan, Ulyanovsk and Chishma consistently appear regardless of years of testing to form a single galaxy. The greatest variability data show Bezenchuk and Penza. Second, the system of statistical parameters of an estimation homeoadaptibility at genotypes tested along an ecological vector is developed. It is determined, that from all complex of investigated parameters at screening on homeoadaptibility it is expedient to use estimations of adaptive ability on Kilchevsky, Khotyleva (GAA and $S^2_{SAA}$). Thirdly, the circuit of movement of a breeding material on points of an ecological vector is developed. The method is approved in time creative association of breeders “Ecada”. Created using this method cultivars of spring bread wheat Ecada 6, Ecada 70, Ecada 66, Ecada 109 and Ecada 113.

# OCCURRENCE OF *SEPTORIA* LEAF BLOTCH IN ALGERIA AND ASSESSMENT OF WHEAT RESISTANCE

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Septoria tritici (*Mycosphaerella graminicala) and* Septoria nodorum (*Leptosphaeria nadorum)* causal agents of *Septoria* leaf blotch of wheat occur throughout the major wheat growing regions in Algeria. The Septoria diseases are the source of major damage on susceptible varieties on bread and durum wheat. Surveys have been performed during the last decade covered wheat growing areas of eastern and central regions (Annaba, Skikda,Tizi Ouzou, Boumerdes, Algiers) and sub- littoral (Guelma, Souk Ahras, Constantine, Sétif, Mila, Bouira). The disease development was always observed except during 2000-2001 and 2001-2002 (excessive drought conditions). The surveys showed that *Septoria* diseases are more prevalent in coastal areas and sub-littoral where risk is very high. The surveys also revealed the presence of both septoria species (M. tritici and *L. nodorum*), but septoria tritici was more prevalent. Algerian National Wheat improvement Program conducted in collaboration with ICARDA conducts routine screening for resistance to septoria since 2005. A collection of 150 durum wheat and 100 genotypes of bread wheat were tested under natural conditions at two septoria hot spots representing high and low rainfall areas, where the foliar diseases are normally expressed each year under field conditions. Wheat lines that carry resistance to *Septoria* leaf blotch were identified. Resistant lines were tested under controlled condition. Introduced and local germplasm with resistance to septoria were identified.

**Key words**: *septoria leaf blotch, wheat, resistance, survey, Eastern Algeria*.

# SELECTION OF SPRING HARD-WHEAT ON THE QUALITY AND SALT TOLERANCE

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Food security of the country on the basis of competitive products is the main purpose of agriculture, which is one of the leading sectors of the economy of Kazakhstan. Much of the agricultural land in Kazakhstan is in the zone of risky agriculture. Bioclimatic potential of Kazakhstan is several times lower than in the USA, Europe and many regions of Russia. Durum wheat in Kazakhstan is a priority crop. Area under culture, make annually - 230-240 thousand hectares. At present time, there were two problems with selection of durum wheat to seek ways to stabilize the level of yield and grain quality at an optimum and economic levels and the creation of varieties with combined resistance to biotic and abiotic environmental factors. Favorable weather conditions during grain filling and ripening in the last 3 years several trials have increased protein content and gluten. Promising lines had higher values of grain quality. The most high-quality grain samples were from the following spring durum wheat - 18063 (Nauriz-6), 18095 (Salauat), 18404, 18585-2,18485-5, 18399 (Lan), 18104 (Ertol), 18602-4 (Milan). According to the results of a 3-year trial are promising for transfer to State sort plot (SSP), they are characterized by high productivity, high macaroni properties, resistance to disease and pests. Evaluation was carried out on the salt tolerance of the procedure V.A.Udovenko. All seeds germinated in water for 2 days. Then, root length was measured in the samples studied. On the third day the seeds were placed in solutions with various salt concentrations where they were grown for another three days and then measured for root length. The results showed that at low salt concentrations 10 Am longer square in comparison with standard Nauryz-6 were 8 samples: 18602-4, 18472, 18001-8, 18404, 18104, 18595, 18567-7, 18585-5. At higher salt concentrations up to 18 At the root of the length of the plants decreased from 8.7 to 42.3%. Longer root preserved specimens marked at 10%. However, some samples of durum wheat at higher salt concentrations were very responsive and dramatically reduced the length of the root, such as Nowruz-6 18472-2-3-2, 18339, 18485-2, 18595, 18567-7, 18585-asm, at 30.4 , 26.7, 28.6, 38.5, 23.3, 23.8, 25.9, 42.3, 32.4% respectively. Slightly reduced the length of the root number 18036-30 (by 8.7%) and 18409 (5%). Created and transferred to Nauriz-6 SSP 9 varieties of hard spring wheat – Nauryz 6, 7 Nauryz, Nauryz 8, Tom Seymour, Lan, Ertol, Salauat, Milan and Kargala 69. For commercial use in the south, south-east, east and west Kazakhstan recommended high-yielding varieties of hard spring wheat, with high qualities of grain macaroni- Nauryz 2, Nauryz 6, Gordeiforme 254, Lan, Ertol, Salauat, Milan and Kargala 69. Varieties of spring durum wheat Nauryz 2, Nauryz 6, Gordeiforme 254, Lan approved for use in Almaty, Zhambyl, South Kazakhstan, Kyzylorda and East Kazakhstan regions.

**Keywords:** Breeding, line, hybrid, yield, quality, salt tolerance.

# STUDY OF THE FUNCTIONAL STATE OF THE CELL GENOME OF AGRICULTURAL CROPS AS RELATED WITH HETEROSIS

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In some agricultural crops (*Solanum lycopersicum* L., *Gossypium* L., *Triticum* L.) the author estimated the features of hereditary apparatus rearrangement in heterotic hybrids in comparison with parental forms on basis of content of nucleic acids in nucleus, mitochondrion and chloroplast. Such complex approach to investigation of functional state of cellular genome permits to obtain more complete presentation of realization of activity these structures during heterosis effect. So, DNA content per one cell in leaf's tissue in all hybrid combinations was higher than in parental varieties. The number of cells per unit of square of leaf surface was lesser, while the size of one cell was larger. In heterotic hybrids both mitochondrions and chloroplasts may contribute to increasing of cell energy-supply. Probably, that it is manifestation of complementary of coordinated action of genetic systems of these cellular organelles. One can suppose that in case of increased load on nuclear, mitochondrial and chloroplast genetic system of plant cell, the hybrid, which has raised energy-supply for biosynthesis of plastic matter, develops the high heterosis effect. The revelation of general mechanisms of functioning of genetic apparatus in hybrid forms of different agricultural crops permit to recommend the determination of DNA content in somatic cell for prediction of heterosis.

# ANALYSIS OF DIALLEL CROSS FOR SOME QUANTITATIVE TRAITS IN COMMON BEAN (*Phaseolus vulgaris* L.)

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Genetic information on combining ability and the type of gene action that governs the inheritance of economically important quantitative characters can be an immense help to the breeder. Such information can assists the plant breeders in selection of suitable parents and the appropriate breeding procedure. The $F_1$ hybrids excluding reciprocals from a five-parent diallel cross along with the parents were evaluated in a randomised complete block design. Data were recorded on nine quantitative traits. Substantial genetic variability was observed among the hybrids for the traits studied. Combining ability and gene action for green pod yield, plant height, pod length, pod weight and pods per plant were estimated. The study indicated that both general combining ability and specific combining ability effects were significant and important for all traits. Partial dominance for green pod yield and plant height and partial to over-dominance for pods per plant were observed. Dominant genes seem to govern the inheritance of all three characters Viz. Plant height, Number of pods per plant and green pod yield. Combining ability, component variance analyses indicated that the pod yield and two of its components are influenced by both additive and non-additive gene action. Diallel analysis also indicated that expression of four No. of branches per plant100 seed weight Days to 50% flowering and Pod weight of the traits is regulated predominantly by additive gene action suggesting possibility of early-generation selection, while non-additive gene action also plays an equally important role in the control of Plant height and green pod yield. Genotypes Arabhavi-1 and IIHR-909 were good combiners for pod yield traits. While Arka Suvidha was a good combiner for improvement of number of pods per . Association between general combining ability (GCA) effects and mean performance suggested that the performance per se of the genotype should be a good indicator of its ability to transmit the desirable quality attributes to its progenies. Though performance of crosses was found to be independent of parental GCA status, it is evident that at least one of the parents used in hybridization should have more number of pods and pod weight for obtaining better segregants. Recurrent selection and reciprocal recurrent selection could be suitable breeding procedures for rapid improvement.

Key words: Combining ability Diallel *Phaseolus vulgaris* L.

# ASSESSING THE SUITABILITY OF SPECTRAL REFLECTANCE INDICES TO SCREEN CONTRASTING WHEAT GENOTYPES FOR DROUGHT TOLERANCE

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Spectral reflectance indices can estimate drought stress-related traits of a large number of genotypes quickly and cheaply. The objective of this study was to assess the suitability of diverse spectral reflectance indices to screen wheat genotypes for drought tolerance.Diverse spectral indices assessed by active spectral sensing were related to the water content of the aboveground biomass, dry weight of the aboveground biomass and grain yield per hectare of 89 F5 families derived from a half diallel cross among three common Egyptian parents (Sids1, Sakah 93 and Sakha 61) and one common wheat drought sensitive (YecoraRojo) with water deficit stress conditions. Drought stressed conditions were achieved by applying one irrigation before seedling and then two irrigations were applied before complete emergence of florescence with total amount of water 2500 $m^3$ $ha^{-1}$. The results showed that the most spectral indices estimating the water status of plant such as normalized water index, water band index, reflectance ratio $R_{940}$ : $R_{960}$, reflectance ratio $R_{1000}$ : $R_{1100}$, and reflectance ratio between water band index and normalized difference vegetation indexwere able to distinguish genotypic differences in drought tolerance. These indices showed a strong linear relationship with destructive assessed parameters water content of the aboveground biomass, dry weight of the aboveground biomass and grain yield per hectare. In conclusion, spectral reflectance indices predicting water status of plant under drought stress gave a better association with plant water content at the canopy level indicating that its potential application in precision phenotyping.

# ASSESSING THE SUITABILITY OF VARIOUS MORPHO-PHYSIOLOGICAL TRAITS TO SCREEN WHEAT GENOTYPES FOR DROUGHT TOLERANCE

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Success of improving the drought tolerance of genotypes requires effective and reliablescreening traits in breeding programs. The objective of this study was to assess the suitability of various morpho-physiological traits to screen wheat genotypes for drought tolerance. A segregating F5 population of 89recombinant inbred lines (RILs) derived from a half diallelcross among three common Egyptian parents (Sids1,Sakah 93 andSakha 61) and one common wheat drought sensitive (YecoraRojo) was evaluated in a field under water deficit stress conditions in randomized complete blocksdesign with three replications.Drought stressed conditions were achieved by applying one irrigation before seedling and then two irrigations were applied before complete emergence of florescence with total amount of water 2500 $m^3$ $ha^{-1}$. The morphological traits (plant height, number of tillers and green leaves, leaf area of flag leaf and green leaves and dry weight of aboveground biomass) and physiological traits (leaf area index, water content of aboveground biomass and stomatal conductance) were measured at 90 days after sowing.The results showed significant genotype effects for most traits. Principle component and cluster analysis exhibited strong relationships between grain yield,flag leaf area, late stay green area, water content of aboveground biomass,leaf area index and stomatal conductance. It was concluded that measurement of leaf area index and stomatal conductance by nondestructiveequipment provide new and feasible screening methods for detecting genetic variation in drought tolerance under field conditions.

**Keyword:** drought stress, leaf area index, screening criteria, stomatal conductance

# ASSESSMENT OF GENETIC DIVERSITY AMONG POPULATIONS OF *ONOBRYCHIS. CORNUTA* USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS

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*Onobrychis cornuta* subsp. *cornuta* is a species of *Onobrychis* belongs to the Dendrobrychis section of Fabaceae family. In Classification based on morphological characteristics, different populations with some various morphological features such as flower color are in subsp. as *O. cornuta* subsp. *cornuta.* In this study, random amplified polymorphic DNA (RAPD) marker was used to assessment of genetic diversity among populations of *O. cornuta* with the pink and white flowers collected from Zonuzagh-Kuhkamar region of East Azerbaijan province. RAPD analysis using 4 random primers generated 257 bands, as the average number of bands for each primer was 64.2 bands. The amplified products of the RAPD profiles ranged from 100 to 1400 bp. Genetic similarity among all accessions was calculated according to Simple Matching (SM) similarity index, using the similarity of qualitative data (Simqual) routine. The dendrogram was constructed using the unweighted pair group method average (UPGMA) clustering procedure as available in NTSYS-pc 2.02. Accordingly, the samples were placed in 2 groups with the pink and white flowers. According to Nei genetic distance matrix using GenAlex 6.5, genetic distance and genetic similarity existed between populations were 0.105 and 0.900 respectively. Existing high similarity between populations could be due to ecological conditions in region. But, the existing populations in two groups showing there is the possibility of separating two sub species from *O. cornuta*. In conclusion, the RAPD method successfully discriminates among two populations *O. cornuta*. Therefore, RAPD provides rapid results, is less time-consuming and less expensive, and gives information about genomic variability below the species level.

**Keywords:** *Onobrychis cornuta*, genetic diversity, PCR, RAPD

# THE DETERMINATION OF MORPHOLOGICAL AND AGRONOMIC PROPERTIES OF SOME CULTURE AND WILD PEA GENOTYPES IN K.MARAŞ CONDITIONS

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This study was carried out to determine some morphological and agronomic traits differences among 4 peas genotypes obtained from the natural vegetation and culture, and in order to compare the genotypes in the view of examined of the characteristic, Kahramanmaras Sutcu İmam University, Faculty of Agriculture, Department of Field Crops in the years of 2010-2011 and 2011-2012. The study was carried out according to the randomized complete block design with four replications for two years between genotypes which were determined the morphological and agronomic differences. According to the results of the two-year combined the analysis of variance, genotypes between to the number of days to flowering, plant height, number of pods per plant, 1000-grain weight, grain yield per decare, in spite of the average rate was a statistically significant difference in terms of features, the genotypes of dry straw yield property the difference was statistically insignificant. It was determined that the wild pea genotypes could be used in the studies of development of breeding appropriate in the Kahramanmaras ecology of the food pea types.

**Key Words:** Pisum sativum, wild pea, breeding, genotypes, grain yield, yield component

## A NEW APPROACH FOR PLANT BREEDERS: PROTEOMIC STUDIES

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Since information obtained from genomic studies is limited, proteomics, which is an advance of genomics, become more important in the evaluation of the biological events. Proteomics is to analyse proteins expressed by genom under certain conditions and in a spesific tissue (plant, animal, microorganism tissue), that is proteomics is to identify proteom. The main goal of proteomics studies is the understanding of proteins including their identification, characterization, and quantification of proteins in whole cells, tissues, or body fluids. Proteomics methodologies require techniques to separate and quantify individual plant, animal, microbial proteins and identify those proteins. In this presentation, we review the current proteomics technologies which include two-dimensional gel electrophoresis (2-DE), two-dimensional differential in-gel electrophoresis (2D-DIGE), one-and two-dimensional liquid chromatography (1D-LC and 2D-LC), mass spectrometry (MS) and protein microarray technology.

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## CHICKPEA (*CICER ARIETINUM* L.) *IN VITRO* MICROPROPAGATION

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Breeding and genetic transformation improvement needs suitable and reliable protocols development. This is especially essential for recalcitrant plant such as grain legumes. For chickpea, the establishment of a repeatable micropropagation protocol is needed to promote plant regeneration. Mature embryos were cultured on Murashige and Skoog (MS) medium used alone or supplemented with plant regulators, to induce shoots and roots formation either via callogenesis or directly.

***Key words:*** Cicer arietinum L., mature embryos, plant regulators.

# CLASSIFICATION OF WHEAT VARIETIES WITH BIOCHEMICAL CHARACTERISTICS AND RAPD MARKERS

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The forty-eight wheat varieties studied with antioxidant enzymes and RAPD markers. Seventy primers used for DNA amplification of which 10 primers of them showed suitable banding patterns. These primers produced 73 polymorphic bands with mean value of 7.3 for each primer. The cluster analysis on based of Nei's distance and UPGMA method, distinguished four different groups. Based on PCoA three coordinates accounted for only 61.7% of variation, which indicated the proper distribution of markers in the surveyed wheat genomes because of relatively low percentage determined by the three first coordinates. Activities of antioxidant enzymes including catalase (CAT), glutathione peroxidase, ascorbate peroxidase (APX) and superoxide dismutase and amounts of malondialdehyde, total protein, $H_2O_2$, Na, K and Cl were measured. Cluster analysis classified varieties in three groups. Karkheh, Arta and Alborz Varieties had the lowest catalase, $H_2O_2$, malondialdehyde and considerable antioxidant enzymes. Genotypes of this group were identified as resistant varieties which could be used in breeding programs.

**Keywords:** Antioxidant Enzymes, Cluster Analysis, PCoA

# CORRELATION AND PATH COEFFICIENT ANALYSIS FOR PROTEIN YIELD IN CONFECTIONARY SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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Path coefficient analysis was used to separate direct and indirect effects of studied traits on protein yield, and to identify traits that could be used as selection criteria in confectionarysunflower breeding. Correlations between different traits are an aspect that should be kept in mind for better planning of breeding programs in sunflower.In this paper, we have studied the interdependence of protein yield and seed oil content, kernel oil content, seed yield, kernel protein content, weight of 1,000 seeds, seed kernel ratio and seed hull ratio. The research was conducted during three vegetation seasons on 22 experimental confectionary sunflower hybrids, produced within the breeding program at the Institute of Field and Vegetable Crops. Among the largest number of examined traits, significant and highly significant correlations were found. With the analysis of simple correlation coefficients a weak negative interdependence was determined between kerneloil content, kernel protein content,weight of 1,000 seeds, seed hull ratio with protein yield.Positive but weak correlation was determined betweenseed oil content, seed kernel ratiowithprotein yield anda positive very strong correlation of seed yield(0.458$^{**}$) withprotein yield. The seed oil content had a highly significant direct negative effect on protein yield (DE=-0.734$^{**}$).The mass of 1,000 seeds had weak negative direct effect on protein yield.Kernel protein content and kernel oil content has demonstrated a weak direct positive effect on protein yield. Path coefficient analysis for protein yield at phenotypic level showed that the positive direct effect was maximum for seed kernel ratio (DE=1.340$^{**}$) followed by seed hull ratio (DE=0.992$^{**}$) and seed yield (DE=0.657$^{**}$).This indicates that seed yield, seed kernel ratio and seed hull ratio have a high influence on protein yield.

**Key words:** confectionary sunflower, protein yield, yield components, correlations, path coefficient analysis, conventional breeding

# CREATING INITIAL FORMS OF SPRING WHEAT IN RELATION TO CLIMATE CHANGE

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Agricultural production has always been and remains dependent on climatic changes occurring. The grain belt of Northern Kazakhstan is mainly located in the area of so-called risk-prone agriculture, which is characterized above all by a short growing season and a pronounced continental climate. Compounding the problem of selection is the peculiar environmental situation with extreme abiotic years irregularly alternating with favorable ones. The unpredictability of this change places exceptional demands on plant varieties. Growing conditions for spring wheat in the steppe regions are characterized by a high moisture deficit~~s~~ and high daily temperature amplitudes. Precipitation is the main source of moisture for fields. During the growing season it is not only the amount of rainfall that is important, but also its distribution over time. Whereas previously satisfactory and good moisture conditions were observed during the growing season in 36% of years, over the past ten years, every second year has been characterized as arid (2004, 2006, 2008, 2012), and 2010 – dry, with a hetero-thermal coefficient during the growing season of only 0.3. In this regard, it is important in properly selected source material with a known range of variability of traits and identified genes (Merezhko, 1994). Identification of the range of variability was aided by large-scale screening of the global gene pool (about 2000 samples) in the Baraev Centre collection for productivity, early maturity, grain quality, disease resistance, as well indicators limiting the production of crops. To enrich the hereditary information of ~~a~~ the new source of material, a global gene pool of spring wheat with a known range of variability of traits, and donor varieties notable for early maturity, yield, plant height control, response to light, etc. is drawn into the selection process. Hybridization is carried out both in the field and in biotechnological greenhouses. The created source material is extensively studied, and promising lines are used to create varieties resistant to abiotic factors.

# CREATION OF NEW VARIETIES OF PERENNIAL GRASSES ON THE BASIS OF COMPLEX HYBRID POPULATIONS IN NORTHERN KAZAKHSTAN

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In Kazakhstan, most arable land devoted to feed crops is occupied by perennial grasses. With the right mix of species and varieties for different zones and necessary care, they provide cheap, varied and nutritious food. Examples are wheatgrass, wild-rye, bromegrass, and different types of wheat grass. Viable seeds make a significant contribution to improving crop yields, and product quality and variety. The climate in the North of Kazakhstan is continental, drought-prone, even dry, and cold, with moderate or little snow in the winter. With annual precipitation of 250-350 mm and evaporation from 450 to 600 mm, it is characterized as anarid zone. The Baraev Centre conducts selection work, using traditional and modern breeding techniques - creating complex hybrid varieties, including synthetic ones using polycross breeding aimed at creating new varieties of haybromegrass and pasture grasswild rye characterized by high drought tolerance, winter hardiness, high nutritional and seed productivity, high forage quality, and disease resistance. Examination and evaluation of the original material is carried out using both fieldand laboratory methods in everyday natural conditions.One of the important stages in the formation of synthetic population is determining the combining ability (CS) in their components. A large role in determining the CS is accorded to the polycross-test. Polycross organizational schemes and polycross interbreeding allow us to estimate both the general and specific combining ability of perennial grasses for hay-making and grazing areas. Selection of components was conducted for the formation of synthetics in the steppes of Northern Kazakhstan not only in terms of the CS, but in conjunction with assessment in accordance with other economically important traits and characteristics in order to avoid the loss of valuable genotypes. The use of polycross provides a promising breeding material with high combining ability to create high-yielding, winter-hardy, drought-resistant varieties of perennial grasses for hay-making and grazing. This method results in the creation of high-yield crops for North Kazakhstan conditions:  Shortandywheat grass, brome Ishimskiy anniversary, Akmola emerald, bromegrass Tselinograd anniversary, Shortandy pasture.

# DEVELOPMENT OF NEW VARIETIES OF SAINFOIN WITH HIGH NITROGEN-FIXING POTENTIAL.

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The most common of Northern Kazakhstan legumes is sainfoin. Cockshead has the unique ability to enter into symbiosis with rhizobia, forming nitrogen-fixing nodules and for vegetation to absorb up to 125-480 kg/ha of nitrogen from the air each year. This provides a high yield of low-cost vegetable protein without the use of chemical fertilizers. But in the arid steppes of Northern Kazakhstan during the formation of the sainfoin root system nodules on the roots are not formed due to lack of moisture in the soil. The task of research in this regard is to establish new and promising varieties and lines of sainfoin with high nitrogen-fixing ability. To increase the nitrogen-fixing capacity of sainfoin, the seeds were inoculated before sowing with promising new lines of plants. An experimental drug of nodule bacteria (nitragin) obtained in a microbiology laboratory from local strains of nodule bacteria for sainfoin, Rhizobium simplex (Rs.-5is for sainfoin) was used. The dimensions of symbiotically fixed nitrogen were counted by a chromatographic method of comparison with a non-legume crop culture. Field studies were carried out through competitive variety trials. The objects of research are well-known varieties of sainfoin crops an improved sand variety, and the promising new lines of sainfoin, K-185 and K-209, inoculated with nitragin. The research in crops of different varieties and lines of sainfoin showed that inoculation of new lines of seeds with nodule bacteria promotes more active nitrogen fixation than in plants, which have not been treated with nitragin. On average, during the sainfoin growing season the maximum number of nodules on the roots of the plants were observed in the variant with nitragin in line K-185 and observed 81 pc. on one plant. As a result, the line K-185 uptake of atmospheric nitrogen was 192.8 mg or 83.4% of total nitrogen. Improved sand varieties of sainfoin and K-209, when inoculated with rhizobia, formed several smaller nodules, their number reaching up to 40 pcs. on one plant. By using the chromatographic method for determining the nitrogen-fixing ability in new lines of sainfoin K-185 and K-209, it has been found that, during plant growth, fixed nitrogen atmospheres were respectively 491 and 458.7 mg/m, and that the total balance of nitrogen was 84%, owing to rhizobia inoculation the new lines have a more active ability to fix atmospheric nitrogen than the standard variety of sainfoin. Thus, the promising lines of sainfoin K-209 and K-185 are the primary forms for creating new varieties of sainfoin with a high potential for nitrogen-fixing in the conditions of the Northern Kazakhstan.

# ENCAPSULATED SOMATIC EMBRYOS AND SHOOT TIPS OF RAPESEED (*BRASSICA NAPUS* L.): AN EFFICIENT WAY FOR STORAGE, TRANSPORT AND MULTIPLICATION OF PLANT MATERIAL

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The present paper reports the encapsulation of Somatic embryos and in vitro-derived shoot tips of rapeseed (*Brassica napus* L.) for evaluate somatic embryos response to different storage periods and germplasm exchange purposes. In this experiment, the effects of several concentrations will be studied for: a) sodium alginate as gelling agent; b) calcium chloride as complexing agent; c) preparation of sodium alginate and d) IAA concentration for enhance root formation in re-growth shoot tips after recovery. At other experiment, encapsulated somatic embryos (ESEs) were encapsulated in 2% sodium alginate, stored for several periods (10, 20, 30 and 40 days) at 4°C. Results showed that, a gelling matrix of 4% sodium alginate and 1.4% calcium chloride were found most suitable for formation of ideal beads in shoot tips. Encapsulated shoot tips exhibited the best shoot development on Murashige and Skoog (MS) medium supplemented with 2 mg $l^{-1}$ BAP and 2mg $l^{-1}$ IAA (70.2 %) followed by hormone-free MS basal medium (63.19%) and distilled water (62.16%). Furthermore, it illustrated that 2 mg $l^{-1}$ IAA produced a highest root in plantlets derived from encapsulated shoot tips. The second experiment results indicated that Maximum conversion frequency of 55.5% was obtained from encapsulated embryos cultured on MS medium without plant growth regulators stored for 10 days. The longer duration of cold storage, caused the less in plantlet recovery. This work indicates that encapsulated somatic embryos of canola could be regenerated for a limited period time.

# EVALUATION OF DROUGHT TOLERANCE IN BREAD WHEAT GENOTYPES USING MORPHO-PHYSIOLOGICAL TRAITS

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Drought is a major abiotic stress that is threatening the producing and survival of many crops such as cereal. Wheat is grown on arid agricultural fields and drought often causes serious problems in wheat production on these fields. For the purpose of identifying drought resistant cultivars and evaluating physiyo -morphological characteristics 20 genotypes of bread wheat , along with three check cultivars were evaluated for some important traits related to drought tolerance , including germination stress index (GSI), rootlet length, coleoptiles length, canopy temperature (TC), Leaf temperature (LT), Leaf water loss (LWL), flag leaf length, relative water content (RWC), Chlorophyll content (SPAD), stress tolerance indices (STI and Tol) and other morpho-physiological traits under field and laboratory conditions. The experiments were conducted in RCBD with three replication in two conditions (rainfed and supplemental) in dryland agricultural research institute, sararood station, Kermanshah, in 2009-2010 cropping seasons. Germination test in laboratory indicated significant variations. At the germination and early seedling stage the genotypes Pyn/Bau// Vorona/Hd2402 and Crr/Attila performed better than the others.  Rootlet and coleoptiles length was reduced as water potential decreased. In field conditions results of analysis variances indicated significant differences among genotypes for traits with the exception of relative water content (RWC). Leaf and canopy temperature increased due to drought stress. Result obtained in this experiment indicated that drought stress significantly decreased the chlorophyll content. The simple correlation coefficients revealed that STI had high and positive significant relation with germination percent, grain yield, and other characteristics including chlorophyll content, flag leaf length, number of seeds in spike and biomass. The genotype Kauz”s”/Machuhete produced the highest values for the grain yield, number of seeds in spike, 1000- kernel weight and STI compared to all the other genotypes.

**Key words**: Bread wheat, drought tolerance, morpho-physiological traits

# EVALUATION OF DROUGHT TOLERANCE IN CUMIN (*CUMINUMCYMINUM*L.) ECOTYPES IN FIELD CONDITION

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In the arid and semi-arid tropical regions where drought is a major constraint, cumin is one of the most agriculturally valuable plants. The aim of this research was to identification of drought tolerant genotypes in cumin. Tolerance level of cumin ecotypes to drought conditions were assessed based on some tolerance indices in a randomized complete block design with two replications in field experiment. Five drought tolerance/susceptibility indices including mean productivity (MP), geometric mean productivity (GMP), and stress tolerance index (STI), stress tolerance index (TOL) and susceptible stress index (SSI) were calculated based on grain yield under drought and normal conditions. Based on principal components analysis method2 sub-populations from pars province identified as the most drought tolerant ecotypes. Therefore ecotypes were identified could be valuable resources for identification of genes responsible for drought tolerance in molecular plant breeding. Results showed MP, GMP and STI indices were more effective in identifying high yielding cultivars in diverse water scarcity whereas TOL and SSI indices were useful to determine resistant cultivars.

# EXPLOITATION OF HETEROSIS - AN APPROACH FOR ENHANCING DROUGHT TOLERANCE AND YIELD IN POSTRAINY SEASON SORGHUM

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Post-flowering drought stress is the major production constraint in postrainy sorghum (*Sorghum bicolor* (L.) Moench) grown on more than 4.5 m ha on residual soil moisture, concentrated mainly in India. Drought adapted land race cultivars are still widely grown in the postrainy season. Sorghum produced during this season is prized for its grain and stover quality. Development of hybrids adapted to drought was suggested as an avenue to improve postrainy sorghum productivity and hence to contribute to ensure food security. An experiment was conducted to identify stable heterotic hybrids under drought conditions. We generated 354 new hybrids by crossing postrainy adapted parents during 2009 postrainy season and evaluated them in 2010 postrainy season in an augmented design at ICRISAT-Patancheru, 75 promising hybrids were selected. The selected hybrids were evaluated in replicated trial during 2011 postrainy season at ICRISAT-Patancheru and 51 hybrids were selected based on their superiority for agronomic traits and grain yield. The selected 51 hybrids were evaluated in a multi-location replicated trial using RCBD over three locations of India (Patancheru, Rahuri and Parbhani) during 2012 postrainy season for assessing their yield potential under drought conditions. Drought was imposed in the field by giving only two irrigations at critical stages of plant growth, panicle initiation stage that coincides with 30 days after sowing and flowering stage which coincides with 60 days after sowing and stopping irrigations after that. Drought adapted popular landrace cultivars were used as controls in the experiment. No rainfall received in all three test sites after stopping the second irrigation at 60 DAS and the genotypes experienced drought. Data were recorded on agronomic traits, grain yield and grain quality traits. The crop was harvested at physiological maturity stage. Combined analysis of multilocation-data indicated that of the 51 hybrids tested, 16 hybrids showed high yield under drought conditions and possessed farmers preferred grain quality attributes. Three hybrids significantly out yielded the controls and remaining 13 hybrids were not significantly different from the controls. The selected hybrids flowered early and possessed bold, pearly white grains which are preferred traits by farmers and consumers. These hybrids can be eventually commercialized after testing for specific adaption. Our experience in exploiting heterosis through the development of hybrids and selection for yield and drought tolerance in alternative seasons proved to be a very promising approach for enhancing grain yield and drought tolerance for postrainy season adaptation.

# FEATURES OF GAS EXCHANGE DAILY DYNAMICS IN VARIOUS WHEAT VARIETIES UNDER DROUGHT CONDITIONS

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Study of the dynamics of leaf area formation and dry biomass accumulation in various wheat varieties under drought is of great practical importance. Daily dynamics of $CO_2$ gas exchange is of much importance for assessment of adaptation and comparison of the assimilating activity of various winter wheat genotypes under the moisture stress. Daily changes is photosynthetic intensity of the both investigated varieties (Baraketli-95 and Girmizi bugda), irrespective of the leaf, are expressed as the curves with a peak in the morning hours depression at the noon and a relatively lower and shorter rise and faster drop associated with the sunset. Total $CO_2/dm^2$ assimilation of the 8th leaf of Baraketli-95 and Girmizi-bugda under moisture stress and irrigation was equal to 103 and 113 mg $CO_2/dm^2$ day and 72 and 93 mg $CO_2$ day, respectively. While the hourly average intensity of photosynthesis was estimated to be 7.8 and 8.4 mg $CO_2/dm^2$ hour for Baraketli-95 and 6.2 and 7.1 mg $CO_2/dm^2$ hour for Girmizi-bugda, under moisture stress and irrigation. The study results show that varieties Baraketli-95 and Girmizi-bugda have similar values for the daily gas – exchange dynamics, photosynthesis raise, total assimilated $CO_2$ and its hourly average. Also, water stress impact on photosynthetic activity as well as the critical period of water stress is similarly reflected by the photosynthetic parameters in both genotypes.

# FLAG LEAF REFLECTANCE EFFICIENCY AS INDICATOR FOR DROUGHT TOLERANCE IN DURUM WHEAT (TRITICUM DURUM DESF.) UNDER SEMI ARID CONDITIONS OF ALGERIA

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The present study was led on the experimental site of ITGC (Technical Institute of Field Crops) station of Setif, Algeria during two cropping seasons (2010/2011 and 2011/2012). This study aims to evaluate the efficiency of using Mesurim Pro (Version 3.3) software in the measure of the reflectance at Red (654 nm) and Blue (450 nm) (RB) wavelengths, and to investigate the spectral behavior of the relationship between reflectance at RB, Grain yield, Senescence parameters and Chlorophyll content in set of durum wheat genotypes and evaluate the relationships between drought resistance indices and reflectance at Red and Blue. The reflectance is measured using the numerical image analyses (NIA). The results of the present study indicated that the two different conditions of growth (stress and irrigated conditions) had different considerable effects on all traits tested during the two cropping seasons. The best negative and significant correlation between flag leaf reflectance at Red, Blue, Grain yield and drought resistance indices suggest the efficiency of using the reflectance for the predicting of grain yield and screen tolerant genotypes in durum wheat. In addition, the best correlation between leaf reflectance and senescence parameters suggest that the genotypes with slow senescence have low values of leaf reflectance. All this results prove the efficiency of using Flag leaf reflectance at Red and Blue as suitable tool for screening in durum wheat cultivars for high grain yield and under drought condition.

**Key words:** Durum wheat, flag leaf reflectance, drought indices, irrigation, Senescence, Chlorophyll.

# FLAG LEAF SENESCENCE IN DURUM WHEAT AS SELECTION INDEX FOR GRAIN YIELD UNDER DROUGHT CONDITIONS

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The relationships between leaf senescence parameters and yield components were examined in ten cultivars of durum wheat, *Triticum turgidum* subsp. *durum* (Desf.) Husn., grown in the high plains of Setif, eastern Algeria. Leaf senescence was estimated during grain filling by numerical image analysis (NIA) and by transmittance, measuring chlorophyll degradation with a chlorophyll meter. Senescence parameters were calculated to characterize the evolution of senescence with time. Cultivars ranking differed for senescence over time and senescence parameters, indicating that multiple measurements during the grain filling period and use of multiple parameters are required for accurately comparing the dynamics of senescence among cultivars. Genotype effects were significant for most parameters estimated by NIA, but not for parameters measured by transmittance. A highly significant correlation was found between senescence values (averaged across cultivars) estimated by NIA and transmittance but no correlation was found between the two methods for any of the measured parameters. For each method, a significant negative correlation was noted between senescence averaged across measurements and the date of mid-senescence (defined as the sum of temperatures corresponding to a senescence value of 50%). A significant correlation was noted between grain yield and the date of mid-senescence calculated by the NIA method. No association was found, however, between senescence parameters (measured either by NIA or transmittance) and grain weight or grain growth rate. The study evidenced the potential interest of NIA methods for a more precise analysis of the dynamics of senescence and a comparison of cultivars for this trait. Together with previous experiments, it however confirmed the strong influence of environmental conditions on the average level, onset and maximal rate of senescence, the ranking of cultivar for those traits, and the association between senescence and yield.

**Key Words**: Durum Wheat, numerical image analysis, measurement, genotype, senescence, transmittance method

# GENETIC AND QTL ANALYSIS FOR AGRONOMIC TRAITS IN A TUNISIAN DOUBLED-HAPLOID BARLEY POPULATION

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Fifty-nine doubled-haploid (DH) barley lines and their two parents 'Roho' and 'Line90' were planted in a randomized complete block design with three replications at the research farm of Superior Agronomic School of Mograne. They were evaluated for the nine agronomic traits: heading date (HD), plant height (PH), spikes number per meter (SN), ear length (EL), number of seeds per spike (NSS), 1000-grains weight (TGW), biomass (BM), seed yield (SY) and harvest index (HI). Analysis of variance indicated the presence of some superior transgressive lines. Heritability estimates were more than 0.7 for HD, NSS and TGW. Genetic correlation analysis indicated significant association among some traits particularly HD with SN and TGW; and also SY with PH, EL and BM. Furthermore, it was shown that the spike type have a significant effect on all traits except PH and HI. The segregation of 34 SSR markers were used for quantitative trait loci (QTL) mapping. For the nine agronomic traits, 19 QTLs with additive effect are mapped on eight chromosomal positions of 2H, 3H, 4H, 6H and 7H. Phenotypic variance explained by these QTLs varied from 4.6 to 76.5%. This analysis showed that the two parents contributed to improve agronomic traits by providing favorable alleles.

**Key words:** *Hordeum vulgare*, doubled-haploid population, genetic analysis, agronomic traits, quantitative trait loci.

# IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES UNDER LOW TEMPERATURE IN WINTER WHEAT

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Cold is one of the main abiotic stress causing winterkill of winter wheat. In winter cereals, frost tolerance is associated with the occurrence of a cold-hardening which is triggered by induction or repression of cold responsive genes after exposure of plants to low but non-freezing temperature (LT) for certain periods of time. In order to detect new differentially expressed genes at the different point of cold acclimation period two promising winter wheat lines (‘5899-16’ ir ‘5450-1’) were cold-acclimated at +4 °C for 6 weeks in the plant growth chamber. cDNA was synthesized from mRNA of crown and leaf tissues collected in three biological replications at 0, 2, 4 and 6 weeks of cold acclimation. cDNA-AFLP analysis was performed using 48 primer pair combinations, which generated 522 transcript-derived fragments (TDFs). 19 TDFs (3.6 %) were identified as being differentially expressed (presence/absence) between cold acclimated and non acclimated wheat. 13 TDFs (68.4 %) were up-regulated and 6 TDFs (31. 6%) were down-regulated within 2 weeks after the start of the cold acclimation. All 19 TDFs were excised from gels, cloned and sequenced. BLASTx search of the GenBank non-redundant (nr) sequence database demonstrated that 12 of the TDFs belonged to known sequences with putative functions related to metabolism (7), signal transduction pathways (2), transport (1) and protein modification (1). Further expression analysis of these genes using real time RT-PCR will confirm or deny their involvement in the cold acclimation process of winter wheat.

# IDENTIFICATION OF WHEAT BREEDING MATERIAL RESISTANT TO LEAF RUST *PUCCINIA RECONDITA* F. SP. *TRITICI*

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Resistance to leaf rust *Puccinia recondita* f. sp. *tritici* is the most important objectives in Kazakhstan. This disease is one of the major factors that adversely affect wheat yield and quality, reducing by 30-50% yield. The development of donors and potential breeding lines resistant to stripe rust is a very important task. The aim of the present study was to screen 63 accessions, including commercial cultivars and elite advanced wheat lines from Kazakhstan and Belarussia, with markers linked to effective leaf rust genes. For the identification of Lr-gene sources, STS J13, STS Gb and STS J09 markers (http://maswheat.usdavis.edu) associated with known effective genes (*Lr9, Lr19* and *Lr24*) were used in screening the accessions. Using STS marker J13, associated with *Lr9*, five carriers of this gene (Belarusian cultivars Rassvet, Daria, Visa, Toma and cultivar from Kazakhstan Samad) were identified. Resistance to leaf rust in these cultivars on a natural background was within the 5R-20MR. Two Belarusian elite lines KSI16/12 and KSI22/12, 1 Russian cv. Pallada and 8 of Turkey-CIMMYT elite lines with *Lr19* were identified using the STS GbF/R primers. 16 elite wheat lines with STS marker J09 generated the DNA fragment associated with *Lr24*. Among them Almaly/GF92, Almaly/Umanka, 4 lines Naz/Obrij, 3 lines 428d/MK-122A, 2 lines Naz/Renan, 1 line Naz/Immun78, 4 lines Naz/Umanka. Genetic and pathological work selection in different breeding nursery revealed to select 20 wheat lines that combine resistance to leaf rust in productivity.

# IMPACT ENVIRONMENTAL OF GROWING ON VIABILITY OF SEEDS

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The influence of soil and climatic conditions on the formation and properties of abundant crop seed quality calls for an environmental approach in the organization of seed production. This raises the need to identify favorable areas and micro-watersheds for high-quality seeds in this large region of the country. For this reason, Kazakh Scientific – Research Institute of Farming and Plant Growing initiated research in all agro-ecological zones of the south, southeast, east of Kazakhstan. The objects of the study were promising and approved for use in the Republic of Kazakhstan varieties of winter and spring wheat. The studies were conducted on the piedmont plain of Trans-Ili Alatau, 2nd foothill zone (Sarkand), middle (St George), foothill-dry (Zhambylky), dry steppe (Shiely), mountain-meadow and steppe (Zyryanovskiy) zones. The results showed that all the studied varieties of seeds of different ecological points were viable respectively vigor and germination of seeds, the figures in the zones were within 95-97%. Grain moisture, depending on the ecological zones was on grades from 7.1% (St George SSP) till 18.0% (Ziryanovski SSP). Coarse grain from varieties of winter wheat depending on the meteorological conditions formed in the dry steppe zone, where the average weight of 1000 grains is 44.0 and the lowest was in the foothill areas, 34.7 g. Highest yield obtained in the varieties grown in the medium-band (SSP George), where he was from 14.7 till 18.9 kg / ha. If we consider the percentage of injury to the seed zones, it was in the range from 61.0 till 74%. Thus, the winter wheat variety Vitreous 24 more seeds were subjected to injury in the foothills, piedmont dry areas - 74% less than it was injuries seeds grown in the dry zone, 64.5%. Seeds of winter wheat Karla more were injured in a dry steppe, dry foothill areas (Shiely GUS) - 73.0% less likely in foothill areas. Seed varieties Almali more damaged in the foothill areas, 74.0%, to a lesser extent in the dry steppe - 61.5%. On the sort of injury Farabi seeds for all zones within 71.5%. Damage to the seed grown in the mountainous zone (Ziryanovski GSM), up by grades 70,5-71,5%. By varieties of spring wheat degree of injury was in the zones 67-72%. The results of experiments to determine the intensity of the initial growth showed that the highest they have been in the seeds of all the studied varieties grown in the piedmont zone (Sarkand SSP). On average, according to grades on the 10th day in the area rose 90-92%, while in the dry foothills of 71-74%, respectively. Along with high growth vigor in seeds during germination the seedlings were formed with five roots, and seeds with dry foothill zone dominated seedlings with three spines. Seeds of winter wheat Jubilee 60 grown under dry-band (SSP Shiely) showed high strength increase (85%) compared with the other studied in the area of winter wheat (Karla, 81%, 75%, Almali, vitreous 24 - 76%). Seeds of spring wheat varieties Pamyat 47, Zhenis middle mountain zone (St George SSP) on this indicator inferior seed varieties of winter wheat, where the force of their growth was 70-72%, compared to 74-87% in winter. Low levels of growth compared to other regions are in the seeds of winter wheat and Bulava, Mironovskaya 808 grown in the mountainous zone (Ziryanovski SSP), the force of growth was in the range 71-76%, and the seeds of spring wheat varieties Alem, Lyazat from the same zone had the force of growth, respectively, 71 to 73%. Thus, according to studies revealed that the extent of injury and the intensity of the initial conditions affect the growth of seeds of growing seed varieties and biological features.

**Keywords:** variety, seed ecology, germination, moisture content, particle size, injury, strength growth.

# INFLUENCE OF ENVIRONMENTS ON THE AMOUNT AND STABILITY OF GRAIN YIELD IN THE MODERN WINTER WHEAT CULTIVARS. II. EVALUATION OF EACH VARIETY

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Cultivars grown in the production were selected and tested for three consecutive years at eight locations in Bulgaria; those were representative for the entire territory of the country and had contrasting soil and climatic conditions for growing of the crop. Multiple statistical methods and approaches were applied to evaluate the adaptability of each cultivar by grain yield against the background of the complex genotype x environment interaction. Significant variations of grain yield were found among the investigated cultivars regardless of their specific response to the year conditions and the location. The interaction genotype x environments was significant and high, and was in essence of non-linear type. The changeable environmental conditions caused different reactions of the cultivars, which allowed dividing them into groups according to the plasticity and stability, they demonstrated. The variation in this experiment determined through principal component analysis reached level four, which is comparatively rare for this trait. On the whole, PC1 had low value (49 %), while PC2 was high (16 %). The investigated cultivars differed not only by grain yield but also by their plasticity and stability under changeable environments, nevertheless of the genotype effect being about 12 % for the entire experiment. It was found that each cultivar can give high grain yield at high stability regardless of its genetic potential for quality. Best balance between grain yield and stability was found in cultivars Aglika, Demetra, Iveta (first quality group), Galateya, Slaveya (second quality group) and Todora, Kristal and Pryaspa (third quality group).

# INOCULATION EFFECT OF ENDOPHYTIC BACTERIUM (*BACILLUS SP.*) ISOLATED FROM WILD RICE *ORYZANIVARA* ON SRI LANKAN TRADITIONAL RICE VARIETY MA WEE

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Rice *(Oryza sativa)* feeds the 50% of world population. Nitrogen (N) fertilizer is a major cost of rice production. Sri Lankan wild rice *Oryzanivara* thrives without N fertilizer. We have isolated an endophytic bacterium from *Oryzanivara,* which was identified as *Bacillus megaterium* or a very closely related species based onits 16SrRNAsequence. We studied the effect of inoculation of Sri Lankan traditional rice variety Ma wee with the *Bacillus*isolate. A complete randomized design (CRD) with 10 replications was carried out in greenhouse. There were four treatments based on inoculation and N at an equivalent concentration of 25 kg/ha; [inoculated and fertilized (I/F), inoculated and non-fertilized (I/NF), non-inoculated and fertilized (NI/F) non-inoculated and non-fertilized (NI/NF)]. Total chlorophyll content (TC) and plant height (PH) were measured at 5th week during vegetative stage. First panicle length (PL), number of filled grains (FG) and filled grain weight (FGW) were recorded and harvest index (HI) was calculated. A significant positive effect ($p<0.05$) of inoculation was identified for TC in I/F and I/NF versus NI/NF; PH was highest in I/F (130.25±3.56cm)versus the lowest in NI/NF (107±0.40 cm). I/F, I/NF and NI/F showed significantly($p<0.05$) higher PL (24.63±0.87, 24.02 ±1.07, and 22.03±1.16 cm) and FGW (1.14±0.11, 1.13 ±0.12and 1.04±0.14g) respectively than NI/NF (18.73 ±2.26 cmand 0.65 ± 0.11 g). I/F and I/NF had a significantly higher HI (21.16 ± 1.53 % and 23.4±1.41%) than in NI/NF (15.4 ± 2.19%). Significantly lowest FG was recorded from NI/NF (32.71 ± 4.03)in contrast to I/F, I/NF and NI/F (53.50±4.41, 49.25± 4.11 and 45.42 ±4.94 respectively). Our experiment indicates that our bacterial isolate may reduce the requirement ofSri Lankan traditional rice for N fertilizer.

**Keywords:** *Bacillus megaterium*, endophytic bacterium, *Oryzanivara,* Sri Lankan traditional rice

# MAJOR CHANGES IN PEROXIDASES SYSTEM UNDER COLD ACCLIMATION IN *MEDICAGO*

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The production of a crop is challenged by abiotic and biotic stresses. Temperature is one of the most important environmental factors controlling seed germination and seedling heterotrophic growth and also limiting crop distribution. During crop establishment, extreme temperatures can decrease plant emergence and lead to drastic losses in crop yield and quality. Up to 15 percent of the world's agricultural production is lost to frost. Germination and seedling growth are stages that are rarely a specific and primary target for breeders, increasing knowledge on tolerance to extreme temperatures could lead to possible genetic improvements (Dias et al. 2010). It is of vital significance to understand plant resistance mechanisms and cultivate new varieties with high resistance. The genus *Medicago* has emerged as an important experimental species. The development of annual *Medicago* seedlings under a regime of low temperature defers a species to another one. Changes in isozymes of peroxidases activities are generally related to stress responses. To minimize oxidative damage, plants have evolved various enzymatic and nonenzymatic defence mechanisms to detoxify free radicals and reduce oxidative stress. The aims of this work was to investigate biochemical changes in contrasting cold tolerance annuals *Medicago* populations originate from different Algerian eco-geographique sites and try offer some referential criteria in terms of biochemical tools in *Medicago* annuals population with high tolerance, as well as their selection and breeding.

# MOLECULAR CHARACTERIZATION OF FINGER MILLET (*ELESUINE CORACANA* L.) GENOTYPES USING INTER SIMPLE SEQUENCE REPEAT (ISSR) MARKERS

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Molecular characterization of the 32 finger millet genotypes was done using Inter Simple Sequence Repeat (ISSR) markers to assess the genetic diversity at State Level Biotechnology Center, MPKV, Rahuri, M.S. India during 2012. These promising 32 finger millet genotypes were selected from field evaluation of 65 genotypes during *kharif* 2009 and 2010. Among the 42 ISSR primers screened 20 primers produces polymorphic bands. It produced a total of 83 scorable bands out of which 75 were polymorphic and eight bands were monomorphic. Maximum scorable bands were observed using the primer IS-8 (7 bands), followed by ISSR-827 (6 bands). The least number of bands were reported in the primer ISSR-814 and ISSR-8386 (2 bands each), followed by IS-13, ISSR-855, ISSR-8082 and ISSR-8932799 (3 bands each). The maximum number of bands were observed in the genotype KOPN 926 (65 bands), followed by KOPN 892 (62 bands) and KOPN 922 (61 bands). Whereas KOPN 241 and PR 202 (29 bands each) reported least number of bands followed by VL 149 (30 bands) and KOPN 892 (31 bands). Similarity analysis using ISSR markers revealed moderate to high diversity among the finger millet genotypes under study, with the similarity index value ranging from 0.409 to 0.907. Maximum diversity was observed between the genotypes KOPN 370 and KOPN 241 (0.409), followed by KOPN 892 and KOPN 241 (0.433) and KOPN 338 and KOPN 241 (0.437). Maximum similarity was observed between the genotypes KOPN 338 and KOPN 922 (0.907), followed by KOPN 926 and KOPN 922 (0.905) and KOPN 865 and KOPN 922 (0.894). The 62 genotypic combinations showed the similarity index above 0.80, whereas 94 genotypic combinations reported similarity index between 0.75 to 0.80 and 88 genotypic combinations reported similarity index between 0.70 to 0.75 showing high similarity between these genotypes. The UPGMA based clustering analysis grouped 32 genotypes into four mega-clusters. It shows highest 24 genotypes in cluster I sub-grouped into six subclusters, followed by cluster III (4 genotypes with two sub-clusters) and cluster II (3 genotypes), whereas cluster IV was monogenotypic. This ISSR analysis study revealed that the genotype KOPN 241, KOPN 370, KOPN 892 and KOPN 338 can be considered as parents of interest and crossed with elite material to develop new breeding population in finger millet.

**Key words:** Finger millet, Molecular diversity, ISSR markers

# OBTAINING MAIZE (*ZEA MAYS L.*) LINES UTILIZING BY DOUBLED HAPLOID TECHNOLOGY AGRONOMIC AND MOLECULAR CHARACTERIZATION

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**The core activity of seed sector and seed is plant breeding and variety development. The progress in achieved science, technology and economy becomes accelerated and advanced to have new plant variety in 20 th century. Most critical stages of maize breeding is to improve inbred lines which has highest general and specific combining ability. This kind of working takes long time, needs high budget and labor force. Having inbred lines which will be used for hybrid development takes at least 7-10 years. Nowadays double haploid (DH) lines produced by in vivo induction of maternal haploids are prevalent in maize (*Zea mays L.*) breeding. Haploids in maize can be obtained either through in vitro or in vivo. Haploid technique utilizing by anther culture for reducing times has been used for many years as well but not become widespread because of low success rate. Success rate is getting higher by using inducer lines in recent years and DH technology has been applied in maize breeding program especially by commercial seed companies. In vivo DH technology reduces breeding cycle to 2-3 seasons for obtaining inbred lines process. The other advantages are maximum genetic variance, complete homozygosity, reduced expenses etc. Agromar Seed Company has started to used this technology since 2011. Haploid and doubled haploid line's molecular characterization and genetic diversity identified by marker assisted selection (MAS) . Having two generations in one season in greenhouse facilities has also been used. 20 different donor x inducer crossing process had been done in 2012-2013 season and 4105 putative haploid seeds were identified. The induction rate in this working may vary % 8-18. As a result 75 DH-lines were obtained at the end of 2013 season and crossing process for having hybrid has been going on. Among 75 DH lines, 40 DHL were screened by SSR and 39 were identified as a homozygous.**

# PARTICIPATORY DEVELOPMENT AND SELECTION OF A NEW SET OF CLIMBING BEAN GENOTYPES WITH MORE ACCEPTABLE SEED TYPES AND RESISTANCE TO *PYTHIUM* ROOT ROT DISEASE

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A research project was initiated to develop new climbing bean genotypes with more acceptable seed types, high yield potential and resistance to *Pythium* root rot disease. Using selected popular traditional land races such as Masindi yellow and Kanyebwa and mid altitude climbers (MACs) which are known to possess acceptable seed types, but susceptible to *Pythium* root rot disease as female parent germplasm and MLB 49-89A and RWR 719 as the male parents with un acceptable seed types but resistant to *Pythium* root rot disease, new crosses were made. Both two way and three way crosses were generated. The resulting two way and three way cross hybrid seeds were selfed up to the $F_4$ generation. Starting at the $F_4$ generation, the segregating populations were subjected to participatory evaluation and selection while advancing them up to $F_6 – F_8$ generations. Data was collected on the important agronomic, morphological traits and seed quality traits. Evaluation for reaction to *Pythium* root rot disease was also carried out using both phenotypic and molecular marker techniques. Results on the performance of the new climbing bean genotypes are discussed.

**Key words**: climbing, common bean, seed type, traditional land race

# PARTICIPATORY EVOLUTIONARY CEREAL BREEDING UNDER RAINFED AND IRRIGATED CONDITIONS OF IRAN

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In 2008 we started an evolutionary plant breeding (EPB) program for rainfed barley utilizing 8 kg of a mixture of 1600 $F_2$received from ICARDA. The seed was plantedby a farmer in Dalahoo, West-Iran. Althoughplantedlate, the mixtureperformed well; in 2009 the farmer planted half-hectare.The mixture out-yielded the local barley and performed like the improved cultivar Sararood-1.Based on this success, a bread wheat mixture was made in 2010, utilizing the backup seeds in the seed store, and the seeds of the segregating populations from DARSI breeding program. The mixture was planted in a farmer's field in Sahne (Kermanshah province). Despite a epidemic of yellow rust and lodging problems in the adjacent fields, the EPB population showed good resistance to both rust and lodging, and yielded 3500 kg/ha, whilethe local check, Sardari, yielded 1500kg/ha. In the dry 2010-2011, the evolutionary population out-yielded again Sardari. The same results are observed by farmers in the Semnan province, wherethe evolutionary populations of barley and wheat, grown under irrigated condition show good yield, higher resistance to pests and lower infestation byweeds.

# PROTEOMICS ANALYSIS IN SOYBEAN ROOT INOCULATED WITH COMPATIBLE BACTERIA UNDER FLOODING STRESS- CAN *BRADYRHIZOBIUM JAPONICUM* INDUCE FLOOD TOLERANCE?

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A proteomics approach was used to evaluate the effects of flooding stress on early symbiotic interaction between soybean roots and soil bacteria, *Bradyrhizobium japonicum*. Three-day-old soybean was inoculated with *B. japonicum* followed by flooding. The number of root hairs was increased after 3 days of inoculation. Proteins were extracted from roots and separated by two-dimensional polyacrylamide gel electrophoresis. Of 219 protein spots, 14 and 8 proteins were increased and decreased, respectively, by inoculation under flooding compared to without flooding. Increased level of 6 proteins in flooded seedlings compared to untreated seedlings was suppressed by inoculation in seedlings under flooding. Differential abundance of glucan endo-1,3-beta-glucosidase, phosphoglycerate kinase and triosephosphate isomerase based on their localization in middle and tip of root, indicated that they might be related to increase in number of root hairs. These results suggest that disease/defense, energy and metabolism related proteins may be subjected to regulation in flooded soybean seedlings, when inoculated with *B. japonicum* and this regulation may lead to increased number of root hair during early symbiotic differentiation.

# RELATIONSHIP OF MORPHOLOGICAL TRAITS WITH RAPD AND ISSR MARKERS IN SUGAR BEET

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Assessment of the genetic diversity of different crops on the basis of molecular markers and morphological traits is the most common practical work, however less studies were done aimed at the combined use of molecular and morphological characteristics in sugar beet. This paper presents the results of the morphological assessment conducted in the experimental

area of Genetic Resources Institute in 3 replications using RCBD (Randomized Complete Block Design), also molecular data were described. Random amplified polymorphic DNA (RAPD), inter microsatellite (ISSR) markers and morphological parameters on 5 quantitative traits were used to estimate 42 sugar beet genotypes. The original matrix based on these results was constructed to calculate the genetic distance and similarity and the dendrogram was created. The value of Nei's genetic distance (RAPD-analysis) and Jaccard's genetic similarity indices (ISSR-analysis) ranged from 0.03 to 0.24 and from 0.359 to 0.71, respectively. The Mantel test conducted to compare the matrices of two different marker systems was significant, $r = 0{,}92$ **. So it showed a high correlation between the matrices and concordance of dendrograms created based on these data. As a result of the study of relationship between morphological parameters and ISSR - RAPD matrices significant correlation was determined ($P < 0{,}01$). The correlation coefficient (r) between morphological parameters and RAPD-ISSR matrices was 0.506 and 0.508, respectively. Significant correlation between morphological features and molecular markers can be explained by high heritability and stable character of these parameters. Thus, both marker systems along with noted motphological traits can be recommended as an effective tool for the evaluation of genetic polymorphism of sugar beet genotypes.

# RESEARCH AND ESTIMATION OF MORPH PHYSIOLOGICAL TRAITS IN SELECTION OF WHEAT

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The farmer varieties are not input–responsive and therefore they don't fit the needs of the agricultural develop med, which is mostly based on high-input technologies (high fertilizer rates, modern crop management practices, etc). The appropriate use of new achievements of the crop breeding, identification and evolvement of yield related morph- physiological traits in the breeding process and proper selection of parental forms in crosses are the challenges to be tackled by breeders. Study of the dynamics of leaf area formation and dry biomass accumulation in various wheat varieties under drought is of great practical importance. We have attempted to study the effect of the moisture stress on the leaf area formation dynamics and dry biomass accumulation during the ontogenesis. Two local wheat Azametli-95 and Girmizigul-1 were used as the study material. It should be noted that fast increase in the leaf area for both genotypes was observed at the beginning of the ontogenesis in both various moisture stress and irrigated. Maximum values for the leave area of Azametli-95 and Girmizigul-1 were recorded in, at the end of the booting. Thus the obtained data provides evidence that the leaf area and the leaf dry biomass accumulation dynamics are influenced not only by the plant development stage and genotype, but also by environment, especially by such strong factor as water stress.

# SCREENING OF TWO RICE GENOTYPES (AMBER33 AND AMBER BAGHDAD) FOR DROUGHT TOLERANCE USING CELL SUSPENSION CULTURES AND PLANTING TECHNIQUES

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Seeds of two rice genotypes Amber33 and Amber Baghdad were presoaked in 1.5mM of Sodium azide (SA) for 4 hrs which is the optimum dose for mutagenesis with SA that caused 40% reduction in seedlings height. This dose gave the highest genetic variation and less sterility in both genotypes. Calli from both SA treated and non-treated genotypes were induced from mature embryos on appropriate medium while cell suspension cultures were initiated by placing about 100mg callus pieces into 250ml flasks containing 100ml of Murashige and Skoog, (1962) medium (MS) supplemented with 0.5mg/l kin (Kinetin) and 2.0mg/l 2,4-D (2,4-Dichlorophenoxyacetic acid), then placed on a rotary shaker at 100rpm for 30days. Growth curves of cell suspension cultures were examined during a range of culture periods 0, 5, 10, 15, 20, 25 and 30 days. In all cell lines, the growth rates of cells were initially slow but as the culture proceeded, they increased and accumulated great amounts of biomass over a period of 20 days. The best inoculums for cell plating were determined by plating aliquots of 1.0, 1.5, 2.0, 2.5, 3.0, 3.5 and 4.0ml of cell cultures into 20ml solidified MS medium poured into Petri dishes. Packed cell volume (PCV) and the number of colonies were recorded after four weeks of cell plating. Inoculums convenient for cell plating were inoculated into MS medium supplemented with different concentrations of PEG6000 (0.0, 0.5, 1.0, 1.5 and 2.0%) for screening and selecting cell lines tolerant to drought. Shoot formation was induced on MS medium supplemented with NAA (Naphthaleneacetic acid) and IAA (Indole 3-acetic acid) at 0.5mg/l and 4.0mg/l BA (Benzyle adenine). Proline and carbohydrate concentrations were determined in regenerated shoots of plated cell suspension cultures. Results showed no significant differences between the two genotypes in respect to PCV, mean no. of colonies after screening on different PEG concentrations, mean no. of shoot/cell aggregate, proline and carbohydrate concentrations while these parameters significantly increased at 1.5mM SA treated genotypes compared with untreated. Results also revealed a significant reduction in mean no. of colonies, mean no. of shoot/cell aggregate and carbohydrate concentrations with the increasing of PEG concentration especially in SA non-treated genotypes. Proline concentrations significantly increased with the increasing of PEG concentration in the plantlet leaves regenerated from cell suspension cultures and the highest value was recorded in 1.5mM SA treated genotypes.

# SOYBEAN YIELD AND SEED GERMINATION POTENTIAL OF GENOTYPES FOR RESISTANCE TO STINK BUG COMPLEX

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The soybean yield and seed quality can be decreased by stink bugs incidence during the production process of seeds. The selection of genotypes with potential traits for stink bugs resistance can provide parameters that will assist the selection of new soybean lines in breeding programs; therefore the identification of soybean genotypes potentially resistant to stink bugs is a relevant subject of study. This work aimed to compare the yield and seed germination parameters of several soybean genotypes under stink bugs attack. Twenty-four soybean genotypes were evaluated in presence and absence of chemical insect control, at 2012/2013 season. The experiments were conducted in a randomized block design with five replicates, at the Experimental Station of Anhembi (Department of Genetics, USP, ESALQ, Brazil). The following parameters were evaluated: i) seed yield (SY, g plot$^{-1}$); ii) healthy seed weight (HSW), g plot$^{-1}$), iii) seed germination (%G) and iv) resistance index estimation [% reduction = (HSW SY$^{-1}$) 100]. After ANOVA analysis, a significant interaction ($p \leq 0.05$) among genotypes and control systems was observed for the most evaluated parameters (except for % reduction). Among the selected genotypes, five could be considered as potential lines for productivity traits and, other four genotypes had great germination percentage in both presence and absence of insects. At least nine lines showed the lowest values for the resistance index estimation (% reduction) in the both control systems, highlighting LQ1050 line.

# THE ASSESSMENT OF PLANT PROPERTIES IN IRANIAN FENNELS FROM PERSPECTIVE OF CLIMATE EFFECTS

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Fennel (Apiaceae family) is used in food, cosmetic, and medical industries. In this study, 50 ecotypes of Fennel (*Foeniculum vulgare* Mill.) from all over Iran were collected and some plant properties were studied in two years. Results indicated these ecotypes were divided into three groups of long term (250 days), middle term (180 days) and short term plants (120 days). With considering of climate features in the origin regions of these ecotypes and plant properties of the ecotypes, it was found that phenological properties and subsequently morphological properties are completely affected by climate properties of origin regions. Required time to complete the life cycle in each ecotype exactly was matching with the number of months that simultaneously proper temperature and humidity exist. Long term ecotypes had the highest amounts of plant height, viability and inflorescent number because of stability of proper situation for high vegetative growth and subsequently high reproductive growth, and the lowest amount of weight of 1000 seed because of high inflorescent number. Any relationship between seed yield and essential oil content with climate was found. Iranian fennel has a wide diversity and in every climate, over time especial adapted plants to the local climates was produced, and in term of conservation of genetic reserves especially about those genotypes with low viability it is necessary that some conservation programs should be done. By demonstration of climate effects on plant properties, we should be more concerned about climate changes because we don’t know how our world will be affected by that.

**Key words:** Iranian Fennels, Plant Properties, Climate Conditions, Climate Changing

# THE EFFECT OF SALINITY ON SEED GERMINATION AND SEEDLING GROWTH IN CUMIN (*CUMINUM CYMINUM* L.)

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Salinity is one of the most important factors that limit plant growth production in the word. To evaluate the response of cumin in germination stage to salt stress this study was assessed in a completely randomized design with three replications. Sodium chloride were used to simulated salt stress to 25, 50, 75, 100, 125 mM and distilled water were considered as a control. Some traits such as germination rate, root and shoot length, wet weight of shoots, root and shoot dry weight and electrolyte leakage were measured. Results showed that the effect of various salinity levels on germination factors was significant. By increasing salinity level electrolyte leakage were increased. Since the length of shoot of seedling showed less decline at 75mM compared with 50 mM. Seem that cumin has a special mechanism to reduce the negative effects of salt stress on its shoots in 75Mm.

# USE OF PHYTOPATHOGENIC FUNGI TO PROTECT CEREALS AGAINST WEEDS

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Being widespread on the fields of agricultural crops, weeds are able to cause significant crop losses (up to 10-15%). The most harmful weeds for cereals are *Cirsium arvense, Echinochloa crus-galli, Vincetoxicum funerbe, Cynanchum acutum, and species from the genus Carduus.* Regular treatments with herbicides can result in changes in the structure of weed species and initiate an appearance of new herbicide-resistant weed forms. Today the use of phytopathogenic fungi as a very efficient and safe tool to provide a biological control of weeds becomes an attractive alternative to the use of chemical control agents. The search for fungal pathogens that can be used for the biological control of weeds from the genera *Carduus, Cirsium, Echinochloa, Vincetoxicum,* and *Cynanchum*, has been carried out in the Krasnodar region of Russia. The preformed phytopathological and molecular studies have made it possible to identify phytopathogenic mycromycetes representing potential biological control agents: *Puccinia suaveolens* (for *Cirsium arvense*)*, Puccinia calcitrapae var. centaureae* (for different species of the genera *Carduus*)*, Ustilago trichophora* (for *Echinochloa crus-galli*)*,* and fungi from the genera *Phomopsis* and *Cercospora* (for *Vincetoxicum* and *Cynanchum*, respectively). Methods of the plant inoculation and inoculum production have been developed, and the pathogenicity of the selected fungi towards their host plants has been studied in their natural habitats. Basing on the *Xcelsius Present 2008* system, the web site http://phytofungi.weebly.com/index.html has been created that reflects the localization of weeds and phytopathogenic fungi, which are potential biocontrol agents, in the Krasnodar region of Russia. The maps of distribution of fungal weed pathogens are created on the basis of the Google map system. They can be shown as satellite, topographic, and relief maps of different scale. Special symbols are developed to show pathogen location points. The systems of the geolocation and spatial search of fungal pathogens and their host plants are planned to be developed in the future.

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# VARIABILITY, HERITABILITY AND ASSOCIATION ANALYSIS FOR YIELD, YIELD COMPONENTS AND KERNEL QUALITY IN SWEET CORN (*ZEA MAYS* L. VAR. *SACCHARATA)*

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The objective of this study was to determine genetic variability, heritability, and genetic advance, genotypic and phenotypic correlations of yield, yield components and kernel quality traits in sweet corn varieties. The present research was conducted during 2009 and 2010 growing season in Eskisehir, mid western Turkey. Seven sweet corn varieties (Lumina, Merit, Sunshine, Jubile, Challenger Yellow Baby and 2201) were used as materials. The trials were set up in randomized complete block design with four replications. Yield (husked, dehusked and fresh kernel), plant height, number of leaves per plant, ear weight (de-husked, husked), ear length, ear diameter, number of rows per ear, number of kernels per row, 1000 seed weight were determined as yield and related traits. Dry matter content, soluble solid concentration, protein, sugar and starch contents were determined as kernel quality characteristics. Analysis of variance observed highly significant differences for all the examined traits in both years. Sugar content, soluble solid concentration (for both years) and number of leaves per plant (in 2009) revealed the highest genotypic and phenotypic coefficient of variation values. Sugar content, soluble solid concentration (for both years) and starch content (in 2010) showed high heritability with high genetic advance. These characters can be improved efficiently by individual selection or breeding strategies in the examined populations. Positive correlations were found between yield (husked, dehusked and fresh kernel) and yield components except 1000 seed weight. Husked ear weight and dehusked ear weight (for both years) could be used as the main criteria for all three types of yield improvement when selecting in the studied materials. Also, significant correlations were estimated between yield-yield components and kernel quality in this study. Sugar content had significant negative correlations with fresh kernel yield and plant height (in 2010).

# BREEDING OF PEANUT (*ARACHIS HYPOGEAE* L.) VARIETY (*OSMANIYE-2005*) TOLERANT TO IRON DEFICIENCY CHLOROSIS

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This study was conducted in University of Çukurova, Faculty of Agriculture Field Crops Department in between 1993 and 2002 years. The objective of this research was to breeding high yielding and tolerant to iron deficiency chlorosis peanut variety. In this study, the crossing breeding method was used and plant selection was made according to "Pedigree selection" method in segregating materials. NC-7 and 75/1073 varieties were used as parents in this breeding program. Crossing was made in 1993 and harvested $F_1$ seeds. It was started to selection single plants at $F_2$ and continued to $F_5$ stages. The single plants were selected according to tolerance to iron clorossis, pod size and quality and pod yield. The selected lines were tested in seventh, eighty, ninth and tenth years. As a result, a breeding line is known [2000-19-B-(K)] was determined a new groundnut cultivar candidate as a high yield and tolerant to iron deficiency clorossis in 2003. According to test results, "The Registeration Comitte" has diceded to registration of [2000-19-B-(K)] line as OSMANİYE-2005 new variety.

# BREEDING PROGRESS OF SPRING WHEAT IN WESTERN SIBERIA AND THE PROTECTION OF BREEDING ACHIEVEMENTS IN RUSSIA

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According to the data of spring wheat trials that have been run on state sites in Western Siberia, there have been authoritative growth on 1,8% per year in yeld productivity for the last 31 years. With the average yeld productivity 3 t/ha, there have been groth on 1,3 t/ha – from 2,3 to 3,6 t/ha. The progress in breeding has contributed to the growth of average yeld productivity in main areas of the region. For instance, in the conditions of the growth of maximum temperatures in Spring-Summer period from 1961 to 2011, annual yield productivity growth of grain crops was 1,7% in Omsk region. The potential of grain yield productivity of the contemporary spring soft wheat varieties is more than 6,0 t/ha. However, financial receipts from royalty for using breeding achievements are inconsiderable. The system of the cooperation between patentees and licensees is one of the actual problems in modern Russia. The legal acts on the above-mentioned issue are reflected in The Civil Code of the Russian Federation, Part 4, Chapter 73 «The right to breeding achievements». Russian legislation divides definitions of author's right and sole right. Sole right of patentee consists of any entity's receiving license for dealing with seeds from patentee. Not only patentee, but also government bodies began controlling legality of seed using after accession of Russia to the World Trade Organization (WTO). Nevertheless, the problem of royalty receiving for seed sowing on private farmer fields remains debating.

# BREEDING WHEAT (*TRITICUM AESTIVUM* L.) WITH ENHANCED BIOACTIVE COMPUNDS

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Increasing interest in human nutrition has focused plant breeders' attention on the extent of variation and the genetic control of bioactive compounds in order to select new wheat varieties with improved nutritional values as the basis for a healthy cereal-based diet. The objectives of plant breeders are therefore to increase this variation using classical breeding and biotechnological tools, to combine existing germplasm rich in bioactive compounds with good agronomic and technological quality traits. The experiments carried out in the frame of HEALTHGRAIN FP6 EU project identified genotypes with high levels of water-extractable (WE-AX) and total arabinoxylans (TOT-AX). Yumai-34 and Seu-Seun 27 are outstanding for both traits. These genetic resources were used in breeding by crossing them with adaptive varieties with good agronomic performance as well as good breadmaking quality. This combination of properties makes it possible to produce healthy food products containing a high amount of dietary fibre from wheat. The efficient introgression of genetic resources into elite varieties by backcross breeding requires the screening of the progeny with molecular markers to detect the presence of the selected trait. Germplasm developed with mutations in granule-bound starch synthase genes (Sgp-A1, Sgp-B1 and Sgp-D1), which contain starch with an increased proportion of amylose was backcrossed with commercial wheat varieties that are adapted to various growing regions of Europe and have good processing quality, in order to obtain double or triple null mutant genotypes adapted for commercial production.

# COMBINING ABILITY THROUGH LINES × TESTER ANALYSIS AND HERITABILITY STUDIES IN UPLAND COTTON

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Line × tester analysis and heritability studies were carried out in upland cotton during 2011-12 at the University of Agriculture, Peshawar, Pakistan. Five lines (CIM-446, CIM-473, CIM-506, CIM-554 and SLH-284) and three testers (CIM-496, CIM-499 and CIM-707) were crossed through L × T mating system to generate 15 $F_1$ hybrids. Genotypes revealed significant ($p \leq 0.01$) variations for all the traits. $F_1$ hybrids showed significant increase over parental means. Mean squares due to lines were significant ($p \leq 0.01$) for earliness, bolls and seed cotton yield plant$^{-1}$. For bolls sympodia$^{-1}$, bolls and yield plant$^{-1}$ and lint %, the testers showed significant ($p \leq 0.01$) differences. The L × T interaction mean squares were significant ($p \leq 0.01$) for all traits except lint %. The earliness, bolls sympodia$^{-1}$, bolls and yield plant$^{-1}$ and lint % were controlled additively, while boll weight was controlled non-additively. In genetic variation, the line x tester contribution was maximum followed by lines and testers. Lines (CIM-473, SLH-284) and pollinators (CIM-707, CIM-496) were leading general combiners. $F_1$ hybrids (CIM-473 × CIM-496, CIM-473 × CIM-499, SLH-284 × CIM-707, SLH-284 × CIM-496 and CIM-506 × CIM-707) involve general combiners and revealed best performance for yield and lint traits. Heritability was moderate to high with appreciable genetic gain for majority traits. Except lint %, the correlation of yield was positive with other traits. However, bolls sympodia$^{-1}$ and bolls plant$^{-1}$ were the major contributors in managing seed cotton yield. $F_1$ hybrids with high × high, high × low and low × high general combiners can further improve the yield related traits in early segregating populations.

# MUTANT VARIETIES OF SOYBEAN, TOBACCO, CHICKPEAS AND THEIR DEVELOPED CHARACTERISTICS

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In this study, TAEK A-3 and TAEK C-10 soybean varieties with high yield, fat and protein content, TAEK-TUTLUER and TAEK- PEŞKİRCİOĞLU tobacco varieties for blue mold resistant, TAEK-SAĞEL chickpea variety with higher yield, antracnose tolerance and short cooking time featuring from irradiation of seeds to registration process of mutation breeding and related data presented. In addition, the cool climate cereals, legumes and industrial crops of effective dose of the mutation breeding studies forming the basis of (to ED50) determined and the method and the results of this method are given.

**Key words:** soybean, tobacco, chickpeas, mutation, mutation breeding, gamma rays, radiation

# PROSPECTS OF ASSOCIATION MAPPING IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

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In two sets of cotton (*Gossypium hirsutum* L.) germplasm, one mainly from China and the other from Pakistan, extent of linkage disequilibrium was assessed by using the same set of 98 SSR primer pairs. At significant threshold values of $r^2 > 0.05$, 3% and 7.1% SSR marker pairs showed a significant pairwise LD in Chinese and Pakistan *G. hirsutum* germplasm respectively. In the Chinese germplasm, two long stretches of LD blocks were observed on chromosomes D4 and D11, extending to a distance of 81 cM and 138 cM respectively. In *G. hirsutum* germplasm from Pakistan, long haplotypic block of 180 cM was observed on chromosome D5. The percentage of SSR loci pairs in LD in Chinese *G. hirsutum* germplasm was much lower as compared to germplasm from Pakistan and the previous reports of studies in *G. hirsutum*. This study shows that association mapping has potential and prospects to detect significant and reliable marker-trait associations in cotton and can be successfully employed in molecular breeding programs of cotton.

**Keywords:** Cotton- Linkage disequilibrium-Haplotypic blocks

# CEREALS BREEDING FOR APHIDS RESISTANCE

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The main obstacle to the successful development of aphid resistant cereal varieties is the occurrence of new virulent insect biotypes. Differential interactions with major genes for resistance were shown for *Sitobion avenae* F., *Rhopalosiphum padi* L. in wheat and for *Schizaphis graminum* Rond. in sorghum. Moreover, differential interaction of minor genes for greenbug resistance in sorghum with the insect genotypes was found. Consequently, aphid adaptation does not depend on phenotypic expression and genetic control of resistance. Resistant varieties with various genetic basis have to be cultivated. The gene pool of soft and durum wheat are poor in resistant forms. Among 4527 accessions tested only 48 were slightly infested under field conditions. Some varieties possessed the antibiosis to *R. padi*. Analysis of wild wheat (1043 accessions) showed an appreciable heterogeneity in resistance to *S. avenae* and *R. padi*. The species with $A^u$, $A^b$ and $A^bGD$ genomes were the most rational to be used in breeding. Resistance controlled by the G genome is overcome by the pests. Resistance to *S. graminum* was studied in 5059 sorghum accessions and 25 highly resistant lines have been isolated. Only cultivated sorghums had very effective greenbug resistance. Inheritance of resistance to *S. graminum* in some accessions was studied. We identified 15 genes for greenbug resistance in sorghum. At least 7 genes are of great interest for breeding.

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# CLASSIFICATION OF WHEAT VARIETIES WITH BIOCHEMICAL CHARACTERISTICS AND RAPD MARKERS

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The forty-eight wheat varieties studied with antioxidant enzymes and RAPD markers. Seventy primers used for DNA amplification of which 10 primers of them showed suitable banding patterns. These primers produced 73 polymorphic bands with mean value of 7.3 for each primer. The cluster analysis on based of Nei's distance and UPGMA method, distinguished four different groups. Based on PCoA three coordinates accounted for only 61.7% of variation, which indicated the proper distribution of markers in the surveyed wheat genomes because of relatively low percentage determined by the three first coordinates. Activities of antioxidant enzymes including catalase (CAT), glutathione peroxidase, ascorbate peroxidase (APX) and superoxide dismutase and amounts of malondialdehyde, total protein, $H_2O_2$, Na, K and Cl were measured. Cluster analysis classified varieties in three groups. Karkheh, Arta and Alborz Varieties had the lowest catalase, $H_2O_2$, malondialdehyde and considerable antioxidant enzymes. Genotypes of this group were identified as resistant varieties which could be used in breeding programs.

**Keywords:** Antioxidant Enzymes, Cluster Analysis, PCoA

# DETECTION OF POLYMORPHISMS AMONG NAKED BARLEY USING AGRO-MORPHOLOGICAL, HORDEIN, RAPD AND ISSR MARKERS

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The objectives of this study were to estimate the genetic diversity of 63 naked barley genotype using agro-morphological traits, biochemical and molecular markers and to determine the relationships of genetic distance estimates obtained from these methods. Among traits, a considerable diversity was observed for peduncle length, 1000-grain weight and grain yield per plot. 10 patterns in the area C hordein, and 13 patterns in the area B hordein were observed; and in total 32 bands and 32 patterns were observed. A total of 290 bands were observed using 16 RAPD primers, of which 222 (76.5%) were polymorphic. The total number of amplification products per primer ranged from 10 (S18) to 29 (S32) with an average of 18.12 bands per primer. In inter-simple sequence repeat (ISSR) analyses, a total of 283 alleles were detected, among which 261 alleles (92.2 %) were polymorphic. The number of alleles per primer ranged from 9 (ISSR-3) to 26 (ISSR-15) with an average of 17.7 alleles per ISSR primer. The results in this study suggested that, although the analysis of hordeins, RAPD and ISSR markers could successfully be used to investigate the genetic diversity of the barley accessions, the ISSR markers were superior to hordeins and RAPD markers in the capacity of revealing more informative bands in a single amplification. Whereas that all of investigated genotypes were from ICARDA, high level of diversity was observed in the samples through agro-morphological traits, storage proteins and molecular markers, which could be used in future breeding programs, widely.

# ESTIMATION OF NATURE AND MAGNITUDE OF HETEROSIS AND COMBINING ABILITY OF IMPORTANT TRAITS IN MAIZE (*ZEA MAYS* L.)

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Maize is a C-4 plant thus produces high productivity per unit area in comparison to other cereals. Maize is one of the promising crop for food, feed and industrial utilization. However, its protein is deficit in essential amino acids particularly, lysine and tryptophan. To overcome this deficiency, quality protein maize (QPM) with sufficiently higher quantity of lysine and tryptophan has been developed. Quality protein maize (QPM) has nearly twice the amount of lysine and tryptophan, which make the protein of QPM equivalent to 90% of the milk protein. The biological value of normal maize protein is 45%, while that of *o2* maize is 80%. QPM holds superior nutritional and biological value and is essentially interchangeable with normal maize in cultivation and kernel phenotype. The availability of QPM Donors developed at CIMMYT has paved the way for development of QPM hybrids. These QPM donors are being used to convert local lines into QPM lines with local agronomic back ground. Such local lines should combine well and exhibit high heterosis with QPM Donors. Keeping this in view eight QPM lines from DMR, New Delhi was used as Testers and ten local inbreds from BHU maize programme were taken as Lines into a Line x Tester crosses. The crosses were attempted during Kharif 2012 and main trial was conducted during Rabi 2012-13. The heterosis and combining ability estimates were calculated as per Line x Tester analysis (Kempthorne, 1967). The line x tester studies revealed that lines V 351, CM 141 and V 335 are good combiner against testers CML 141, CML 176 and CML 161 respectively for yield and yield contributing traits. SSR markers phi057, phi112 and umc1066 are being used for marker assisted selection conversion programme for quick conversion of local lines into QPM lines. The crosses CM 141 x CML 176 and V 335 X CML 161 are promising combination and will be converted into QPM lines having agronomic back ground of CM 141 and V 335.

# EVALUATION OF RICE, MAIZE, MILLET AND SORGHUM BY GRAIN AMYLOSE CONTENT FOR BREEDING PROGRAM

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Amylose content - on of the main composing criterions in rise grain quality evaluation. It is the right indicator of food rise nutrient quality. Rise amylose content separates to high (0-3%); low- (10-19%); middle - (20-24%) and high amylose (>25%). The 265 rise samples analyzed, including 235 - breeding. Whole changeability amplitude of variety genofund on amylose content is from 7.2 to 23.7% dry mass and among distributed among the next researched genotypes: with a very low content less than 10%-noted in 35.7% genotypes, with a low content (10-15) - 50%; middle content (15-20) -12.9%; more than 20% of amylose -1.4% genotype, including Zarya cultivar (20.2-24.7%); with a high content >25%> - is not founded. Collection and breeding Kaz SRI (Podolskih A., Baibosinova S.) of rise material characterized with a presence of highamylose genotype (16.4-27.8%)) and high protein (7.2-13.8%)), thus in minor number. The collection material (Taranov O.) had in its composition low glutinose forms (0.2 - ....). In the Kazakhstan content and correlation of amylose and amylopectine researched in the great degree for the crop the quality of its limited with a starch quality – first of all for the rise and maize. In connection of field mecessity for the health and functional food researches took the development on barley, oat and rise amylose. Increasing interest in the crops such as millet with an amylose content of 19.6% to 27.0%, and sorghum from 19.6% (Victoria, Kazakhstan) to 26% (Karlikovoe, Russia). The Kazakhstan rise varieties grain amylose content changeability varies 7.0-15.4% (to 24.3%), the barley from 14 to 27%, and oat from 1.2-12%, wild wheat relatives 19.6-31.5%, triticale 24-43%, maize 18-29%, millet and sorghum 19.6-27.8%. The healthy food focusing the plant breeding to create varieties combines the technical and nutritious properties.

# FACULTATIVE BREAD WHEAT VARIETIES AND INTERNATIONAL COOPERATION IN KYRGYZSTAN

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Among cereal crops in Kyrgyzstan main food crop is bread wheat (*Triticum aestivum L.*) Bread wheat occupies about 50% of total cultivated area under agricultural crops. Bread wheat is cropping area has grown from 300 thousand to 450 thousands hectares. Wheat breeders of Kyrgyzstan of multi-year targeted breeding created high-yield varieties of bread and durum wheat varieties were developed for different climatic zones of Kyrgyzstan (Bermet, Tilek, Kyal, Adyr, Asyl, Melyanopus 223 etc.). There are varieties is winter types of wheat. The genetic yield potential of this varieties developed to 10, 0 t/ha and higher. In present time farmers and seed production organization in Kyrgyzstan does not have the opportunity to realize the genetic potential of winter type of wheat. In this current situation in agriculture sectors furthers breeding of new varieties of facultative wheat with resistance to biotic and abiotic factors and high quality grain. Solution of these problems is carried out by testing facultative perspective varieties and germplasm from International Agricultural Center (CIMMYT and ICARDA). In Agricultural Co-operative " MIS " breeding and seed production work of winter, facultative and spring bread wheat are conducted. Purposeful work for creation and improvement of facultative bread wheat varieties for different ecological zones of Kyrgyzstan carried out under CIMMYT (Turkey). Since 2002 through the CIMMYT/ICARDA project were official registration 8 varieties wheat and triticale (Djamin, Almira, Azibrosh, Zubkov, Petr, Alesha, Missim). In present time are tested following nursery: 11KYRG-YT-IRR and 11 KYRG-YT-SA. 18th FAWWON.

# FREE PROLINE FOR CEREALS BREEDING ON THE GENERAL ADAPTABILITY

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The physiological and biochemical mechanisms of cereals metal resistance of among which considerable interest is represented by researches on change of level of a free proline is actual. As objects of research 27 varieties of a winter, spring and facultative wheat registered and perspective in Central Asia. For a germination of 7-day sprouts of wheat put experiences with addition in nutritious solution of the HM various salts in concentration of 20 mg/l. Determination of free proline was performed by the method of Bates. It is established on a big selection material of change of biometric parameters and level of this amino acid at wheat under the influence of TM most widespread in Kazakhstan ($Cd^{2+}$, $Cu^{2+}$, $Zn^{2+}$). TM stimulate accumulation of the proline in leaves of sprouts of all studied wheat varieties against inhibition of growth processes. Activisation of exchange processes connected with increase of level of free proline under the influence of a metal stress a number of varieties, including Bogarnaya 56 differed.High level of free proline was observed at action of ions of $Cd^{2+}$. It is proved that $Cd^{2+}$ ions are the strongest toxicants in comparison with $Zn^{2+}$ that involves activation of cellular mechanisms a stress stability. It is connected with substantial increase of the maintenance of the amino acid in comparison with control: Bogarnaja 56 for 158,3 %, Bezostaja 1 for 136 %. At a variety Progress level of free proline at operation of $Cd^{2+}$ was twice higher in comparison with reaction to $Cu^{2+}$. On accumulation of the amino acid accurate regularity in extent of reaction of wheat varieties on HM action was determined: $Cu^{2+} < Zn^{2+} < Cd^{2+}$. Faculty wheat differed high the maintenance of proline in control that is caused by resilience to their extreme factors of the environment, so the increased adaptive potential. Under the influence of HM there was a considerable accumulation of this amino acid at varieties Intensivnaja and Pamjat' 47 in winter form, especially under the influence of $Cu^{2+}$ and $Cd^{2+}$. Summer forms of faculty wheat reacted increase of free proline level, especially at $Cu^{2+}$ action. For example, the summer form of a variety Intensivnaja was characterized by four multiple excess of proline. The made experiments show the role of proline as endogenous regulator astress stability in reaction to TM action. Researches on use of free proline as a sign for pre-breeding and definition of genotypes - donors of metal stability of wheat are expedient.

# GENETIC CONTROL OF SCALD RESISTANCE IN BARLEY LOCAL SAMPLES

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Scald (causal agent *Rhynchosporium secalis* (Oud.) is a widespread and economically important disease of barley. Evaluation of barley local forms is considered to be one of possible approaches in donors for the resistance identification. To study character of the resistance inheritance 4 local barley samples from China, India and Ecuador were analyzed; they were crossed with susceptible variety Cambrinus, between them and with near-isogenic line with gene *Rrs9.* Hybrid populations were infected with mixture of 27 *R. secalis* isolates from 2 natural populations under field conditions. In $F_2$ from crosses with Cambrinus segregation for resistance corresponded to theoretically expected 15 : 1 and 3 : 1 indicating to the presence in samples k-22299, k-16233, k-27768 2 genes for the resistance and in k-27205 1 gene for the trait. In crosses combinations k-27205 × k-16233 and k-27768 × k-27205 segregation was found (corresponded to theoretically expected 63 : 1) proving nonidentity of their genes for the trait. Segregation for the resistance in $F_2$ from crosses k-27205 × NIL *Rrs 9* (15 : 1) indicated to nonidentity of genes for resistance to scald in these samples. In crosses of other 3 local samples with NIL *Rrs 9* in $F_2$ all plants were resistant. The results allow us to suppose the presence of different genes for the resistance in local barley samples under study.

# GENETIC DIVERGENCE ANALYSIS ON SOME BREAD WHEAT GENOTYPES GROWN IN ETHIOPIA

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An investigation was carried out with 49 bread wheat genotypes to assess the genetic diversity for yield and yield related traits. The Unweighted Pair Group Method using Arithmetic Averages (UPGMA) technique was used for the analysis. The genotypes were evaluated for 17 Characters and showed wide variability for the components studied. The cluster analysis grouped the 49 bread wheat genotypes into 22 different clusters. This indicates the presence of wide diversity among the tested genotypes. From cluster mean values, genotypes in cluster 9 and 13 deserve consideration for their direct use as parents in hybridization programs to develop high yielding wheat varieties. The genotypes in cluster 3 and 16 may be used for improvement of protein and gluten contents, early maturity and other desirable characters other than grain yield. The result of the principal components analysis revealed that nine principal components (PC1 to PC9) accounted nearly 80 % of the total variation. It was also noted that differentiation of genotypes into different clusters was because of the small contribution of few character rather than the cumulative effect of a number of characters. The information obtained from this study can be used to plan crosses and maximize the use of genetic diversity and expression of heterosis.

# GENETIC STRUCTURE OF DURUM WHEAT POPULATIONS BY ISSR MARKERS

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Inter simple sequence repeat (ISSR) marker were used to characterize and assess genetic diversity in durum wheat accessions from the Morocco, Ethiopia, Southeast of Turkey, Lebanon, Kazakhstan, China and Mongolia. In total 15 ISSR primers were used for amplification of DNA fragments. In this experiment 221 loci were scored which 163 of them were polymorphisms. Among the studied markers although UBC808, UBC840, UBC864 and UBC812 markers produced highest the number of total and polymorphic bands, they showed highest of Polymorphism Information Content (PIC). The results obtained suggested that these primers can be used to study of genetic diversity of durum wheat accessions. Cluster analysis showed that the observed genetic diversity in durum wheat material sampled in different part of the studied countries is geographically structured. The samples from Turkey and Lebanon are genetically similar and the samples from Mongolia showed highly genetic distance from the rest studied populations. Also the results of experiment showed that the genetic diversity from Southeast of Turkey, Lebanon, Morocco and Ethiopia samples was more than the samples from Kazakhstan, China and Mongolia. The results show that the diversity of samples belonged to the regions near the East Asia begins decrease, thus it is possible to conclude that the region of Africa with Fertile Crescent is the main center of durum wheat diversity.

# GENETIC VARIATION OF MINERAL ELEMENT CONTENTS IN GRAIN OF MOROCCAN DURUM WHEAT GENOTYPES

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Wheat is one of the most produced cereals in the world. It is considered as the main human food crop. It constitutes a staple food for varied uses. Wheat is an excellent health building food since it is a good source of protein, minerals vitamins and of other beneficial bioactive components (phytochemicals and dietary fiber components). Micronutrient malnutrition arising from minerals deficiency especially zinc (Zn) and iron (Fe) deficiency has emerged as a serious health concern worldwide. Now it afflicts over 3 billion people around the world (United Nations System Standing Committee on Nutrition 2004). These deficiencies are caused by habitual diets that lack diversity overly dependent on a single staple food. Thus, the nutritional importance of wheat proteins should not be underestimated, particularly in less developed countries where foods made from wheat like bread, noodles, couscous, burghul and other products may provide a substantial proportion of the diet. Genetic enhancement of crops with elevated levels of micronutrients and the development of genetically enriched wheat varieties through breeding is considered as a promising and cost-effective approach for diminishing micronutrient malnutrition problem. High levels of these nutrients can be found in landraces and old low-yielding varieties. Wild germplasm of wheat is also a rich source of useful variability for grain iron and zinc contents (Cakmak et al. 2000; Rawat et al.2009). This type of germplasm can be effectively utilized for enhancing the micronutrient status of the elite wheat cultivars. This will contribute to improving the health and livelihood of numerous resource-poor, micronutrient-deficient people in many developing countries. The objective of this study is to screen Moroccan durum wheat germplasm including old and modern varieties and landraces for macro-and micronutrients composition in the grain. Results showed wide variation in macro- and micronutrients content. This variation was related both to the genotype and the environment. Range values obtained for macro and micronutrients expressed in mg/Kg were: K (3700 -5500), Na (450-610), P (2010-3980), Ca (1130-2070), Mg (940-2650), Cu (11-21), Mn (29-55), Fe (35-43), Zn (21-38). The evaluated germplasm formed an interesting source of favorable nutrients especially zinc and iron that might be very desirable in breeding activities for improving nutritional quality of wheat.

# GENETICAL DETERMINATION ON OF THE SPRING TYPE OF DEVELOPMENT IN WHEAT *TRITICUM AESTIVUM* L.

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Genetically determination of vegetation period in wheat *T. aestivum* is polygene: it depends on expression of main genes *Vrn*, *Ppd*, *Eps* and the other factors, which are modified by environment conditions. Among tested varieties wheat of spring type (85 varieties) it was founded out the occurrence of genotypes (%) was *Vrn1 vrn2 vrn3* 24,6; *vrn1 Vrn2 vrn3* 15,3; *vrn1 vrn2 Vrn3* 12,9; *Vrn1 Vrn2 vrn3* 37,6; *Vrn1 vrn2 Vrn3* 7,1; *vrn1 Vrn2 Vrn3* 1,3; *Vrn1 Vrn2 Vrn3* – 1,2. Ultra-early-maturing varieties of wheat with gene *Eps* have genes *Vrn1 Vrn2 Vrn3* and *Vrn1 Vrn2*. The development rates of such varieties are controlled by *Eps*. According our date, gene *Eps* in presented by block of polygene's with little effect, determining uninterrupted changeability, and coupled with gene which may by Mendel 'method. By combination of early maturing genes we obtained more early maturing lines. Among intermediate wheat *T. aestivum* (33 varieties) the occurrence of genotypes (%) was *Vrn1 vrn2 vrn3* 27,3; *vrn1 Vrn2 vrn3* 51,5; *vrn1 vrn2 Vrn3* 9,1; *Vrn1 Vrn2 vrn3* 6,1; *Vrn1 vrn2 Vrn3* 3,0; *vrn1 Vrn2 Vrn3* 3,0. Intermediate wheat is characterized by high sensitivity to day length and frost resistant what contribute to winterizing. Intermediate varieties of wheat have both dominant *Vrn* genes and genes controlled frost resistance.

# GREENBUG RESISTANCE IN BARLEY ACCESSIONS FROM ASIA

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The most modern barley varieties are susceptible to economically important aphids. For breeding purposes a study of local accessions to identify new effective genes for resistance is very promising. Resistance of 1358 barley accessions from East and South Asia to the greenbug (*Schizaphis graminum* Rond.) was evaluated in laboratory under artificial invasion. Heterogeneous forms with different expression of resistance to Krasnodar greenbug population have been detected. High level of aphid resistance was found in landraces from China (44 accessions), Japan (2), Mongolia (2), North Korea (1), India (7), Nepal (1), Afghanistan (33), Pakistan (8). Resistance in these 98 accessions is under control of alleles not identical with alleles of the previously identified *Rsg1* gene because cultivar Post carrying this gene was susceptible to the Krasnodar greenbug population. Differences in genetic control of the resistance in landraces from China and North Korea were revealed.

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# HETEROSIS STUDIES FOR SOME AGRONOMICAL TRAITS IN OATS

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The benefits of increased vigor which often occur crossing unrelated plants or animals have been recognized for centuries. Hexaploid oat genotypes E44, K1, A45 and A52 belong to A. *sativa* and A. *byzantina* species were crossed. In the study, heterosis, heterobeltiosis and standard heterosis values were calculated for 11 traits on 12 hybrids belong to K1 x E44 (10 hybrids), K1 x A45 (one hybrid) and K1 x A52 (one hybrid) with the parents. According to results, oat hybrids had higher values over the parents for all investigated traits. K1 x A52 population had the highest plant height (PH, 201.0 cm), tiller number (TN, 22) and 1000-grain weight (1000-GW, 47.1 g) and the highest stem diameter (SD, 9.0 mm), flag leaf width (FLW, 4.0 cm), panicle length (PL, 53.0 cm), grain number per panicle (GNP, 98.0) and, grain weight per panicle (GWP, 3.2 g) were obtained from K1 x A45 population, while K1 x E44 population had the highest flag leaf length (FLL, 42.7 cm), single plant grain yield (SPGY, 42.6 g) and biomass (B, 108.7 g) values. Results suggest that the magnitude of hybrid vigor differed by traits and depending on hybrid combinations. Heterosis values were ranked between -26.8 and 282.3%. However, heterobeltiosis values were between -45.6 and 248.0%, and standard heterosis values were range in -2.7 to 419.0%. The highest heterosis and standard heterosis values (282.3 and 419.0% respectively) were determined for SPGY in K1 x E44 population while the highest heterobeltiosis value (248.0%) was determined for B in K1 x A52 population.

**Key words;** oat, heterosis, heterobeltiosis, standard heterosis, agronomical traits

# IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES UNDER LOW TEMPERATURE IN WINTER WHEAT

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Cold is one of the main abiotic stress causing winterkill of winter wheat. In winter cereals, frost tolerance is associated with the occurrence of a cold-hardening which is triggered by induction or repression of cold responsive genes after exposure of plants to low but non-freezing temperature (LT) for certain periods of time. In order to detect new differentially expressed genes at the different point of cold acclimation period two promising winter wheat lines ('5899-16' ir '5450-1') were cold-acclimated at +4 °C for 6 weeks in the plant growth chamber. cDNA was synthesized from mRNA of crown and leaf tissues collected in three biological replications at 0, 2, 4 and 6 weeks of cold acclimation. cDNA-AFLP analysis was performed using 48 primer pair combinations, which generated 522 transcript-derived fragments (TDFs). 19 TDFs (3.6 %) were identified as being differentially expressed (presence/absence) between cold acclimated and non acclimated wheat. 13 TDFs (68.4 %) were up-regulated and 6 TDFs (31. 6%) were down-regulated within 2 weeks after the start of the cold acclimation. All 19 TDFs were excised from gels, cloned and sequenced. BLASTx search of the GenBank non-redundant (nr) sequence database demonstrated that 12 of the TDFs belonged to known sequences with putative functions related to metabolism (7), signal transduction pathways (2), transport (1) and protein modification (1). Further expression analysis of these genes using real time RT-PCR will confirm or deny their involvement in the cold acclimation process of winter wheat.

# LENTIL SINGLE-PLANT PROGENIES SELECTED IN THE ABSENCE OF COMPETITION EXHIBIT QUANTITATIVE RATHER THAN QUALITATIVE G×E INTERACTION

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Breeders are commonly faced with confusing G×E interaction, that is over-environmentally expressed in qualitative (different genotype rank) and/or quantitative manner (significantly differing performance). The aim of this study was to investigate the kind of G×E interaction in 30 lentil genotypes, derived through single-plant selection among ultra-spaced individuals of a lentil population in Orestiada (Site 1). These lines along with the mother population as check were tested in honeycomb R31 experiments at Site1 and Thessaloniki (Site2). Linear correlation for inter-location performance was strongly positive ($r$=0.62, $P$<0.001), depicting consistent rank and thus absence of qualitative G×E interaction. Even though originated from Site1, the 30 lines, as well as the check, recorded significantly higher yields at Site2 compared to Site1 (35% and 72%, respectively), indicating quantitative G×E interaction. The previous result is reasonable since the mother germplasm is a landrace collected from areas closer and thus more adaptable to Site2. Nevertheless, compared with the mother population, out of the 30 lines only 5 over yielded the check in Site2 (3-18%), while in Site1 22 lines yielded from 3 up to 47% higher. Consequently, progeny lines appeared more adaptable to the Site1 where selection had been performed. This result clearly shows that in breeding not only area of selection but those to evaluate selected progenies play a crucial role in identifying promising genotypes and thus should be chosen with caution. Involving the first for progeny evaluation is important to recognize the outstanding progenies, while multi-locate experimentation is needed to succeed in broad adaptation.

## Acknowledgement

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# MEASURE OF STABILITY AND JOINT REGRESSION ANALYSIS FOR YIELD AND YIELD COMPONENTS IN 22 GENOTYPES OF GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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Twenty two groundnut (*Arachis hypogaea* L.) genotypes collected from International Crops Research Institute for Semi Arid Tropics (ICRISAT) and local sources (Samaru, UNILORIN and UNAAB) were cultivated in Lagos ($6^0$ 36’N, $3^0$ 34’E) and Abeokuta ($7^0$ 10’N, $3^0$ 20’E) to determine the genotypes adaptability and performance. Data collected were subjected to combined analysis of variance, joint regression and stability analyses. Highly significant ($\alpha \leq 0.01$) differences were obtained for the main effects of genotype, location x year and genotype x location x year while, significant ($\alpha \leq 0.05$) differences due to locations was recorded. 56% of the variability in pod yield was accounted for by the genotype whilst 7% by location Significant GXE for yield and quantitative characters studied was an indication of differential genotypes performance over different environments. The three stability parameters used jointly rated ICG-8490, ICG4412, ICG-442, ICGY-5M-4746 and ICG-IS-3584 as stable genotypes. On the bases of adaptation and yield, varieties ICG-4998, ICG-2106, ICG-4598, ICG-IS-11687, ICG49-85A and UGA-7-M are recommended for cultivation in the study ecology.

**Key words;** Groundnut; Genotype x Environment interaction; Stability; Environment

# POSTULATION FOR ADULT PLANT RESISTANCE GENES IN WHEAT CULTIVARS TO LEAF RUST

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In the breeding programs of the world countries the wheat donors of Adult Plant Resistance to leaf rust are used since these wheat cultivars provide for durable disease control. There were 16 accessions of *Triticum aestivum subsp. aestivum* and 8 lines of synthetic wheat (*x Aegilotriticum sp.)* possessed APR from National Small Grains Collection, the USDA-ARS. The goal of researches was revealing APR genes in the wheat accessions by specific reaction of plants to leaf rust isolate-testers. Twelve isolate-testers of *Puccinia triticina* differed virulences to set of wheat lines with genes: *Lr12, Lr13, Lr22a, Lr22b, Lr34, Lr35* and *Lr37* were selected. APR genes were postulated in 9 wheat accessions by the phytopathologic testing. Genes *Lr37* and *Lr13* in wheat accessions were marked often. Adult plant resistance in CM 23091-1M-2Y-0Y, Myna“S”, 11-1462-2c-2c-3c was caused these genes. The gene *Lr37* with unknown gene was postulated in Moncho“S”, Torim 73, ND 63-74. The genes *Lr13* and *Lr22b* were found in Pergamino, Gaboto M.A.G., and genes *Lr12, Lr13* and *Lr22b* were identified in 11-1462-1c-1c-4c. Gene *Lr12*+ was determined in ND 460 and *Lr13* was in BW27858 to make a comparison of monogenic lines sensitivity. Gene *Lr13* with unknown genes were postulated in samples CASS97B000441S and CASS97B00054S. The combination of two genes of APR *Lr13* and *Lr22b* were in sample CASS97B00046S. There were no postulated APR genes for several samples of wheat accessions because of lacking leaf rust pathotypes virulent to them.

# POWDERY MILDEW RESISTANCE IN WHEAT (NORTH – WEST REGION OF RUSSIA)

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Powdery mildew caused by *Blumeria graminis* f. sp. t*ritici* Golovin is a serious and widespread foliar disease of wheat in regions with cool, wet conditions. The most economical and environmentally safe means for controlling this disease is selection resistant cultivars. But high resistance of new varieties is limited by appearance of fungus biotypes with corresponding virulence. That is why the research of new resistant forms as well monitoring of fungus population is of a great importance. Many resistance genes have been introduced to common wheat (*Triticum aestivum* L.) from related species. We founded that resistance of most accessions of *T. monococcum* L. to the fungus population is determined by dominant genes, in rare case – by recessive gene differed from *pm5*. Einkorn is resistant to the disease during many years and may be source of effective genes for common wheat. Gene *Pm12* (derived from *Aegilops speltoides* Tausch.) is effective against fungus population in north-west region. The field population of fungus in this region had virulent to *Pm1, Pm2, Pm4, Pm6, Pm8, Pm9, Pm10, Pm10+15, Pm11, Pm19*. The test lines with *Pm3 (a,b,c,d), pm5, pm7* and *Pm18* had strong leaf chlorosis. Thee test-line Wembley 14.31 (*Pm12* gene from *Ae. speltoides*) and test-line BR 93N (*Pm16* gene from *T. dicoccoides Körn.*) had immunity to fungus field population. At the seedling stage only test-lines with *Pm12* and *Pm16* had immunity; the others were susceptible to the disease.

# SELECTION OF INITIAL MATERIAL OF CEREALS RESISTANT TO *FUSARIUM* FUNGI

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Breeding of cereal cultivars resistant to *Fusarium* fungi causing Fusarium Head Blight, Root Rot and Snow Mold is the important problem all over the world, including Russia. Genetic diversity of world gene accessions was studied for selection of breeding sources resistant to *Fusarium* fungi. Ecological and genetic differentiation of species of host plant was taken into account. More than 5000 wheat and barley cultivars from different genetic groups were screened with identification of different types and rates of disease severity of root rot and snow mold. There was 6,7% resistant lines from winter accessions of bread wheat (*T. aestivum)*, 8,8% - from spring accessions of bread wheat, 1,4% - from spring accessions of durum wheat (*T. durum)* selected by screening to resistance. The high resistance was shown for *Triticale* lines. The samples from *Aegilops aucheri, Ae.ovata, Ae.columnaris, Ae.triuncialis, Ae.koteshyi* species were resistant to fusarium diseases. Distribution of resistant wheat lines dependent on their geographical origin. Winter wheat cultivars with moderate resistance to Fusarium root rot were dominated in Western Europe (Icsu – France, Horpacsi – Hungry, Yasen – Bulgaria etc.) and in North America (Chiefkan, Archamp, Benni, Coker 9227 – USA etc.). Resistant spring bred wheat cultivars were revealed within 8 ecological-geographical groups presented majority of countries. The focus of interest was on accessions introduced from North and South America, India, as well as international and regional nurseries (Laura - Canada, Achut - Nepal, Vectis - USA, BVF-2 - Mexico etc.). Durum wheat cultivars with moderate resistance were dominated in the Mediterranean regions and in the southwesten Asia (Aya de Carvo - Portugal, 80/57 – Italy, Ak-bugda - Dagestan, k.6397 - Georgia, k.6397, k. 36269 - Armenia). The origin of wheat cultivars with high resistance to snow mold was West Europe (Glockner, Agent, Aron - Germany, Szemes - Hungary, Turda 81 - Rumania, Sol IV - Sweden). At present in Russia there do not exist resistant to Fusarium Head Blight and Root Rot resistant barley cultivars. However some cultivars of barley are tolerant as Omskiy 90, Omskiy 89, Sonet, Povolzhsiy 65, Elf, Raushan, Nutans 533 and others.

**Keywords:** *Fusarium*, wheat and barley cultivars, breeding

# SELECTION OF INITIAL MATERIAL OF WHEATS RESISTANT TO THE MOST HARMFUL DISEASES

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With the purpose of creation of Germplasm of Wheat Donors and Sources Resistant to Several Harmful Pathogens more than 5000 spring and winter wheat accessions from different genetic collections (USDA-ARS, VIR, “Arsenal”, CIMMYT) were evaluated for resistance to leaf rust, septoriosis and powdery mildew. The scheme of the evaluation and screening sources and donors of wheat was created and include the following ways: Evaluation for resistance to cereal populations of diseases in infectious nursery and greenhouse; Selection wheat varieties with different resistance types; Identification resistance genotype in wheat cultivars using phytopathologic testing, hybridization and PSR-analysis; Studying the main phytopathologic components of partial resistance on wheat cultivars; Screening sources and donors of wheat characterized genetic diversity and group resistance. As a result of evaluation for resistance of wheat accessions in the infectious nurseries located in Central-Nonchernozem and North-Caucasian regions there were selected the samples of winter and spring wheat resistant to Puccinia triticina, Septoria sp., Blumeria graminis and to complex of pathogens. The main resistance types to leaf rust and Septoria in collection wheat accessions were identified. The genotypes with high level of partial resistance to leaf rust and Septoria and combining different resistance types to make for durable resistance to harmful diseases were identified. As a result of repeated estimations of the best productivity accessions of SHWs from NSGC there were confirmed their group resistance to mildew and leaf rust. The genes of juvenile resistance to leaf rust were identified in 90 wheat cultivars from different genetic collections by the method of phytopathologic testing and PCR-analysis. The best SH wheat accessions with economically valuable traits can be recommended for screening high productivity and very resistant wheat cultivars.

# SELECTION OF INITIAL WHEAT MATERIAL FOR RESISTANCE TO *STAGONOSPORA NODORUM* AND *SEPTORIA TRITICI* FROM DIFFERENT GENETIC COLLECTIONS

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At the present time septoriosis has leading position among the big number of nocuous fungi diseases of crops. Everywhere epidemics of the disease occur 4-5 times in every 10 years and crop losses can reach 40-50%. The species of *Septoria* are the most widespread. In the ARRIP infectious nurseries (the Central region of the Russian Federation) the long-term researches for resistance of wheat cultivars from different genetic collections to *St. nodorum* and *S. tritici* were carried out: ARIPI collection - 570 samples, Germplasm Resources Information Network (GRIN) - 1815 samples, CIMMYT collection - 132 samples. A mix of pathogenic races as an infectious background was used for field test. Wheat cultivars from all tested collections were characterized by leaf susceptibility to *St. nodorum*. Five leaf resistant to *S. tritici* cultivars from GRIN collection were selected. Fifty-five ear resistant cultivars to *St. nodorum* were revealed in GRIN collection including accessions from Brazil, the USA, Bulgaria and Mexico. Six resistant wheat cultivars from ARIPI collection were resistant to *St. nodorum* including what accessions from Brazil and China. Cvs. Anderson, Long 94-4081, Cooperation Calquin, Prointa Superior, Buck Arrayan represent the greatest interest resistant not only to septoriosis but also to leaf rust and powdery mildew.

# SPACE-PLANTED RATHER THAN DENSELY SEEDED CONDITION PREDICTS BETTER CROP YIELD OF GENETICALLY HOMOGENEOUS MAIZE LINES

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It has been asserted that objective comparison of maize genotypes for grain yield performance is hard to accomplish at a single dense stand, due to variation in optimum population. Ultra-low density to preclude plant-to-plant interference for inputs has been proposed as a unique presupposition to tackle the problem. To investigate the issue, 31 diverse in yielding ability inbreds were tested at 0.74 versus 6,666 plants/m$^2$ under normal and water-stressed regimes at three locations, forming six across-density environments. In overall, the 31 lines averaged 102 - 697 g/plant and 3,160 - 13,760 kg/ha when spaced and crowded, respectively. At the ultra-low density, all the 15 among environments linear correlations were very high ($r$=0.83-0.95, $P$<0.001). At the typical density, two out of the 15 $r$ values were non-significant, eight indicated moderate correlation (0.36-0.56, $P$<0.05-0.01), and five were above 0.59 to meet the $P$<0.001 level. Consequently, the absence of competition rather than the typical density exhibited less genotype by environment interaction. The overall yield at the dense stand used as index of crop yield potential was positively correlated with the across-environment genotype performance at both densities. However, the ultra-low density gave considerably higher $r$ values, i.e. averaged 0.86 (0.81-0.90) against 0.77 (0.59-0.90), hence foresaw better the crop yield. The results were contrasting with the recommendation that there is no relationship between yield of isolated plants and crop yield, which presumably is valid when tested genotypes are heterogeneous, due to catalytic role of the yielding by competitive ability interference at the dense stand.

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# BIOLOGICAL POTENTIAL OF FACULTATIVE WHEAT IN KAZAKHSTAN CONDITIONS (BIOMASS PRODUCTIVITY, IRON AND ZINC CONTENT IN THE GRAIN)

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Trace elements content, including iron and zinc content in grain wheat are very important for human health. Genotypes and environmental conditions are the main factors as to generate not only the highest grain yield, but also the content of minerale elements in wheat grain. In 2004-2005. in four regions of the country Almaty, Zhambyl, South Kazakhstan and Kyzylorda seeded 25 genotypes of winter bread, including facultative wheat (Intensive, Kazakhstan 10 and Pamyat 47). The minimum content of iron and zinc in these grain wheat genotypes varied from 19-23 and 15-20 mg /kg, and a maximum of 45-50 and 52-59 mg / kg. Cultivars Intensivnaya, Kazakhstanskaya 10 and Pamyat 47 for all the studied areas formed a high iron content (59 mg/ kg), zinc (28-42 mg / kg) in grain. On three main areas of the Republic winter sowing identified areas with a high content of iron and zinc: in Almaty region - Sarkandskiy, the South Kazakhstan Region - Lengerskiy; Zhambyl region - Zhualinsky. For the optional wheat tendency of increase laboratory germination of seeds with high content in grains of iron and zinc. So cultivars Pamyat 47, with iron content 44 mg / kg and Zinc 52 mg / kg, laboratory germination was 76% in cultivars Intensivnaya with an iron content of 31 mg/kg and Zinc 32 mg/kg was 74%. The accumulation of maximum raw biomass is related to the leaf surface area (r = 0,88), the level of chlorophyll (r=0,62). Maximum raw biomass (148.1 kg / ha) was observed in 10 cultivars of Kazakhstan in making zinc fertilizer to the soil with a dose of 23 kg and seed treatment $ZnSO_4$-348 g / t (143.4 kg / ha) of Pamyat 47 cultivars.

# VALIDATION AND DEPLOYMENT OF RESISTANCE-LINKED SCAR MOLECULAR MARKERS FOR MARKER-ASSISTED BREEDING OF THE COMMON BEAN

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The efficiency of SCAR molecular markers in selecting plants resistant to Anthracnose, Angular Leaf Spot and Pythium Root Rot fungal diseases of common bean in the marker-assisted backcrossing program was assessed. Two Anthracnose resistance linked markers, SAB3 (linked to *Co-5* gene) and SH18 (linked to *Co-4*$^2$ gene), a *Pythium* Root Rot resistance linked marker, PYAA19$_{800}$, and an Angular Leaf Spot resistance linked marker OPE4$_{709}$ **(linked to Phg-2 gene)** were validated for possible use for introgression of multiple disease resistance in the market-type climbing bean variety NABE 12C. DNA was obtained using FTA Whatman protocol from the susceptible parental genotype, NABE12C, and from the three resistant parents: RWR719, G2333 and Mexico54, which are the sources of resistance to Pythium Root Rot, Anthracnose and Angular Leaf Spot, respectively. DNA amplification products indicated that the three markers SAB3, SH18, and PYAA19$_{800}$ were polymorphic in the parental genotypes and could effectively be used in selection. These SCAR markers are now being used in the molecular marker-assisted backcrossing program at the Uganda National Beans program to aid the improvement for multiple resistance to the major diseases in NABE 12C. On the other hand, SCAR marker OPE4$_{709}$ was monomorphic in the same parental genotypes and is not suitable for the marker-assisted selection in the backcrossing program of interest. An alternative marker is now being developed based on DNA sequence information available from the PhaseolusGenes database.

**KEY WORDS:** Common bean (*Phaseolus vulgaris*), SCAR markers**,** MAS, Resistance, *Pseudocercospora griseola*, *Pythium spp.*, *Colletotrichum lindemuthianum*.

# DEVELOPMENT OF SUNFLOWER (Helianthus annuus L.) PARENTAL LINES WITH BROOMRAPE (Orobanche spp.) RESISTANT AND HIGH OLEIC ACID CONTENT BY USING MOLECULAR TECHNOLOGIES

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**Sunflower is one of the most important oil crops in Turkey and provides 46% of vegetable oil production. It has the biggest cultivation area and production among other oil crops in the country as well as it is in first rank of vegetable oil production. Broomrape (*Orobanche spp*.) species are the biggest field problem of the Thrace-Marmara region where the 75% of sunflower production is provided and effect 100% of the yield. On the other hand, high content of oleic acid in the sunflower oil is an important criteria of the oil composition which is prefered for human nutrition and it has been an important technological feature of the species that are used in sunflower agriculture. Beside human health, quality of sunflower oil meal in animal feed rations is an important feature of preferred range to obtain ethanol in the scale of consumption. Production of sunflower varieties with high content of oleic acid is increasing rapidly around the world. In mentioned study, it is aimed to determine new sunflower genotypes with broomrape resistance, high grain yield and high oleic acid content by integrating molecular technology into conventional breeding and to develop these new variaties. Agromar's study which began in 2011, Broomrape resistant lines and the high content of oleic acid lines were imported from abroad and formed starting materials of Restorer and B (maintainer) parental lines. In the present program, field and greenhouse studies are carried out to obtain two generations per year from 13 pieces of genetically different materials. Resistance to broomrape is determined by conventional pathological test for each generation in the laboratory (Velasco et al. 2007; Grenz et al. 2008); sunflower genotypes with high content of oleic acid is determined by using molecular markers (Berville et al. 2009). Field study in 2013, is carrying out with 465 pieces of HO (high content of oleic acid) and *Orobanche* resistant candidate lines which are different stages of selfing.**

# AMYLOSE CONTENT IN WHEAT, BARLEY and triticale BREEDING ON THE GRAIN QUALITY

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It is known that product quality taken on the base of functional starch property, it depends on the basic starch polysaccharides (amylose and amylopectine). Heightened interest to healthy food focusing plant breeding on creating new cultivars blended together technological and nutritious properties. Those lines used in Europe wheat breeding to create specialized cultivars with good nutrition properties. For genetically analyses commercial cultivars and international research cultivars researched and differentiated on low amylose (up to 10%) and high amylose (>25%). Most part of Kazakhstan variety genofund and KASIB (Kazakhstan-Siberian Nursery) 4-5 and KASIB 6-7 genofund presented with the amylose content samples 11-20% (62% of KASIB 4-5 and 77% of KASIB genotype). Low amylose samples matched above 12-13%. This cultivars are: Altayskaya 50, Novosibirskaya 29, Lutescense 54, Lutescense 424 and *Udacha* (KASIB 4-5) and Omskaya 36,Omskaya 37, Fiton 156 and Lutescxense 166, SP 94(KASIB 6-7). We systematically studied amylose content for barley varieties genofund, begun in 1993harvest, maximally presented by varieties (72 cultivars) and regions. Three cultivars: Arna, Prestiz and Tcelinnay 91 characterized by high amylose content. Amylose content in the malt samples was high in comparison with other technological types. By international nursery of ICARDAwinter barley collection materials result founded the samples with a amylose content over 25% (higher than usually 20-25%). They are 5 samples: Robur/Miraj 1, 308/80 m l , Alpha/Durra//CWB 117-77-9-7, Robur/Miraj and Rihane-03 (check), which may be considered as the high amylose source (25.8-27.1%). In the breeding nursery Kazakhstan winter triticale (Kozhahmetov K.K.) identified genotypes with 38-42% amylose content, stable to 3 reproductions of both the grain and flour.

# APPLICATION OF EMBRYO CULTURE METHOD IN COMBINATION WITH GAMMA IRRADIATION AND ULTRA SONIC

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New mutant lines with change architecture, increased oil content, increased 1000 seed weight, resistant to *Plasmopara halstedii*; *Phomopsis helinthi, Septoria helianthi Ellis et Kellerman* and parasite *Orobance cumina* were developed using Embryo culture method in combination with ultra sonic or gamma irradiation at sunflower immature zygotic embryos. Some mutant lines showed very good combining ability. Line 12002 R (developed trough Embryo culture method at immature zygotic embryos in combination with gamma irradiation) – paternal component of commercial hybrid Rada and line 12003 R (developed trough Embryo culture method at immature zygotic embryos in combination with ultra sonic) – paternal component of commercial hybrid Yana were realized. Hybrid Rada considerably exceeded with 2.3-7.7 % the mean standard (the Bulgarian commercial hybrid Albena and French commercial hybrid Diabolo) by seed yield. The vegetation period is 115 days. The hybrid Yana considerably exceeded with 7.6 % – 14.4 % the mean standard (the Bulgarian commercial hybrid Albena and French commercial hybrid Diabolo) by seed yield. It's vegetation period is 110 days. The two hybrids possessing immunity to the parasite *Orobanche cumana* population of races A-G, immunity to *Plasmopara helianhi-* races 300, 330, 700 and 731, immunity to *Phomopsis* and *Macrophomina* and tolerance to *Phoma.*

**Key words:** sunflower**,** *Helianthus annuus*, Embryo culture, gamma rays, ultra sonic, mutant lines, resistance, *Plasmopara halstedii*; *Phomopsis helinthi, Septoria helianthi Ellis et Kellerman*, parasite *Orobance cumana*

# ASSESSMENT GENOTYPE*ENVIRONMENT INTERACTION IN BARLEY CULTIVARS WITH REGRESSION METHOD

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It is perceived that barley cultivation has flourished since 9000 years ago. Due to versatile and hardy nature, barley is grown worldwide for staple food, industrial and medicinal uses. Barley is used in form of malt, beer, syrups, malt ova and delicious chocolates. In order to evaluate the stability and determine the highest yielding variety, 15 genotypes of barley were studied in this research. The experiment was conducted in a randomized complete block design with three replication in five locations (Esfahan, Ahvaz, Kerman, Gonbad Kavoos, Mashhad) during growing season of 2011-2012. Combined analysis of variance for grain yield showed significant differences between environments and genotype × environment interactions. Based on the stability parameters of Eberhart and Russel Regression, Nosrat that had higher yield than the average and regression coefficient of 1 (approximately), were more adapted cultivars. However, Karoon, Sahra, Torkaman, Gorgan 4, Nimrooz and MB-83-14 cultivars showed specific adaptation to better and Valfajr, Makooei, Bahman, Yoosef and W-79-10 cultivars to poor environments. Also, according variance of deviation from regression Nosrat variety with lowest value was known as stable genotype in all environments.

**Keywords**: Interaction, Genotype*Environment, Stability, Regression

# BIO-PHYSIOCHEMICAL AND PHENOLOGICAL RESPONSES OF FABA BEAN (*VICIA FABA* L.) TO INDUCED WATER DEFICIT CONDITIONS

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Seeds of five faba bean varieties were field grown under three water irrigation regimes for two seasons 2011-2012 and 2012-2013. Also, seeds grown on ½ MS-basal media supplemented with 0, 5, 10 and 15 % (W/V) PEG-induced water deficit environments for four weeks under growth chamber controlled conditions. The results showed significant decrease in seed yield and its components due to water deficit. Hassawi2 was superior under all irrigation conditions, compared with the other varieties. Osmotic potential in leaf tissues of seedlings grown under PEG-induced water deficit was significantly decreased leading to chlorophyll degradation. Total chlorophyll (TC), maximum quantum yield of photosystem II (PSII) (Fv/Fm) and photon yield of PSII (FPSII) dropped significantly under water deficit conditions compared to control. Increasing PEG concentration significantly decreases the germination percentages; shoots height, chlorophyll content and PSII mediated photoreactions. On the other side, osmotic stress increased crude protein, free proline and Malondialdehyde contents in faba bean leaves. Shoots of all genotypes seedlings and root length of Giza Blanka and Hassawi2 were decreased gradually by increase the osmotic stress. However, Goff1, Hassawi1 and Gazira2 roots were shorter under low PEG concentration (5%) then increased with osmotic stress increase. Estimates of RWC, proline and protein showed that Gazira 2 and Hassawi2 had the highest values under water deficit conditions while lowest values were recorded for Giza Blanka. MDA highest decrease was recorded in Gazira 2 and Hassawi2 under water deficit in comparison to control condition. These findings indicate that Gazira 2 showed better protection under water deficit and has different drought tolerance mechanisms. Meanwhile, seed yield potential of Gazira 2 was very low under well and low water. However, Hassawi2 recorded the highest seed yield under different water irrigation treatments and ranked second for bio-physiochemical studied characters. These results provide the basis to establish of multivariate criteria for drought tolerance screening in faba bean breeding and genomics programs.

**Key words:** faba bean, PEG -water deficit, Chlorophyll fluorescence, PSII, Protein, Proline, MDA, RWC.

# BREEDING OF MAIZE HYBRIDS ON THE PRODUCTIVITY AND QUALITY OF GRAIN IN THE SOUTH-EAST OF KAZAKHSTAN

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Research on the development of corn hybrids of high genetic potential yield and quality of grain held in the south-east of Kazakhstan. Soil test area light brown, medium-textured, the climate is continental with large annual and daily air temperatures and lack of moisture during the growing season, so the cultivation of maize is possible only with irrigation. The object of study-inbred lines, local selected varieties, synthetics, especially valuable and promising hybrids. The study of combining ability for different maize genotypes revealed patterns of manifestation of combining ability. In the selection, establishment and improvement of the raw material used visual selection, topkrossnye and diallel crosses. The main method in the creation of new combinations was the use of a hybridization of inbred lines of different ecological and geographical origin. Special attention is paid to research on the creation and improvement of material to provide donors dvuhpochatkovosti, remontant, erektoidnosti arrangement of leaves, and the use of sister crosses. The average yield of precipitated most in three years in the late-maturing hybrids respectively CVT ranges from 129.5 to 138.5 kg / ha, the excess over the standard of 12.5 t / ha to 30.9 t / ha or 12.7 to 21.2 %. Three-year results of the counting of the interphase periods show that the number of days from germination to flowering panicles for late-forms on average 66-70 days to flowering ears of 66-73 days, the number of leaves 16-20 are different productivity, resistance to stem and root lodging , in affection diseases. Research with the State variety trials produced two hybrid feed direction under the name of the Merey 75 and Tauelsizdik NE-20) with a starch content of 70.0% and grain protein 12%.

# CALLOGENESIS AND STRAINS SELECTION *IN VITRO* IN *POTENTILLA RECTA* L. SUBSP. *LACINIOSA* (WALDST. ET KIT. EX NESTLER) NYMAN

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Recently the plants of genus *Potentilla* L. are used as decorative plants and drugs in medicine. Alternative way of plant biomass (sources of the biologically active substance) obtain is *in vitro* cell and tissue cultures. Strategies for the selection of high-producing strains are based on the variability, i.e., “somaclonal variation” that is induced by *in vitro* methods (Dougall, 1987). The aim of this work was to study the features of *P. recta* subsp. *laciniosa* callus formation *in vitro*. The possibility of callus formation *in vitro* on modified Pierik medium has been shown. The strains of *P. recta* callus which are differ by light - brown color, compact texture and low vitrification have been selected during the experiment. In this case significant discrepancies in the quantitative characteristics of the obtained strains due to the type of explants, its placing on the media and physical factors of cultivation have been found. As a results of adaxial placing of leaf pieces on the culture medium the callus with higher growth rate have been obtained. In this condition maximal accumulation ability of fresh (60.7 ± 1.05 mg / explant) and dry (8.1 ± 0.6 mg / explant) callus biomass has been established.

# CHLOROPHYLL CONTENT OF THE CULTIVATED LENTIL (*LENS CULINARIS* MEDIK.) IN COMPARISON TO WILD SPECIES

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Global productivity of lentil (*Lens culinaris* Medik.) is limited by major biotic and abiotic stresses. Drought is one of the most destructive stresses in lentil production and causes to high yield losses. Chlorophyll content of leaves is an indicator for determining the resistance/tolerance to drought since it can be used determining photosynthetic activity and drought resistance. In this study, chlorophyll content of 16 accessions representing seven taxa, *Lens culinaris* ssp. *culinaris* Medikus*, L. culinaris* ssp. *orientalis* (Boiss.) Handel-Mazetti*, L. culinaris* ssp. *tomentosus* Ladiz., *L. culinaris* ssp. *odemensis* Ladiz.*, L. lamottei* Czefr.*, L. ervoides* (Brign.) Grande, and *L. nigricans* (Bieb.) Godron was measured with SPAD 502 plus chlorophyll meter in greenhose conditions to identify photosynthetic activity. The highest chlorophyll content was observed in *L. nigricans* (PI 572344) with 45.5 SPAD, while the lowest chlorophyll content was in *L. orientalis* (PI 72900) with 27.3 SPAD. To improve in drought resistance/tolerance in the cultivated lentil, the trait of *L. nigricans* could be transferred from *L. nigricans* to the cultivated lentil because they can easily be crossed.

# COMBINING ABILITY AND HETEROSIS OF ZP MAIZE INBRED LINES FOR GRAIN YIELD

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A diallel analysis was used to evaluate combining abilities and heterosis of six maize inbred lines and their $F_1$ hybrid combinations for grain yield. Parental inbred lines and their 30 $F_1$ hybrid crosses (with reciprocals), were included in a randomized complete block design (RCBD) with four replications, in two densities, during three years, according to the Griffing's Method 1 and Model I (fixed effects). Analysis of variance indicated the high significance for genotype, environment, and G x E interaction effects. The high significance values for general combining ability (GCA), specific combining ability (SCA), reciprocal effects (RE), maternal effects (ME and nonmaternal effects (NME) were estimated. Average grain yield for inbred lines ranged from 2,282 t/ha to 8,269 t/ha, and for hybrids from 3,853 t/ha to 15,216 t/ha. Inbred line L6 had the highest values of GCA for grain yield (0,451), which can therefore be used in further breeding programs as sources of genes for this trait. The highest SCA values for grain yield were recorded in hybrid combination L5 x L3 (2,059) and the lowest one in combination of two parent lines with similar genetic background L3 x L4 (-1,184). GCA/SCA ratio was 0,187 suggesting much greater role of non additive gene effects. The high, positive and statistically significant values of heterosis for grain yield were obtained. The highest heterosis 150.32% (L1xL3) and 146.62% (L1x L4), was determined in combinations with inbred line L1 with high GCA. Significantly higher values of SCA and heterosis were estimated in the crosses of genetically unrelated parents.

# COMPARISON OF CHEMICAL COMPOSITION OF TWO DURUM WHEAT (TRITICUM DURUM L.) AND BREAD WHEAT (TRITICUM AESTIVUM L.) GERM OILS.

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Wheat belong to the genus Triticum, as annual plants of the family Gramineae or Poaceae, grown in many countries, including Tunisia with one million hectares annually. Wheat grain is a particular fruit, caryopsis and the outer envelope is adherent to plant seed material. During milling, envelopes (hulls) are separated from the grain (endosperm + embryo). The embryo or germ is the essential part of the seed to plant reproduction and is containing a lot of fat (about 15%) or oils. The processing method used for the extraction of wheat germ oil is Soxhlet extraction. Normal hexane (n-hexane) is commonly used for edible oil extraction. Comparison of the extracted oil of durum wheat germ and Soft wheat germ showed a marked difference in their chemical composition. The basic chemical composition analyses revealed low values of dry matter (14.77g /100g of durum wheat germ and 19.87g /100g of Soft wheat germ), low amounts of total ash content (5.3g/100g of durum wheat germ and 4.99g /100g of Soft wheat germ) and high fat contents (17.12g /100g of durum wheat germ and 15.96g /100g of Soft wheat germ). The yield of extraction by Soxhlet was about 13.12% for durum wheat germ and 11.22% for soft wheat germ. The fatty acid composition of these two wheat germ oils indicates the presence of C18:2, C16:0 and C18:1. The major one is C18:2 with 56.68% for Soft wheat germ oil and 53.43% for durum wheat germ oil. However, 9 compounds were identified in the oil of the aerial part of wheat germ extracted by Soxhlet process.

**Keywords:** Germ oil, Durum and Soft wheats, fatty acid composition, chemical composition.

# DENSITY AND PLANT ARRANGEMENT ON CALENDULA OFFICINALIS L. YIELD

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Calendula officinalis L. has healing antiseptic and anti-inflammatory actions, among others. In 0rder study the effect of plant density and arrangement on quantitative and qualitative performance of calendula officinalis L. herb, an experiment was carried out in research field of Islamic university,chalus in 2011-2012. Applied experimental design, was factorial design in the form of randomized complete block design with three replicates. Experimental treatments have been consisted of the distance between the row in two levels of $R_{1=}$30 cm, $R_2$=40 cm and the distance on the row in three levels of $I_{1=}$10 cm, $I_{2=}$20 cm, $I_{3=}$30 cm and the cultivation method in two levels of $P_{1=}$rectangular and $P_{2=}$zigzag. Studied characteristics consisted of flower diameter size,number of seed in flower,100 seed dry weight and flavonoid content. The results showed that the plant density and arrangement had significant effect at 1% ($p \leq 0.01$) and 5% ($p < 0.05$) level on the flower diameter size,number of seed in flowers,100 seed dry weight and flavonoid content.Also maximum flower diameter size ,maximum number of seed in flower and maximum 100seed dry weight and maximum diameter flavonoid content obtained in 30 cm distance between the row and 30 cm distance on the row treatment and zigzag cultivation method ($R_{1\times}I_{3\times}P_2$).

# DETERMINATION OF STAY GREEN WITH NDVI (NORMALIZED DIFFERENCE VEGETATION INDEX) IN THE WINTER WHEAT GENOTYPES UNDER STRESS CONDITIONS

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NDVI is a spectral index of the green color in plants and can have several uses in crop research, but the main use is studying “stay green” proper. This investigation was conducted in Transitional Zone Agricultural Institute, Turkey in 2011-2012 agricultural years under IWWIP (International Winter Wheat Improvement Program, CIMMYT). This experiment was performed in the RCBD with 4 replicates (replications of 2 and 4 had cut in the late tillering stage) and trial was planted following safflower crop which extracted moisture during the previous season. NDVI had used for 10 weeks from stem elongation stage to maturity. Under-study traits were also included: peduncle length, plant height, heading date. The data on cut and uncut treatment were recorded separately. ANOVA showed highly significant differences among wheat genotypes for all studied traits, uncut and cutting treatment. However, genotype × treatment interaction for yield, days to heading and NDVI were significant, but for plant height and peduncle length were non-significant. Coefficient of variation for NDVI was 7.12% and heritability estimated was 0.857. A positive and significant correlation was observed between NDVI and days to heading under cut and uncut treatment. But between heading date and yield were observed negative significant correlation. This shows the value of stay-green to obtain cumulative effects together with other traits to further improve adaptation under stress. Cumulative effects to improve stress adaptation may be achieved by introgression stay-green expression traits into new wheat lines, so NDVI parametrs proved to be reliable selection traits associated with grain yield.

# DEVELOPMENT OF INITIAL MATERIAL OF SPRING AND WINTER WHEAT ON THE BASIS OF NEW SOURCES OF RESISTANCE TO LEAF AND STEM RUST

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The genotypes resistant to stem rust were selected in 2010-2011 by the results of evaluation of breeding lines, cultivars and accessions from the collection of the N.I. Vavilov All-Russian Research Institute of Plant Industry (VIR) and Moscow Research Agricultural Institute "Nemchinovka" ("Arsenal" collection). They are winter short-stem breeding line from Bulgaria (VIR catalog number 96-90) and highly productive cultivar Donskaya Polukarlikovaya (semidwarf) originated by the Rostov Agricultural Research Institute. Both accessions have immune response (0;) to TTKSK race testing in the laboratory conditions (Anisimova et al., 2010).Genes of resistance *Sr17, Sr22, Sr24, Sr31* and *Sr44* were identified in 96-90 accession by PCR analysis. The presence of 5 genes of resistance to stem rust (*Sr9a, Sr17, Sr22, Sr36, Sr44*) was established in Donskaya Polukarlikovaya cultivar. The same genes were identified in winter wheat accession 119-4-06rw obtained by three-species crossing (spring wheat, *Ae speltoides*, *S. cereale*) (Lapochkina, 2005). The accession of spring wheat 113/00$^i$-4 has disomic substitution in chromosome *Ae. triuncialis*, and in laboratory conditions the reaction to pathogen penetration corresponded to 0;. In the field conditions of Ethiopia (infectious nursery) the accession was not affected by stem rust but was late-ripening. Two genes of resistance to leaf rust (*Lr10* and *Lr24*) and two genes of resistance to stem rust (*Sr17* and *Sr44*) were identified in 113/00$^i$-4. The latter two accessions were resistant to leaf and stem rust. The hybrid and backcross populations were obtained from intercrossing of the accessions. At present research of effective genes *Sr* and *Lr* is conducted in individual plants of hybrid populations by means of PCR analysis.

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# DIRECTIONS AND METHODS OF WHEAT AND TRITICALE BREEDING

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In Ukraine, for domestic needs and export, wheat and triticale are grown annually on the area of 6,5-7,0 millions hectares. In area, among the crops, winter forms predominate (90-95 %). Breeding in the leading centers aimed at increasing adaptability to abiotic stresses – drought, heat, winter hardiness; to biotic factors: resistance to leaf, stem, yellow rusts; root rot, blotch spot, Septoria of leaves; loose smut, common bunt; viruses; bacterial diseases and hardiness to pests damage: shoot attaching fly, wheat bug, wheat aphids etc. Quality traits for bread production are: fullness, hardness, vitrescence, volume weight of grains; protein content and electrophoretic profile; quantity and quality of gluten; flour yield and strength; dough extensibility and elasticity; bread volume and values estimated by eye: surface, shape, color of bread crust; bread texture, color and elasticity of bread crumb; general bread making rate). A special varieties are created for confection, macaroni, ethanol and also possessing increased biological value (with dark grains). All these traits are combined with high yield capacity and suitability for use of technical means. At present, the winter bread wheat cultivars are divided in three types: intensive (semidwarf), universal and semi-intensive. There are created in Ukraine 210 winter wheat cultivars, that is 80,5 % of all ones included in to the Ukrainian Variety Register. Triticale breeding is carried out for a cereal (food, industrial and grain feed) and grain-cutting types. From total 25 registered winter triticale cultivars, 22 are bred in Ukraine. All the 16 registered spring triticale varieties have Ukrainian origin.

# DONOR OF COARSE-GRAINED WINTER RYE (*SECALE CEREALE* L.) LARGE-GRAINED

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A widely distributed method of selection of cereals is sorting its weight and volume. Since 1970, the directional selection has been carried out to increase the weight of 100 grains per winter rye plant. Under the influence of selection of the coarsest plants there was a constant, but uneven increase in the weight of 100 grains (picture 1). In the 19th generation of short-stalked coarse population appeared individual plants with a weight of 100 grains of more than 8.0g, the so -called extremes. Table 1 shows a positive asymmetric character of the appearance of classes with an incredibly large grain. In the source material and the previous generations of breeding there haven't been shown up the plants and even the individual grains with such a high weight. In 2009, there was a group of plants with the extreme of the weight of 100 grains of 9.1g. We haven't ever seen such a coarse-grained winter rye in our country and even in the literature. We have the honor of the first to report the phenomenon. After the appearance of coarse extremes parents in following generations of the population there was a kind of a period of stabilization the weight of 100 grains, the modal class clearly manifested, the frequency of the sign showed the character of a normal distribution. The coarse-grained rye the genetically determined sign has been controlling by a series of numerous alleles and is available to artificial selection. Thanks to the prolonged intensive selection the average weight of 100 grains per plant increased from 2.94g to 7.32g or in 2.5 times. The effectiveness of selection for the increasing in weight of 100 grains per plant was systematic, but not even. During 43 generations we could see the periods of fast response to directional selection, the long-term periods of deceleration and even reversing of the average weight of 100 grains. The greatest impact on the efficiency of selection showed the selection differential (36%), the selection intensity (22%), the heritability coefficient in the narrow (10 %) and broad sense (8%). The predicted and realized efficiency of the selection of 43 generations coincided in 37% of cases, so it means the reality of our selection predictions.

# ECOLOGICAL VARIETY TRIALS OF CHICKPEA (*CICER ARIETINUM L.*) IN THE REGION OF ARID STEPPES IN AKMOLA OBLAST, NORTH KAZAKHSTAN

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Cultivation of legumes is usage of unique property to assimilate atmospheric nitrogen for soil improvement, health nutrition and export diversification. In condition of rainless steppes of Akmola oblast of North Kazakhstan held ecological variety trials of chickpea from 2001 to 2013. Had been studied 30 varieties and lines from ICARDA, Russia, Ukraine and Kazakhstan scientific research institution. The cultivation of chickpea in the region had been done due to the existence of stress factors. Because of stress factors the yield varies from 0.2 to 4.0 t ha$^{-1}$. During humid years yield loses because of diseases varies from 15 to 80% or more. Major loses are due to the distribution of fungus *Ascochyta rabiei*. In 2002, 60% of chickpea were spoiled by 90-95%. It was made a selection of steady types of beans that show resistance in 2013 while in same soft conditions only 6 of 30 were spoiled. Basic part of resistant material was received from ICARDA. Also Fusarium wilt caused by fungus *Fusarium oxysporum* was distributed. Desi variety shows stronger resistance than kabuli variety. During some years decrease of yield decreased due to the pest by 30% or more. Those are pod borers (*Helicover paarmigera*), leaf miner (*Liriomyzacictrina*). By ICARDA and scientific center's scientists were made a variety of chickpea Duet of Asia (FLIP 95-65) that conducting governmental and ecological variety trials in Kazakhstan.

# EVALUATION OF HYBRID MATERIAL, ORIGINATED FROM WILD ANNUAL SUNFLOWER SPECIES FOR RESISTANCE TO THE LEAVES PATHOGENS CAUSE GREY (*PHOMOPSIS HELIANTHI*), BROWN (*ALTERNARIA* SP.) AND BLACK (*PHOMA MACDONALDI*) SPOTS ON SUNFLOWER

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The aim of the presented study was selection of hybrid forms, originated from wild annual species *Helianthus debilis*, *H. petiolaris* and *H. praecox*, resistant to grey, brown and black spots on sunflower. On the base of their reaction to agents of three fungus diseases, the breeding materials with immune and resistant type of reaction were selected. The wild sunflower accessions, picked as paternal parents, were beforehand evaluated on artificial infection plot. Vegetation period and seed oil content of the obtained hybrid materials were determined and studied. As a result of evaluation and purposeful selection, some new forms with high resistance to pathogens *Phomopsis helianthi*, *Phoma macdonaldi* and *Alternaria* sp., high seed oil content and different vegetation period were selected. These hybrid forms were characterized also with presence of Rf genes and were included in a program for control of resistance to economically important sunflower diseases and for developing new lines-restorers of fertility.

# EVALUATON OF THE SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) CORE COLLECTION UNDER ECOLOGICAL CONDITIONS OF SAMSUN

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Test safflower genotypes consisting of the safflower (*C. tinctorius* L.) core colllection and three certificated local safflower (*C. tinctorius* L.) cultivars were sown in winter during 2007-2008 at the Experimental Fields of the Agricultural Faculty belonging to the Ondokuz Mayıs University. 205 safflower genotypes provided from the Regional Plant Introduction Station in Iowa/USA and three safflower genotypes (Dinçer, Remzibey and Yenice) were used as seed material. Genotypes were sown in a field nursery design in 4 blocks and the local cultivars were sown at the top, in the middle and at the bottom of every block. The safflower (*C. tinctorius* L.) collection consisting of 205 genotypes were sown with three local cultivars in 3m long rows with a interrow space of 10 cm per hand. Phenological observations were done over whole rows, agricultural characters were determined using 10 plants. Using the characterisation tables of UPOV phenologic characters beginning from emergence up to harvest time and morphological characters such as plant height, number of lateral branches, lenght of lateral brach, head weight, number of heads per plant, number of seeds per head, thousand seed weight etc. were determined. Principal Component Analysis was performed to determine genetic variation based on obtained characteristics and the results displayed that big variation exists regarding inside the safflower (*C. tinctorus* L.) collection.

**Key Words:** Safflower, *Carthamus tinctorius* L., Adaptation, Phenological and Morphological Characters

# GENETIC ANALYSIS OF FABA BEAN (*VICIA FABA* L.) INTER-VARIETAL CROSSES

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Ten crosses representing four inter-varietal combinations among seven faba bean genotypes were used to study the performance and genetic components of variation. The parental genotypes represented *Major* (Luz), *Equina* (Hassawi 1, 2 and 3) and *Minor* (Triple White, Gazira 2 and Kamline) subspecies of faba bean. Results revealed that Minor x Equine crosses surpassed all other combinations in term of yield and hybrid vigor. This was mainly due to the positive effect of no. of pods /plant and no. of seeds / plant. Although Major crosses had heavier seeds and longer pods, the negative impact on the number of pods and seeds /plant led to the reduction of grain yield. Luz (the major type) could be considered as an excellent tester in breeding for number of seeds/pod and 100 seed weight traits. Kamline and Gazira 2 as minor types behaved as good combiners for number of pods/plant and number of seeds/plant. On the other hand, the local Equine type Hassawi 1 and Hassawi 3 were good combiners for number of branches/plant and number of seeds/pod, respectively. Estimates of variance due to GCA and SCA and their ratio revealed the significant contribution to both of them in the inheritance of studied traits with predominant non-additive gene action for most studied characters. Narrow sense heritability ranged from 44.9 for days to maturing and plant height to 90.1 for no. of branches/plant. The level of genetic variability suggests the significance of such materials in improving performance and yielding ability in faba bean breeding program. It is suggested to rely on *Equine*/ *Major* Crosses for improvement of yield potential in faba bean under arid and semi arid climatic conditions.

**Key words:** faba bean, inter-varietal crosses, combining ability, heterosis

# GENETIC DIVERSITY ANALYSIS USING SSR MARKERS AS A TOOL FOR MORE EFFICIENT UTILIZATION OF MAIZE INBRED LINES

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Information about maize (*Zea mays* L.) genetic diversity is very important for hybrid maize breeding. Twenty SSR makers were used for investigating genetic relationships and genetic diversity among 29 maize inbred lines from Maize Research Insitute “Zemun Polje” breeding program. In total, 116 alleles were identified with a mean of 5.8 alleles per locus. Genetic similarity was calculated using Jaccard’s coefficient of similarity and ranged from 0.27 to 0.98 with an average of 0.458. Unweighted Pair Group Method with Arithmetic mean (UPGMA) method was applied for cluster analysis and showed clear clustering. Inbred lines were mostly grouped according to available pedigree data. The results showed that SSR markers could be successfully used in genetic diversity assessment and information about genetic variability could help in more efficient utilization of inbred lines in process of maize hybrid creation.

# GENETIC PERFORMANCE OF VEGETATIVE TRAITS OF MPOB OIL PALM INTERSPECIFIC HYBRIDS

# IN INLAND AND COASTAL SOILS

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Oil palm interspecific hybrids were derived from the North Carolina mating design 1 (NCM 1) involving 236 *Elaeis oleifera* palms as maternal parents and 76 *Elaeis guineensis (pisifera)* palms as paternal parents. The progenies were planted in Malaysia on inland soils of Kluang, Johor and Ulu Paka, Trengganu, and on coastal soil ofTeluk Intan, Perak. There were significant differences between *pisiferas* in Kluang, Ulu Paka and Teluk Intan for all the seven vegetative traits *viz.* petiole cross-section (PCS) rachis length (RL), leaflet length (LL), leaflet width (LW), leaflet number (LN), height (HT) and leaf area (LA). Small PCS, short RL and low HT are favoured by oil palm planters for ease of frond pruning, higher density planting and longer economic lifespan, respectively. The highest heritability due to *pisifera* parents, $h^2_p$ were recorded in Teluk Intan with heritabilities of 74.7% (PCS), 43.1% (RL), 66.2% (LL), 54.9% (LW), 100.0% (LN), 80.6% (HT) and 63.0% (LA). The lowest PCS (8.65 cm$^2$), RL (3.91 m) and HT (0.28 m) were obtained in Kluang by progenies MS2063 [0.142/7833 x W(T)9], MS2083 [0.142/7391 x W(T)9] and MS2081[0.142/7436 x (HE ZE B2 x AVROS 4/12)], respectively. Based on general combining ability (GCA), the lowest PCS (14.36 cm$^2$) and RL (4.40 m) were obtained in Kluang by *pisifera* 181OP7 [W(T)9], whereas the lowest HT (0.46 m) was given by *pisifera* 181OP15 [LN(T)5]. The outcome of this study revealed the importance of utilising suitable *pisiferas* with good GCA as paternal parent in the creation of oil palm intersepecific hybrids with the desired vegetative traits.

# GLUTENIN SUBUNITS AND GLIADIN IN “KASIB” SPRING WHEAT IDENTIFICATION

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According to the analysis of 216 genotypes of spring wheat identified them as belonging to 25 types of electrophoretic spectrum, including 18 types of HMS-glutenin for 188 homogeneous cultivars. Most of the spring wheat KASIB are characterized by the formula 2 * 7+9 5+10 (40% genotypes), and formula 2* 7+9 2+12 – (30%), formula 1* 7+9 5+10 – (8%). The diversity determined by varying chromosome 1A and 1B at the 5 subunits and 1D - 4 subunits HMG. Judging from the distribution of genotypes KASIB nurseries are mostly HMS-glutenin determined high quality baking by: 1A - 2 * (77-79%) and 1 (14-15%) at 1B - 7 +9 (81-82%) and 7+8 (13-15%) by 1D – 5+10 to 60%. This set to included a new subunit “4+10” for 1D for samples Erythrospermum 55/94-01-20 (Pavlodar Research Institute, KASIB 8-9), Fitton 41 (KASIB 8-9) relative to gene pool of high-quality genotypes found in Kazakhstan. Identified cultivars “Iridost” with alleles 5.5+10 on chromosome 1D, previously identified for cultivars Tselinogradka, Tselinnaya 24, Akmola 3 (Abugalieva, Morgounov, 2004). On chromosome 1B cultivars Chelyaba for the entire set was original because they only had 6+8 subunit and in the mix for cultivars Lutescens 29-94; for genotypes: E-607 and E-757 - a rare characteristic subunit 7 *+ 8. The most distant from all cluster genotype OK -1, Fitton 25 and GVK 1916-9  which are wheat-rye 1B/1R-trans location. Wheat-rye translocation (IB / IR) identified more samples for Omsk breeding and West Kazakhstan in each KASIB (except KASIB 4-5), for all samples submitted “Kurgansemena” (except Lutescens 415/00) and “Agrosemkonsalt” (KASIB 8-9 and 10-11), as well as for LLP”Fitton” breeding samples (Fitton 41 and Fitton 43, including CYMMIT shuttle breeding material. Total detected such 30 genotypes of 216.

# IDENTIFICATION OF QTLS RELATED OF AGRONOMIC TRAITS IN RECOMBINANT INBRED LINES OF WHEAT (*TRITICUM AESTIVUM L.*)

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Grain yield and associated agronomic traits are important factors in wheat (*Triticum aestivum L.*) improvement. Knowledge regarding the number, genomic location, and effect of quantitative trait loci (QTL) would facilitate marker-assisted selection. QTL mapping study was conducted in recombinant inbred lines derived the cross between Roshan × Superhead based on randomized complete block design using DArT markers at the agricultural research farm of Shahid Bahonar University of Kerman, Iran in 2011-2012. The genetic map consisted of 347 DArT markers identified nineteen linkage groups, based on composite interval mapping (CIM) that showed 2(2A, 7B), 3(1D, 5A, 5B), 1(3A) and 1(7B) QTLs for plant height, 1000-grain weight, harvest index and number of fertile tillers traits, respectively. These results will provide important information for further functional analysis of yield-related genes in wheat. The molecular markers linked with QTLs for yield-related traits might then be useful for breeding programs in wheat by marker.

**Keywords**: DArT marker, Linkage group, QTL, Wheat.

# INDUCE BUD PRODUCTION OF PURPLE CONEFLOWER (*ECHINACEA PURPUREA* L.) THROUGH CELL SUSPENSION CULTURES

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Purple coneflower (*Echinacea purpurea* L:Asteracea) is a medicinal perennial herb for treating various illnesses. Suspension cultures grow much faster than callus culture and yield large number of uniform cells or cell clusters for the production of large number of somatic embryos which can develop into intact plants. Petiole explants were cultured on liquid media containing MS salts, B5 vitamins, 3% sucrose, 1 mg/l IBA and different concentrations of BA (0.02, 0.1, 0.5, 2.5 mg/l) and BA (0.1 mg/l) + sorbitol (0, 1, 2, 3, 4%). Calluses were sub-cultured at every 7 days interval to the same medium. Experiments were arranged in Complete Randomized Design (CRD) with five replicates. Greenish colour bud primodia grew faster on the medium supplemented with 0.1 mg/l BA and 4% sorbitol comparing to the control and other treatments. However, embryogenic callus was not observed in any treatment. Callus which was taken from cell suspension culture treated with BA was transferred to the MS medium supplemented with 0.6% agar + 3% sucrose with 0.1 mg/l BA for further growth. Exposure of explants to a high level of cytokinin (BA) for long period negatively affects the tissue growth and development, resulting inactive and died explants. Many callus with green buds continued to grow resulting large number of buds. The MS medium 0.1 mg/l BA and 0.01 mg/l NAA increased the germination rate. Because calluses from cell suspension culture proliferated fast and had high plant regeneration potential, this suspension culture system can be used for micro-propagation of elite genotypes to serve as valuable materials for various breeding program.

**Key words**: Purple coneflower, callus, suspension culture, BA, NAA, sorbitol

# MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF FABA BEAN (*VICIA FABA* L.) GERMPLASM

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Drought is considered the leading environmental constraint to crop yield loss due to significant alterations in plant physiology and biochemistry. This study aimed to evaluate morphological and physiological performance of faba bean genotypes under three water treatments, molecular characterization of these genotypes utilizing Amplified Fragment Length Polymorphism (AFLP) and combined physiological and molecular evaluation of these genotypes. Twenty local and introduced genotypes were grown in the net house, College of Food and Agricultural Sciences, King Saud University, Saudi Arabia. Three water treatments were applied which were; field capacity, 50% of field capacity and 25% field capacity (stressed treatment). A split plot design with three replications was used. Results showed high significant differences between irrigation treatments and among genotypes for most of the studied trait. Under stressed treatment, L.4, Kamline, Gazira2 and Gazira1 showed the highest water use efficiency based of economic yield. Pop.3, L.4, Kamline, Gazira2 and ILB4358 showed the highest water use efficiency based of biological yield. At 25% FC, Kamline, 985/252/95, Giza716, Gazira1 and Cairo7 showed ability to avoid water-deficit stress through reducing their relative water content. L4, Gazira1, Kamline, X.735 and Gazira2 showed the highest seed yield under water stress conditions. In terms of biological yield, L4, X.735, 989/309/95, Kamline and Gazira1 showed the highest values. This study demonstrated the power of AFLP markers in detecting polymorphism and estimating genetic diversity in faba bean germplasm. The nine AFLP primer pairs generated a total of 650 differently sized well-resolved peaks (fragments), of which all were polymorphic. In total, 5,168 data points (amplified fragments) were scored with an average of 574 peaks per primer pair across all genotypes, thereby confirming the high multiplex ratio expected for AFLPs. The capability of different primer pairs to generate AFLP loci varied significantly, ranging from 12 loci in primer pair *EcoRI*(GA)+*Mse1*(CTT) to 102 in primer pair *EcoRI*(TC)+*Mse1*(CAA), with an average of 72.22 loci per primer pair.

**Key words**: faba bean, WUE, AFLP, molecular diversity.

# ACCESSING NOVEL GENES FOR CHICKPEA IMPROVEMENT

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Narrow genetic base of cultivated chickpea is a major limitation in improving chickpea production and productivity. Wild *Cicer* species possess high levels of resistance/tolerance to many biotic/abiotic stress and can contribute in broadening genetic base of cultigen. However, long duration of wild *Cicer* species and non-synchronization of flowering with cultivated chickpea is a major obstacle for their utilization in chickpea improvement. The response of wild *Cicer* species was studied for vernalization and extended-photoperiod treatments in three sets. In one set, accessions belonging to eight wild *Cicer* species were given one-month vernalization treatment at 4°C temperature prior to transplanting in pots; in the second set, same accessions were subjected to 24-hours extended-photoperiod after 15 days of transplanting till maturity, whereas the third set served as control (without vernalization and extended-photoperiod). All the accessions responded well both to vernalization and extended-photoperiod treatments and, days to first flowering were reduced by ~70% in *C. reticulatum*, and ~63% in *C. echinospermum* compared to control. Tertiary genepool species showed differential response to vernalization and extended-photoperiod. Days to first flowering were reduced by 29% (*C. chorassanucum*) to 66% (*C. judaicum, C. pinnatifidum, C. bijugum* and *C. yamashite*) under extended-photoperiod and by 53% (*C. judaicum*) to 65% (*C. bijugum*) under vernalization treatment compared to control. Further studies revealed that 18-hours extended-photoperiod is the critical daylength required for reducing crop duration of all wild *Cicer* species. These results would contribute significantly in chickpea pre-breeding by accessing genes from wild species in developing cultivars with a broad genetic base.

# ASSESSMENT OF GROAT NUTRITIONAL ASPECT OF NEW DEVELOPED OAT HEXAPLOID LINES THROUGH INTERSPECIFIC CROSS WITH TETRAPLOID OAT *A. MURPHYI*

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Attempts have been made, to develop high groat protein content lines of hexaploid oat through hybridisation work, aiming the transfer the tetraploid oat species *A. murphyi*'s high groat protein content into three Moroccan common oat cultivars. Derivative hybrid lines were subjected to pedigree selection which yielded ten lines showing a good agronomic performance. Since the derivative lines will be conceived for human consumption; selected lines were assessed for groat protein content. Protein analysis revealed that this trait was improved for the developed lines by 2 to 18% in comparison to their hexaploid parents respectively.

**Keywords:** Oats, tetraploid oat *A. murphyi*, Common oat *A. sativa*, hybridisation, groat protein content

# DETERMINATION OF HERITABILITY AND GENE EFFECTS ON QUANTITATIVE TRAITS IN RICE GENOTYPES

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In order to evaluate heritability and gene action for some of the important quantitative traits in rice, six crosses were conducted among Iranian and foreign rice cultivars in the first year. F1, F2 generation were planted in second and third year respectively. The experiment was done with 25 treatments (six crosses) including 7 parents and their F1, F2 and F3 generations, with three replications on rice Research Institute of Iran (Rasht) in fourth year. Characteristics such as Plant height, tiller per plant, panicle length, and fill and strill grain per panicle and grain yield were measured and evaluated. The result obtained from analysis of variance indicated that mean squares in generation were highly significant for all traits. The generations mean analysis was performed for all traits. The result showed that although, additive, dominance and effects of epistatis were important for inheritance of Plant height, tiller per plant, panicle length, strill grain per panicle and grain yield, dominance gene effect was the most important for them. While the additive gene effect was the most important for traits such as fill grain per panicle. Broad sense heritability for grain yield in sepidrood/Binam cross was less with 49.46% and the highest of it was for fill grain per panicle in sepidrood/Alikazemi with 78.08%.

**Key words:** Rice, Generations mean analysis, Gene effect, Broadsense heritability

# DEVELOPMENT of DOUBLE HAPLOID LINES by *IN VIVO* HAPLOID TECHNIQUE in HYBRID MAIZE BREEDING

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The double haploid (DH) technology has become an indispensable tool of modern maize research and breeding. There are two methods *in vivo* haploid induction in maize which are paternal (androgenetic) haploid and maternal (gynogenetic) haploid induction. In this study, the maternal haploid induction method was applied. RWS, RWK-76 and RWSxRWK-76 inducer materials were used as pollinator. This study was conducted between 2011-2013 years and 200 source populations were used as donors. The donor genotypes are in 600-700 FAO maturity groups. Seeds of 102373 number were obtained by crossing inducer lines with donor genotypes. 16493 seeds from the obtained seeds were selected as putative haploid seeds using a seed coloration marker gene (*R1-nj*). According to the selection, haploid induction rates (HIR) in 2011 and 2012 ranged from 9.14 to 15.24% and 11.40 to 19.14% respectively depending on the inducer genotypes. Putative haploid seeds were germinated at 23 °C in a growth chamber. Coleoptile and root of seedlings were cut and treated with 0.04% colchicine + 0.5% dimethylsulfoxide (DMSO) solution for 12 hours at 20 °C to seedlings. Seedlings were planted viols after washing with water and $D_0$ plants were grown untill reaching 3-4 leaves in growth chamber. Following planting in the field, inbreeding were conducted for the fertile $D_0$ plants during the flowering period. The fertile plant ratios were 57% and 63% respectively in the first and second year of this study. A total of 327 double haploid lines were obtained from this study. The seeds of 140 double haploid lines from the first year were reproduced in the greenhouse. Top-crosses were made with 140 double haploid lines and Mo17, B73, ADK-451 inbred lines testers in 2013. It is used widely and effective method for selecting of double haploid lines with recurrent selection of top-cross in hybrid maize breeding.

# DEVELOPMENT OF DROUGHT-TOLERANT VEGETATIVE (TRIPLOID) BERMUDAGRASS [*CYNODON DACTYLON*]

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To meet increasing demand on green space without further straining water resources requires use of water-efficient landscape plants. Hence, declining water resources necessitates development of drought-tolerant turfgrass cultivars. There is a great deal of variation for drought-tolerance among native bermudagrass germplasm originating from Mediterranean region. The aim of this study is to develop drought-tolerant, vegetative (triploid) bermudagrass cultivars. Native tetraploid bermudagrass genotypes were crossed with a diploid C. *transvaalensis* Burtt-Davy that originated from South Africa, and that possesses high turfgrass characteristics. The crosses were made at Akdeniz University, Antalya, Turkey, greenhouses in 2012. The seeds were germinated, DNA was extracted from the seedlings, and molecular markers were used to identify true hybrids. Phenotypic pre-selection was made among the hybrids and 400 hybrid genotypes were vegetatively propagated, and transplanted in the field with 3 (three) replications in June, 2013. Establishment rates have been recorded. Drought-tolerance and turfgrass characteristics (color, quality, texture, dormancy etc.) will be recorded until 2015. The preliminary observations indicate that triploid (vegetative) bermudagrass cultivars with superior turfgrass characteristics can be developed. New cultivars are expected to combine the drought tolerance of native tetraploid bermudagrass with that of superior turf characteristics of diploid C. *transvaalensis.*

***Key words:*** *bermudagrass, vegetative, triploid, drought-tolerance*

# ENHANCING SPOT BLOTCH RESISTANCE IN WHEAT THROUGH INTROGRESSION OF QTLS USING MOLECULAR BACK CROSS BREEDING

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Two parallel back cross molecular breeding (BCMB) programs were conducted to transfer QTLs imparting resistance to spot blotch disease of wheat caused by *Bipolaris sorokiniana* into cv. HUW 234. This cultivar is a dominant cultivar in the eastern Gangetic plains (EGP) of India for last two decades and contains another QTL *QSb.bhu-2A* (*Xgwm445*) for resistance to spot blotch. In the first case, a QTL *QSb.bhu-2A (Xgwm425*) was transferred from Ning 8201 while in the other two resistant QTLs (*Qsb.bhu-2A and Qsb.bhu-5B*) from Chirya 3 were transferred. In both cases foreground selection for resistance QTLs was exercised using known SSR markers, while background selection was performed using 92 simple sequence repeat loci spread over the whole genome. Foreground and whole genome background selection were done in $BC_1F_1$, $BC_2F_1$, $BC_3F_1$ and $BC_3F_2$ generations. In BCMB involving Ning 8201, twelve $BC_3F_3$ progenies possessing spot resistance QTLs were obtained while 15 were obtained in the program using Chriya 3 as the donor. In both cases the progenies selected showed up to 95.5% genetic similarity with the recipient parent. The derived lines exhibited significantly higher level of resistance against spot blotch under field condition. The mean spot blotch AUDPC of cv. HUW 234 was 1288 while the best three lines developed from Ning 8201 showed AUDPC of 462, 462 and 471, respectively. While the mean spot blotch AUDPC of the Chirya 3 derived best three progenies showed AUDPC of 464, 469 and 471 in $BC_3F_3$. In both the cases derived progenies showed significantly higher grain yield and 1000 grain weight than the recipient parent HUW 234 under disease pressure while at par under disease protected condition.

# GENETIC POTENTIAL OF WINTER WHEAT GRAIN QUALITY IN CENTRAL ASIA

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The quality of winter wheat grain varies significantly by cultivars and growing region, not previously differentiated by the type of end-use (baking, confectionery, etc.) in the national breeding programs. In these conditions it is advisable to determine the genetic potential and analyze the actual quality of the grain. Determining the genetic potential requires the classification of varieties for grain hardness and composition of the HMS and the LMS glutenin. The most detailed it was carried to the genofund of wheat from Kazakhstan, Kyrgyzstan (Abugaliyeva, Morgounov et al, 2000; Abugaliyeva, 2000.) As can be seen from the table that most varieties of winter wheat in Kazakhstan, Kyrgyzstan and CIMMYT are a class of grain "hard" and "semihard" (62-95% in different blocks), characterizing them as baking wheat in the respective regions. The "soft" state laser is from 3 to 14% of the studied genotypes. The "soft" grain samples were also detected in small amounts ranging from 2% (Tajikistan) to 11% (Kazakhstan). Varieties are ranked by the HMS-glutenin from 10 max to min 4 t Payne scale for quality and LMS-glutenin from 5 to max min 1. Potential is determined by the genetic composition of the glutenin level subunits of breedered material is high to 75-80%. However, even varieties classified as soft state – Batyr, Komsomolskaya 103 were characterized by very high-grade baking qualities and new registered cultivars Kanditerskaya. It is therefore important not only to identify potential quality, but also its implementation in the specific growing conditions of the region. For a winter wheat breeding it is important the optimization combining quality with the level of productivity, especially in drought conditions the separation process such as the use of wheat

# WHEAT BREEDING PROGRAM IN SELGEN INC., PLANT BREEDING STATION UHRETICE

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SELGEN Inc. continue the tradition of breeding activities by its predecessor breeding companies, inaugurated at the beginning of last century (1903 - 1905) under the guidance of prominent agricultural specialists. Hundreds of varieties which have helped in advancing plant production have been developed and registered in Czechoslovakia (later the Czech and Slovak Republics) and in many other countries for almost a hundred years. Selgen is from one hundred % Czech company. SELGEN´S primary focus is the breeding of new varieties of field crops.The main program is the wheat breeding program in Stupice and Uhretice stations. The breeding program started in 1921 in Stupice and in 1956 in Uhretice. Fifty four cultivars of winter wheat and twenty one spring wheat and were registered by 2011 in both stations. Cultivars of SELGEN Inc. winter wheat are planted on 24,5 % of multiplication area and spring wheat is planted on 36,5% of multiplication area in 2010. The most used method is the pedigree method with ears selection in Uhretice plant breeding station, testing offspring in yield, abiotic and biotic stress resistance, bucking or feed quality, agronomical properties. In some special programs as selection of rht-gens we use plant selection. New cultivars and advanced lines are plant in different agronomical conditions, different preceding crops (maize, cereals), sowing rate and sowing time. These field trials give information for farmers how to lead the plants to the best results. The breeding process and its results, which are new cultivars of wheat, help to improve yield and quality agriculture production. Breeding and creating cultivars in each country specific conditions give a stability of the production. But it is a long process and it should be its concern of each http://slovnik.seznam.cz/?q=government of&lang=en_cz government to support this work and save national breeding.

# MODELS OF NEW VARIETIES OF SPRING BARLEY

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In order to improve the efficiency of selecting the best genotype throw the phenotype in each agro-ecological zone is necessary to develop and validate the parameters of optimal agroekotype including soil and climatic characteristics, the length of the growing season, sharing the most harmful diseases and pests. In the justification of the model of new varieties is very important is the choice of the main signs on which to predict plant production process. To create the models of spring barley varieties for rainfed and irrigated lands of South-East of Kazakhstan we carried out ecological breeding work. The starting material used accessions from the world collection, local varieties and hybrid populations. They differed by the drought resistance, early maturity, resistance to diseases and pests, high productivity, good quality indicators. Model of varieties with established properties are best implemented using crossbreeding of genetically different parents. In this case, it is necessary to study combining ability of involved parent forms. We found that the limiting factors in producing high yields of spring barley on irrigation are nutrient status, moisture content of plants during the growing season, the adaptive properties, the presence of weeds, diseases and pests. Drought resistance and heat resistance - the main indicators characterize varieties of rainfed agriculture. For breeding is very important combined into one genotype these figures. They are determined not only transpiration rate as architectonic plants, shape of the bush, thick and pubescent of leaves, with a capacity of root system. The long-term theoretical research breeding and genetic parameters (intensity and variability of agronomic traits interaction “genotype x environment”, the value of a combinational accessions, heritability in the broad and narrow sense, selection differential and a shift in the selection), and direct selection work outlined elements of the structure of yields, plant biology and architectonics. On the basis of the above-noted indicators formulated models of future varieties.

# MORPHOLOGICAL AND ELECTROPHORETICAL CHARACTERIZATION OF INBRED MAIZE LINES

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In this research, the lines which were developed by Department of Field Crops, Faculty of Agriculture, University of Namık Kemal, were used as a material. Various morphological characters were examined in the 50 inbred lines and the basic statistical analysis was performed. According to the results; it was determined that the data collected on tassel formation 66 - 85 days, silking 63 - 82 days, leaf area 204.750 - 717.620 cm$^2$, plant diameter 1.230 - 2.160 m., plant vigour 2 - 4, ear length 6.50 – 21.00 cm., number of fudsper ear 34 – 475 , 1000 seed weight 123.600 – 363.600 g., cob diameter 5-11 cm., cob weight 3.00 – 53.40 g. and grain yield was between 7.400 – 131.100 units. In addition, the band patterns of gliadin protein of inbred lines were determined with SDS – PAGE method, and the number of the bands and the spreading of the bands to the gliadin regions according to ratio density data of the genotypes were examined. As result of the electrophoresis examinations, it was established that the band number of the gliadin proteins in the inbred maize lines was between 11 - 20, the relature mobility of the genotypes was between 18 – 90 kDA and according to the gliadin regions the bands were mainly in the omega region, beta and gama regions follow this. It was found out that the relature mobility was minimum in the alpha region. The determined band patterns were used to establish the similar lines.

**KeyWords:** *Zea mays* L., morphological character, inbredline, SDS-PAGE, gliadin electrophoresis, electrophoretic character.

# PATHOGEN GUIDED RESISTANCE BREEDING: BENEFITS AND PITFALLS

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Accessing adequate amounts of nutritious, safe, and culturally appropriate foods in an environmentally sustainable manner is important for a growing population. The current approach promotes the sustainable intensification, using less water, fertilizer and pesticides to obtain greater yield. Although crop loss due to pest and pathogens in a changing environement is still high, frequentuse of pesticides in modern agriculture poses major risks if used improperly. Exploitingnatural plant disease resistance is highly attractive. Sequencing of pathogen and plant genomes is revolutionizing knowledge-based resistance breeding. Use of NGS helped uncover potential effectors, provided information on their loci, evolution and role in pathogenicity. Mass screening of plant varieties without the pathogen to identify new sources for resistance to prevailing isolates became possible. The prevailing isolates may differ between regions and countries andthus a commercial resistant line in one location may not confer resistance to the same pathogen in another region or country. Use of NGS in effector discovery from pathogens, molecular plant breeding programs and biomarker development will be discussed, and advantages and disadvantages of pathogen informed strategies will be presented.

# PROSPECTS OF ASSOCIATION MAPPING IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

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In two sets of cotton (*Gossypiumhirsutum* L.) germplasm, one mainly from China and the other from Pakistan, extent of linkage disequilibrium was assessed by using the same set of 98 SSR primer pairs. At significant threshold values of $r^2$> 0.05, 3% and 7.1% SSR marker pairs showed a significant pairwise LDin Chinese and Pakistan *G*. *hirsutum*germplasm respectively. In the Chinese germplasm, two long stretches of LD blocks were observed on chromosomes D4 and D11, extending to a distance of 81cM and 138cM respectively. In *G*. *hirsutum*germplasm from Pakistan, long haplotypic block of 180 cMwas observed on chromosome D5. The percentage of SSR loci pairs in LD in Chinese *G*. *hirsutum*germplasm was much lower as compared to germplasm from Pakistan and the previous reports of studies in *G*. *hirsutum*. This study shows that association mapping has potential and prospects to detect significant and reliable marker-trait associations in cotton and can be successfully employed in molecular breeding programs of cotton.

**Keywords:** Cotton, Linkage disequilibrium, Haplotypic blocks, Association mapping, Molecular breeding

# SELECTION OF PROMISING SAFFLOWER GENOTYPES UNDER CONTRASTED ENVIRONMENTAL CONDITIONS

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Safflower is a suitable crop for Moroccan conditions. A set of Moroccan and introduced cultivars as well as international accessions were evaluated at Oujda (eastern Morocco) during 2009-2010 for conventional and late sowing under two water regimes. The objective was to select genotypes with specific and large adaptation to the contrasted environmental conditions. Genotypes were planted in 3 m rows spaced 0.80 m following a completely randomized design without replication. Sowing was done on February in 2009 and on December in 2010. Morphological, physiological and agronomic traits, in addition to the drought sensitivity index, were considered in this study. Results showed there were significant differences between genotypes for all traits in both years, except thousand seed weight (TSW) in 2009. Also, water regime affected significantly all traits, except number of branches per plant and TSW in 2009 and leaf area, number of heads per plant and seed oil content in 2010. Genotype x water regime interaction was significant for all traits, except number of branches per plant, number of heads per plant, TSW and seed oil content in 2009, and TSW in 2010. The accessions 9869 and PI262421 exhibited high performance under full water regime conditions, whilst the accessions PI271073 and PI250076 were the most efficient under drought conditions. Furthermore, these last two as well as the accession PI306685 were the most stable, showing low drought sensitivity index under the different environmental conditions. All this material could be selected and used in safflower breeding program as promising germplasm to develop good and adapted varieties for Moroccan conditions.

# THE PROBLEM OF CLIMATE WARMING AND THE OBJECTIVES OF SPRING SOFT WHEAT BREEDING IN WESTERN SIBERIA

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The problem of climate warming in Western Siberia is the issue of the day as well as in world agriculture. Estimation of the dynamics of average daily temperature change and amount of precipitations during decades from May to September has been made from 1971 to 2011. There has been marked the authoritative rise in temperature in the second decade of May on the average 0,1 Cº per year. Critical period of the spring wheat plant development (from stem elongation to ear formation) coincides with high temperatures and precipitation deficit in the third decade of June and in the first decade of July in most of the years. The foregoing stipulates yield depression. Yield production correlation coefficient with rain capacity is authentically high in the period mentioned above. The general maximum and minimum temperature increase has been marked during the year. The frequency of dry years is increasing, along with epiphytotics of leaf and stem rust and other diseases. The main objective of the breeding in Omsk region is increasing of drought resistance and resistance to diseases of different wheat varieties. The program KASIB has been working effectively under the direction of CIMMYT since 2000 to solve actual problems of breeding. The varieties Sibakovskaya Yubileynaya, OmGAU 90, Novosibirskaya 31, Novosibirskaya 18 and other varieties, resistant to the conditions of Western Siberia, have been created in recent years.

**Key words:** wheat, climate warning, drought resistance, resistance to diseases.

# USING *DNA* TECHNOLOGIES FOR DEVELOPING INBRED LINES AND HYBRIDS IN MAIZE

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In the paper principles for selection of the valuable QTL's in maize population by DNA markers have been presented. Among the different types of DNA markers simple sequence repeat (SSR) markers were used to identify QTL's responsible for plant productivity, plant height and grain length. Two-locus system on the basis of linked SSR-*markers* proved to be the most effective. The genetic improvement population effect (AG) ranged from 9.1 up to 17.6 % depending on the phenotypic character and $h^2$ level. On the basis of the proposed selection model the method for predicting the population QTL development level was elaborated. It would be possible to predict the valuable trait development level in the next generation. The significant genetic improvement of $F^3$-$F^4$ populations for grain length and individual productivity was obtained. On this basis the gene pool of lines (over 200 inbreds) was selected. The best hybrids developed from marker-origin lines outyielded the national check hybrid by 6.8-7.6 %. As a result of this study the first Ukrainian maize hybrid Dialog developed by DNA-marker selection was registered in 2009. It is a single modified hybrid. The seed production of the hybrid is carried out on the cytoplasmic male sterility base. Its genetic grain yield potential is 11-12 t/ha. In 2012 maize hybrid Dialog 300, the second one developed using MAS technology, passed to the state variety testing.

# PARAMETRIC STABILITY ANALYSES FOR GRAIN YIELD OF BARLEY

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Barley is a multipurpose plant cultivated since ancient time for food, feed, medicinal purposes and malt of alcoholic beverages. Study of genotype × environment interaction has an important role in yield stability assessment of improved materials because crop reaction of stable genotypes is the same in different environments. In this study, genotype×environment interaction of grain yield in 15 barley genotypes were studied in a randomized completely block design with three replication in five locations of Iran during 2011-2012 growing season. The objectives were to assess genotype×environment interactions (GEI), determine stable genotypes, and compare mean grain yield with the parametric stability parameters. To quantify yield stability, four stability statistics were calculated (Environment variance, genotypic coefficient of variation, Wrick ecovalance and Shukla stability variance). The obtained results through all these methods were nearly analogous. According genotypic coefficient of variation statistics and environmental variance (0.68) Valfajr variety with lowest value was known as stable genotype. Fajr 30 variety was able to ecovalance down most (0.95), stability variance (0.16) was introduced as a stable genotype. On the other hand the three highest values of criteria related to the Makooei barley that was unstable genotype. Also cluster analysis based on both criteria ecovalance and stability variance, showed the same category based on these parameters and average performance. Nosrat variety with the relatively low interaction of genotype and environment and above average performance was considered best genotypes for breeding program and recommending to farmers.

**Keywords**: barley, G × E interaction, grain yield, stability

# PERFORMANCE OF MPOB NIGERIAN HIGH KERNEL OIL PALM GERMPLASM X AVROS *PISIFERAS* PROGENIES

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A total of six progenies of the high kernel MPOB Nigerian oil palm germplasm were progeny tested with Avros *Pisifera* in inland soils. The performance of their full-sib families for Fresh Fruit Bunch (FFB) was more than 100 kg/palm/year. The best progeny was PK 2692 (0.149/10426 x 0.174/656) yielding 171 kg/palm/year. The high yield was mainly due to high average bunch weight (ABW 16 kg/bunch/year) and moderately high bunch number (BNO 10 bunches/palm/year). Analysis of variance (ANOVA) showed highly significant differences among the progenies for the three traits. The heritability estimates for FFB were low; less than 10%. Higher estimates were obtained for ABW and BNO. For fruit components, the mean fruit weight (MFW) of the progenies was comparable with standard cross (PK2661 10.75 g/fruit) planted in the same trial. The mesocarp to fruit (M/F) of the progenies were lower than the standard cross (80.97%). The mean M/F for the progenies ranged from 65.53% and 76.75%. This was mainly due to high kernel to fruit (K/F) of the progenies with majority had K/F of more than 10% as compared to the standard cross (8.32%). The kernel to bunch (K/B) were also higher than the standard cross with the best progeny PK 2671 (0.149/10702 x 0.174/211) had K/B of more than 10%. ANOVA showed highly significant differences for all the fruit component traits, indicating high genetic variability for the traits among the progenies. Heritability estimates for the fruit components traits were high except for oil yield (OY 34%) and MFW (37%). Overall, PK 2671 with more than 10% K/B, can be utilized for commercial oil palm high kernel DxP production. To date, a total of 17 palms were selected for high kernel planting material based on FFB production of more than 100kg/palm/year and kernel to bunch of more than 10

# PHYSIOLOGICAL AND BIOCHEMICAL PARAMETERS AT SEEDLING STAGE AND GRAIN YIELD IN MAIZE UNDER WATER DEFICIT

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Being one of the most adverse factors of plant growth and productivity, drought considered a severe threat for sustainable crop production in the conditions on changing climate. This stress triggers a wide variety of plant responses, ranging from cellular metabolism to changes in growth rates and crop yields. Understanding the physiological and biochemical responses to drought is essential for a holistic perception of plant tolerance mechanisms to water limited conditions. To analyze the physio-biochemical basis of drought tolerance, 39 genotypes (including local and introduces maize landraces, as well as introduced maize inbred lines), previously selected as tolerant under field drought, were subjected to 4% PEG-induced osmotic stress under laboratory conditions, at seedling stage. Length, fresh weight and free proline content in roots and shoots were measured. As many yield-determining processes in plants, integrating in a complex way, respond to water stress, obtained yields were correlated to laboratory results. Grain yield/plant of local landraces was in significant positive correlation to growth parameters and in significant negative correlation to proline content, both in roots and shoots. Grain yield/plant of introduced maize landraces was in significant positive correlation to all observed parameters in roots, while in introduced inbred lines was found significant negative correlation to growth parameters, as well as significant positive correlation to proline content for both roots and shoots.

**Key words:** osmotic stress, proline, root, shoot, *Zea mays* L.

# PHYSIOLOGICAL RESPONSES AND RECOVERY POTENTIALS OF CULTIVATED AND WILD WHEAT SEEDLINGS EXPOSED TO HEAT STRESS

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Heat stress is one of the major factor limiting plant growth and survival. Effects of sub-lethal heat application before lethal heat treatment on thermotolerance mechanisms of tetraploid two wild wheats (*Aegilops biuncialis* and *Aegilops cylindrica*), and two durum wheats (*Triticum turgidum* L. cv. Kızıltan-91 and Harran-95) were investigated. Eight-day-old cultivar seedlings were exposed to various elevated temperature treatments; control (23±1°C for 24h), sub-lethal heat pretreatment followed by lethal heat treatment (39±1°C for 24h afterwards 50±1 °C for 1 h), lethal heat treatment (50± °C for 1 h). Effect of heat treatments in seedling length among tetraploid wild species and durum cultivars were determined at the end of the 144 hours recovery period. When plants exposed to direct lethal temperature, seedling lengths was significantly reduced in all genotypes. However sub-lethal treatment enabled the seedlings to tolerate the lethal effects of heat stress, this effect was not observed in Kızıltan-91 that showed greatest resistance to heat compared to other genotypes. These results were also verified by electroleakage data. Heat treatment caused a decrease in relative water content in leaves of all genotypes and it was approximately between 70-80%. While total chlorophyll and carotenoid contents of tetraploid wild species were significantly decreased with all heat treatments, sub-lethal heat pretreatment caused an accumulation in only Kızıltan-91. Moreover, *Ae. cylindrica* was sensitive to heat but it had higher protection compared to other genotypes. This cultivar probably withstand heat with better upregulating protective mechanisms (such as anthocyanin, SOD, APX, CAT, GR etc.) compared to Kızıltan-91.

# PREDICTION OF TRANSGRESSIVE SEGREGATION IN RECIPROCAL CROSSES OF THE CULTIVATED CHICKPEA (*CICER ARIETINUM* L.) AND THE HERBICIDE RESISTANT *C. RETICULATUM* LADIZ

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Transgressive segregants or superior lines to their parents (more fruitful filials) in $F_2$ and later generation have often been observed between interspecific and genetically divergent crosses in many crop species. Also, it was proven that there was a close relationship between genetic distance and heterosis in $F_1$. Therefore, genetically divergent parents based on molecular data have been used for a prediction of heterosis in many vegetables and important field crops. In Aim of the present study was to estimate transgressive segregation in $F_2$ and later generations in reciprocal crosses between the cultivated chickpea (*C. arietinum*) and a mutant of *C. reticulatum* (imidazoline resistant), progenitor of the cultivated chickpea, using heterosis and heterobeltiosis data. Heterobeltiosis rather than heterosis for yield and yield components have been found between reciprocal interspecific crosses. Results obtained on heterobeltiosis indicated that the interspecific reciprocal crosses between *C. arietinum* and *C. reticulatum* could be a good predictor for transgressive segregation in $F_2$ and later generation.

# QTL ANALYSIS OF GRAIN YIELD AND YIELD -RELATED TRAITS USING RECOMBINANT INBRED LINES IN WHEAT UNDER DROUGHT STRESS

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Quantitative trait locus (QTL) analysis of yield and yield -related traits in common wheat was conducted using a set of 75 recombinant inbred lines (RIL) derived from Roshan × Superhead in drought stress. The Diversity Array Technology (DArT) approach was employed for genotyping the population. The skeleton map consisted of 347 markers with a total length of 641 cM and average distance of 1.84 cM between adjacent markers. The length of individual chromosomes ranged between 8 cM for chromosome 7Ato 62 cM for chromosome 3B. Twenty nine QTL were located on 8 chromosomes, 1A, 1B, 2D, 2A, 4A, 5B, 6A and 7B. Four (main spike harvest index, biological yield, number of tillers per plant and number of fertile tillers), Three (grain Number per spike), two (plant height and spike length), one(biological yield of main stem , plant harvest index, length of internode, flag leaf length, grain yield and grain weight per main spike) QTL were detected. These results will provide important information for further functional analysis of drought-tolerance-related genes in wheat. DArT markers linked with QTLs for grain yield-related traits may be useful for marker assisted selection to enhance drought tolerance.

**Keywords**: Wheat, Drought stress, Quantitative trait locus, Recombinant inbred line

# RELATIONSHIP BETWEEN TRANSGRESSIVE SEGREGATION AND GENETIC DISTANCE BASED ON AFLP MARKERS IN *CICER* SPECIES

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Relationship between transgressive segregation and genetic distance based on molecular data has been widely studied in many important plants so far. Results have indicated that molecular divergence among parents has been a good predictor for transgressive segregation in $F_2$ and later generation. The objectives of the study were: (i) to measure the genetic distance among *C. arietinum, C. echinospermum* and *C. reticulatum* based on AFLP markers, (iii) to investigate relationship between genetic distance of the parents based on AFLP markers and transgressive segregation in $F_2$ and later generation. Three *Cicer* species including three accessions of *C. reticulatum,* one accession of *C. echinospermum* and three accessions of the cultivated chickpea (two of '*macrosperma*' and one of '*microsperma*') were crossed. Genetic distance among *Cicer* species was studied 47 AFLP markers. A significant relationship between the genetic distance of *Cicer* species and transgressive segregation for yield and yield components was found. The performance of the hybrids for yield and yield components was higher in interspecific crosses than those of intraspecific crosses. To increase of seed yield and yield components in chickpea, genetic divergent parents should be crossed for transgressive segregation in $F_2$ and later generation. Time, cost and effort will be reduced with these approaches. This study is an example on use of molecular techniques in plant breeding programs.

# SCREENING OF KENYA COMMERCIAL WHEAT VARIETIES FOR RESISTANCE TO THE EMERGING STRAINS OF STEM RUST RACE UG99

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Stem rust disease of wheat caused by *Puccinia graminis* fsp. *tritici* is of major concern because of its devastating effects on susceptible wheat varieties causing yield loss of up to 100%. East Africa has been designated as a "hot spot" of the stem rust pathogen as evidenced by the discovery of a new more virulent race of stem rust characterized as TTKSK or better known as Ug99 and several of its variants in East Africa and South Africa. This study aimed at screening twenty (20) Kenya commercial bread wheat varieties for stem rust resistance at adult stage under artificial disease epidemic simulation. The twenty varieties and three check varieties (controls) were planted in the International Stem Rust Screening Field at KARI-Njoro in a Completely Randomized Block Design (CRBD). A stem rust susceptible variety (spreader) was planted in between the replicates and around the plot, perpendicular to the entries to serve as a reservoir of stem rust disease. The first stem rust disease scores (infection type and severity) were taken when the susceptible check (Cacuke) showed a disease score of fifty percent (50%). Three scores were then taken at seven days interval and Area Under Disease Progress Curve values computed. Thirteen samples of stem rust fungi were collected randomly in the trial plots and analysed with Ug99 SNP markers using Real Time PCR . Eleven varieties Ngamia, Mbega, Chozi, Kwale, Pasa, Yombi, Duma, Kulungu, Mbuni Njoro BWII and Kenya Kongoni showed susceptibility of varying degree ranging from Moderately Susceptible (MS), Moderately Susceptible-Susceptible (MSS) to Susceptible(S) with the most susceptible being Pasa , two varieties Kenya Chiriku and Kenya Tembo showed mixed type infection(M) while seven varieties Eagle10, Kenya Fahari, Robin, Kenya Ibis, Kenya Nyangumi, Kenya Swara and Kenya Kingbird showed varying levels of resistance. Based on readings from one replicate variety Kenya Swara had the lowest AUDPC value of 56 while the highest AUDPC value of 630 was recorded in variety Pasa. Both AUDPC and disease scores showed significant ($P<0.0001$) variation among the varieties. However there was no significant ($P>0.1$) variation among replicates for both disease measures. In the analysis of stem rust fungi using Real Time PCR two genotypes of the Ug99 variant TTKSK were detected. The two genotypes were AF-001ad and AF-001aa and varied at SNP marker positions A023 and and A030 with genotype AF-001ad having Adenine and Cytosine (AC) bases at both positions and genotype AF-00aa having two Adenine (AA) bases at both positions. In conclusion the Kenyan commercial wheat varieties can be categorized as those having adult plant resistance to Ug99 and those that are susceptible to this race.

**Key words:** *Puccinia Graminis fsp tritici,* TTKSK, Ug99, Kenya commercial wheat varieties

# STUDY OF GXE INTERACTION OF TEN MOROCCAN GENOTYPE OF OAT

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Analysis of multi-location and multi-season trials to recommend adapted oat cultivars is an important step in plant breeding programs. Therefore, the aim of this work was to study the genotype x environment interaction in order to define the ideotype for each eco-region. Ten cultivars of oats including four registered cultivars and six selected genotypes were studied for two seasons in three different locations. The results indicated significant ($P<0.01$) effect of genotype, environment and GxE interaction for all studied traits (dry matter yield, seed yield, plant height …). The presence of GxE interaction indicates that cultivars rank differently according to the environmental variation. The analyze of GxE interaction, using AMMI model allowed us to recommend specific adapted cultivars for each eco-region.

Key words: oat, GxE interaction, specific adaptation, AMMI.

# THE GRAIN ZN ACCUMULATION FOR SPRING WHEAT: CULTIVARS AND REGIONS

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WHEAT MINERAL (ZN) Nutrition Information Analysis In Kazakhstan Showed Wide The Regional Variability Of The Grain Mineral Composition. In This Regard, The Study Grain Produced Regions On 68 Points While The Soils And Grain Will Organize Regions And Genotypes Within The Climatic Zones Of Kazakhstan. Zn Content In Spring Wheat Varies Considerably (2004-2005) From 10 Mg/Kg (Shortandy) Up To 80 Mg/Kg (Alginsk), And Middlegrounded Values From 11-12 Mg/Kg (Osakarov And Shortandy) To 41 Mg/Kg (Ruzaev). In General, The Three Sites In The Grain Formed The Lowest Zn Content: Is Osakar, Shortandy (10-13 Mg/Kg) And Kazan (11-22 Mg/Kg). The Maximum Value Of Zn (80-50 Mg/Kg) Was Observed For Cultivars Pavlodarskaya 93, Gedera, Intensivnaya, Kazakhstanskaya Rannespelaya, Omskaya 19, Kazakhstanskaya 15 And Karabalykskaya 3 In Algin And Aytekebie Areas In Western Kazakhstan; Lenger (South), Ruzaev And Shchuchin (East). The Interrelation Between The Accumulation Of The Protein And The Fe Content (0,60-0,89 For Seven Areas) And The Zn Content (0,65-0,82 For Five Areas). The Content And The Zn Concentration Per Mg / Kg And Mg / Grain Correlated At A High Level (0,56-0,97) For The Kazakhstan Genofund. The Content Of Zn Is Characterized By Correlation With Protein Content, The Degree Of Which Depends On The Region, Genotypes And Their Interactions Also As A Correlation: P-Zn (0.40-0.84); S-Zn (0.36-0.91; Zn-Mg (0.39-0.85). For Determining The Influence Degree Of Genotype And Environment Necessary To Unify The Block Of Genotypes, Such For Example As A Kazakhstan-Siberian Network Of Wheat Improvement.

# THE POTENTIAL FOR RESISTANCE BREEDING IN THE GENUS *HELIANTHUS* AGAINST *OROBANCHE CUMANA*, FROM THE BIOCHEMICAL STANDPOINT

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The root parasitic angiosperm Orobanche cumana is a major problem in sunflower cultivation in all south European countries and Turkey. While biological control has so far been unsuccessful, and the application of herbicides is limited for health and economic reasons, only resistance breeding provides a long-term solution. A major difficulty for the breeder is the fast development of new pathotypes of *Orobanche cumana*, which overcome the resistance of newly developed sunflower lines species. Nevertheless, there is still large potential for resistance breeding in the genus *Helianthus*, since very different resistance factors are already known or shall be elucidated. Resistance factors, such as *Orobanche* seed germination inhibitors, were studied in the root exudates of different sunflower lines species. Instrumental analysis of root exudates show the presence of germination inhibitors from the cinamic acid family, the ferulic acid family, the cumaric acid family and benzoic acid. The germination inhibiting activity of benzoic acid by Orobanche seed germination tests under standardized laborarory conditions was shown, but different resistance levels have been observed. The need for molecular biological studies will be stressed. The interdisciplinary collaboration of breeders with biochemists and molecular biologists may lead to more advanced breeding strategies.

**Key words:** sunflower, Orobanche cumana resistance, resistance factors, inhibitors

# THE RESULTS OF COOPERATION OF CHELYABINSK SCIENTIFIC RESEARCH INSTITUTE AND CIMMYT ON SOFT SPRING WHEAT

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In the Southern Urals, Russia, where the everage rainfall is equal to 347 mm, wheat reduces its yield not only because of the drought. Crops suffer from excessive wetting once in 5 years in the steppe and in 30 % of the time in the forest steppe. It is resulted in the lodging of crops, in brown rusted wheat and depletion of seeds (black ear).Yield losses can be up to 64%. The quality of the grain is reduced. Therefore both resistance to drought and waterlogging should be combined in the varieties of wheat. To achieve this goal the productive cooperation of Chelyabinsk Agricultural Research Institute and CIMMYT was started in 2001.This allows to use new genotypes into the selection and to test varieties under different climatic conditions. Such cooperation increases the adaptability of the original and breeding materials to the local conditions. Aristated forms resistant to water stress, genotypes resistant to brown, stem rust are particularly out standing. In 2013 30-50 % of the samples of wheat breeding nurseries in Chelyabinsk Agricultural Research Institute have been taken in hybrid populations created in CIMMYT. Such representation of the selection material indicates the high importance of CIMMYT for selection soft spring wheat in Chelyabinsk Research Institute.

# THE RESULTS OF THE DIRECTED SELECTION FOR REDUCING THE HEIGHT OF WINTER RYE

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The effective selection provides for availability of the necessary original material, the conception of its genetic use, the strategy of receiving and fixing the desired results, the economic mobile tactics of the assimilation results. The directed selection for the height reduction of a winter rye plant has been started since 1975. The most short-stalked plants have been selected every year. The predicted and actual effectiveness of selection, coefficients of heritability, selection differential and genetic clusters have been determined. As a result, the height of the plants has decreased in 5.7 times - from 119cm to 20cm. It is proposed the symbolic of the dominant alelies of genes of the ultra short-stalking in the homozygous state - Hl3HL3. It is determined the relative impact on the effectiveness of the minus selection by height of plants selection differential (38%) and the coefficient of heritability (15 %). The realized effectiveness by reducing of height of winter rye plants in 72 % cases coincided with the prediction. We present genetic and statistical parameters of the average, the cluster analysis of 11 quantitative signs, it is suggested a genetic conception of the practical use of the new donor. Creation of sorts, heterogeneous synthetics and hybrids with yields of more than 10 t / ha is based on the resistance to fallen donors of short-stalking of Gnome 3 (20-25cm), Gnome 2 (50-60cm) and Gnome 1 (90cm). The new created donors redistribute assimilates from the leaves and stems in a pollinated, and improve quality of alpha - amylase complex.

# THE SELECTION OF WINTER RYE (SECALE CEREALE L.) ON PLANT-BREEDING SELECTION AND EXPERIMENTAL STATION OF NOSIVKA

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The doctrine of winter rye selection is focused on yield, quality, resistance to diseases, pests, industrial technologies. Since 1970, the following areas have been developing:

- The selection of a dominant short-stalked, large-grained, non fallen synthetics;

- The genetics of large grain, the creation of large-grained donors, the selection of coarse synthetics;

- The genetics of immunity to flour dew, the creation of donors and the selection of stable synthetics;

- The genetics of immunity to stem and leaf rust, the creation of donors and selection of stable and tolerant synthetics;

- The selection of high-yielding sorts, synthetics and rye hybrids by optimization the photosynthetic potential of plants;

- The selection of sorts, synthetics and rye hybrids with a strong root system;

- The selection of short-stalked, large-grained, resistant to diseases, non fallen hybrids $F_1$.

The plants with genes HlHl have been used by the genetic resource for creation of non fallen sorts. The creative donors of short stems with a height of 19-22cm have been created during 44 years by the directed selection. Thanks to directed selection the weight of 100 grains per plant is increased at 3.4 times. The selection is carried out on the provocative-infectious background to Eresiphe graminis, Puccinia dispersa, Fusarium nivale. The selection for optimization of photosynthetic potential is provided by the erectoidical placing of leaves. The power of the root system is increased with the help of the number of embryonic roots. In the Register of Ukraine there are 11 our sorts with the yields up to 8 t / ha). The large-grained, stable to fallen, with excellent baking qualities, aren't affected by diseases , have the export perspective, don't compete with each other, are able to produce stable yields in different conditions and complementing each other. Such synthetics as Kobza , Lyric, Nalite and Oaza are tested.

# THE SHUTTLE BREEDING OUTCOMES OF KURGAN SCIENTIFIC AND RESEARCH INSTITUTE OF AGRICULTURE (KSRIA)

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The outcome of shuttle breeding is valuable starting material for wheat breeding. The shuttle material of spring soft wheat, made by the KASIB program, is being studied during all the stages of breeding process, in whole from 336 combinations of crossing. Patterns of varieties (234 patterns - 19 TH FAWWON IR 2011-12 and 108 patterns - 19 TH FAWWON – SA) were received from Turkey to enlarge the collection of winter wheat. In 2011-2012 winter period all the patterns died. The second part of the seeds, that had been left as a safety fund, sprang and over-wintered successfully in more favorable conditions of 2012-2013. According to the results of the field screening, 86 patterns (i.e. 25 %) were left for further studying. Thus, international cooperation and breeding material exchange give opportunity to increase genetic material diversity for breeding of spring and winter wheat varieties in Trans-Urals conditions of Russia.

# THE STUDY OF HEREDITY OF PHOTOSYNTHESIS AND DROUGHT RESISTANCE CHARACTERS OF WHEATS AND DETERMINATION OF THEIR DONOR CAPABLE GENOTYPES

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For the purpose of studing the character ofheredity of morphophysiological sings related on drought resistance of wheats varieties was found out that, in celection progeny stabilizing characters of plants depend on biological pecularites of parental pair. It was proved that in hybridization of winter genotypes with spring wheat varieties basic hybrids obtained in male form were those of double feature. In studied hybrids the process of accumulation of dru biomass and dynamics of formation of assimilative surface of leaves and other plant organs were close to parental pair at the beginning of vegetation, but after shooting stage they were similar to maternalrganisms. In studing water regime it was found out that, daily water deficit and water-holding capacity of hybrids were similar to maternal forms and surpasses parental organisms and water deficit intensifies this difference. Photosynthesizing pigments in leaves of hybrid plants was found in maximum amount in heading stage and it was similar to parental one even in breaking plant water supply, decrease of the amount of chlorophylis (a+b) and carotenoids doesn't break the definite appropriateness. The study of photosynthesis intensity indicated that in hybrid plants this process was going as in parental forms and as a result of water deficit weakens in differently both in parental pair and in hybrids depending on biological peculiarities of plants. It was revealed that almost in all hybrid combinations of first generation by the characters of plant growth, length, width and mass of kernel, mass of 1000 kernel, mass of grain in ear is observed effect of heterosis in second generation too, as a result by selecting most valuable sings the efficiency of hybridization may be improved. Comparsion of yielding characters, hybrid guality and parental pair, showed that if the parameters of hybrids in most cases were similar to maternal forms, but by some characters they surpass parental pair. By this way valuable forms of durum wheat hybrids were selected, but manu others are passing competitive strain testing, which enriches local wheat gene fund. It was prepared a recommendation on wheat breeding for creating drought resistant varieties in Azerbaijan condition.

# THE STUDY OF RHIZOBIA SYMBIOSIS WITH BEAN AND ALFALFA GROWN UNDER SALT STRESS

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Worldwide, soils are increasingly attacked by the release of mineral nitrogen from human activities. The use of nitrogen fertilizers to the inevitable consequence, the increase in nitrate content, which may contribute to the production of nitrite and the formation of carcinogenic nitrosamines. The nitrogen fertilizer may also affect the structure and function of the microbial community. Some plants, such as legumes, however, can draw and fix nitrogen gas from the atmosphere through symbiotic association with bacteria called rhizobia. Bean and alfalfa crops are strategic economic and food. In order to study the symbiosis with rhizobia in bean (Vicia faba L.) and alfalfa (Medicago sativa L.) in the region of Biskra, we used soil samples collected from 30 localities. This work has identified several points of ecological and agronomic. The evaluation of potential symbiotic soil of the region of Biskra, by the technique of trapping, show different levels of susceptibility to rhizobial microflora. The effectiveness of the rhizobial symbiosis in two pulses indicates that the biomass dry air and the amount of nitrogen accumulated in the aerial part, depends mainly on the rate of nodulation and regardless of the species and locality. The correlation between symbiotic nitrogen fixation and some physico-chemical properties of soils showed that the symbiotic fixation in both legumes is strongly related to soil conditions of the soil. Salinity disrupts the physiological process of growth, development and particularly that of the symbiotic fixation of atmospheric nitrogen. The physiological characterization, biological and chemical strains indicates that it is nodules by rhizobia that are probably different.

**Keywords:** symbiosis, rhizobia, bean, alfalfa, salinity.

# THE UNIQUE MUTANTS OF BARLEY PRODUCED IN CONDITIONS OF PAMIR

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As a result of long-term works on experimental mutagenesis in conditions of the Western and East Pamir mutants of barley (H. vulgareL.) representing selection, genetic and evolutionary interest have been produced. Mutants are basically received on barley of Jay-kobutak (var. himalaense). Jay-kobutak is a grade of national selection and is sowed on the Western Pamir (Badakshan) at heights up to 3200m above sea level. Plants of the given grade have the following characteristics: a stalk length is 50-60cm, an ear length is 8-10cm, ear density is 11-12, 1000 grains weight is 45-50g. The caryopsis form is oblong. Under the effect of nitrosomethyl urea (NMU) at a concentration of 0.006% in the Western Pamirs 2600m above the sea level Wuhan-1 mutant on a short and erect 25-30cm stem was developed, its ear length is 4-5cm, ear density is 23-24, 1000-grain weight is 33-36g. It is interesting, that this mutant grains have a rounded shape. In the conditions of East Pamir at a height of 3860m under a similar effect of mutagene NMU the rare mutant with the ligule absence of lamina is produced. The genetic analysis has shown that the given character is recessive. Plants of nonligular mutant have length of a stalk 50-55cm, length of an ear 7-9cm, density of an ear 11-12 and weight of 1000 grains 45-48g. As a result of Wuhan-1 и nonligular mutants hybridization the wide range of variability is received. In particular, among others, nonligular round-grained plants are developed. These plants have a stalk of 50-55cm, an ear of 5-7cm, their ear density is 18-19, and 1000-grain weight is 40-42g. The produced forms without doubt are interesting for selection. As well other mutants were produced, such as dwarfs, large-grained, early ripening, which are important for selection and also mutants of genetic-evolutionary interest, such as two-row, rye ear type, etc. Thus, a combination method of experimental mutagenesis and hybridization has not only contributed to a breeding of useful and genetically interesting mutants, but has also identified new botanical forms of barley-nonligular plants with rounded grains.

# TOWARDS AN UNDERSTANDING THE MOLECULAR NATURE OF SUNFLOWER FERTILITY RESTORATION GENES

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The CMS-*Rf* genetic systems are widely used in plant breeding as a basis for hybrid seed production. Recently, they have also been considered as a model for studying the genetic mechanisms of nuclear cytoplasmic interactions. The majority of the known fertility restoration (*Rf*) genes encode proteins containing pentatricopeptide repeats (PPR) motifs and are classified as the *RFL-PPR* gene family. The molecular nature of sunflower *Rf* genes is not yet understood. To test the hypothesis on belonging the sunflower *Rf* genes to the *RFL-PPR* family we used the original models representing the genetic collection of 128 lines with different types of cytoplasmon and alleles in the *Rf1* locus which is responsible for CMS PET1 pollen fertility restoration. The fragments homologous to the *Rf* genes of other plant species have been selected from the Compositae Genome Project database (http://www.cgp.edu/), amplified, cloned and sequenced. All the fragments were shown to contain PPR motifs. Five fragments were polymorphic and the three ones were nearly identical among the genotypes analyzed. One of the fragments contained intron and revealed a polymorphism associated with the *Rf1* functional state. The molecular markers of some PPR-sequences were developed and their co-segregation with the *Rf1* common molecular markers was examined in the F2 of interline crosses.

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# UNDERSTANDING G×E INTERACTION AND ITS IMPACT ON OBTAINING BREEDING OBJECTIVE IN WHEAT GENOTYPES

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Assessing grain yield of a set of cultivars in multi environmental trial, changes are commonly observed in the relative yield performance of genotypes with respect to each other across environments. Understanding the causes of G×E interaction, establishing specific breeding objectives and to identify desirable genotypes ninteen wheat genotypes along with a check cultivar were evaluated under normal and late sowing conditions for yield quantification, heritability and selection response. Analysis of variance showed highly significant differences ($P<0.01$) for spikes m$^{-2}$, grain yield and harvest index, while significant differences ($P< 0.05$) were observed for spikelets spike$^{-1}$ and grains spike$^{-1}$. Rest of the traits showed non-significant differences. The environmental component revealed highly significant differences ($P<0.01$) for all the traits except for grain weight spike$^{-1}$, which exhibited significant differences ($P< 0.05$). However, the G×E interaction showed significant differences ($P<0.01$) only for harvest index. Our results indicated that some bread wheat genotypes performed well under late sowing conditions. Therefore, these genotypes can be used for late sowing in multiple cropping regions or they could effectively be utilized in breeding program to transfer these characters to those varieties which do not perform well under late sowing. Heritability estimates for all yield contributing traits were greater in magnitude under late sowing condition revleaved that selection will possibly be more effective under late sowing environment to reduce the existing gap between normal and late sown wheat crop.

# UTILIZATION OF WEEDY RICE AS BREEDING MATERIALS TO IMPROVE CULTIVATED RICE YIELDS IN SRI LANKA

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Weedy rice (*Oriza sativa f. spontanea*) is now immerging big thread to low land rice cultivation in Sri Lanka as well as in Asia. It is closely associated with cultivated rice and can't distinguish at early stages. It competes with limited resources such as nutrients, moisture and space resulting low or no rice yields due to its high adoptability to wide range of environments. Even it has weedy characters some beneficial characters can use to improve cultivated rice yield while utilization of them as genetic resources in breeding programs. The beneficial characters are less shattering %, high grain filling %, good plant architecture and wide adoptability to limited poor environments (less nutrients, less moisture).There are some important characters in weedy rice that can be utilized to improve cultivated rice with wider adoptability. Therefore the objective of this study is to select best weedy rice accessions as breeding materials to improve cultivated rice yields of Sri Lanka. Collecting weedy rice accessions from different parts of the country and grows in Rice Research and Development Institute field and characterized. Among them select best accessions for breeding programs to do hybridization. Then select best plant types while maintenance of bulk and advanced populations to make stable genotype. Then evaluate selected advanced genotypes for pest and disease reactions and grain quality parameters. Best advanced line subjected to adoptability in different agro ecological zones of Sri Lanka. Finally release new rice varieties containing weedy rice blood.

# DETERMINATION OF STABILITY AND ADAPTATION ABILITY FOR SOME PROMISING COTTON (*GOSSYPIUM HIRSUTUM* L.) GENOTYPES IN EGEAN AND ÇUKUROVA REGIONS

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This study was conducted to determine stability and adaptation ability of some promising cotton (*Gossypium hirsutum* L.) genotypes. The experiment was set out a completely randomized block design with thee replications in five different locations (Menemen/İzmir, Torbalı/İzmir, Söke/Aydın Reyhanlı/Hatay, ve Adana) in 2004 production season. Eight cotton genotypes (BA-119, BA-308, SG-125 Flora, BAX-1302, BAX-1303, BAX-1304 ve BAX-1306) were used as the material of this study. The experiment were examined to stability and adaptation ability of genotypes in point of seedcotton yield (kg/da), fiber length (mm), fiber strength (g/tex) and fiber fineness with six different methods (Finlay and Wilkinson, 1963; Perkins – Jinks, 1968 and Baker, 1969; Wricke, 1962; Shukla, 1972; Francis and Kannenbert, 1978 and Ketata, 1984). The results were evaluated by the aid of stability parameters of different procedures and adaptation ability. Genotypes, environments and genotype x environment interactions were significant for all traits at $P<0.01$ probability level. BA-308 and SG 125 for seedcotton yield, BAX-1302 for fiber length, BA-119 and Flora for fiber strength and BAX-1304, BAX-1306 and Flora for fiber fineness ***were determined as*** a ***good adapted*** genotypes at all environments according to all stability methods.

**Keywords:** Cotton, genotype x environment interaction, stability.

# DEVELOPING PEANUT (*Arachis hypogaea* L.) LEAFSPOT RESISTANT CULTIVARS:

# YIELD EVALUATION OF ADVANCED GENERATION LINES

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Leafspot is a worldwide peanut disease and could cause a yield loss up to 60%. The use of leafspot resistant cultivar is easy, cheap, and environmentally friendly way in peanut cultivation to maintain yield. The objective of the research was to evaluate the yield of 16 peanut lines which developed to be leaf spot resistant and high yielding cultivars. The research was conducted at BAU experimental station Cikarawang located in Bogor, Indonesia, from March to July 2010. Randomized complete block design with three replications was used in the experiment. The lines evaluated were derived from cross between Gajah variety which is susceptible to leafspot and the resistant line named GPNC-WS4. Four Indonesian varieties were used as control, i.e. Gajah, Jerapah, Zebra, and Sima. The result showed that some lines had better level of resistance to leaf spot compare with Gajah variety as susceptible control. Some lines performed agronomic characters, i.e. pod number, filled pod number, pod weight, and kernel weight, which were not significantly different from the control varieties. It showed the potency of the lines to be developed further. Nine best lines with high yield potential and high resistance level to leaf spot from this evaluation were: GWS134D, GWS39D, GWS79A, GWS110A2, GWS39B, GWS134A1, GWS73D, GWS110D, and GWS18A1.

**Keywords:** leafspot resistance level, agronomic characters, environmentally friendly cultivation, high yielding cultivar

# DEVELOPMENT OF SOMACLONES WITH LOW ODAP CONTENT IN GRASSPEA (*LATHYRUS SATIVUS* L.)

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Grasspea (*Lathyrus sativus* L.) is an underutilized legume species which, by virtue of its resilience nature under adverse agro-climatic conditions, is a promising crop for adaptation to climate change scenarios. It is an important legume crop for human food, particularly for low-income people and as animal feed. However, the presence of neurotoxin, β-N-oxalyl-L-α,β-diaminopropionic acid (ODAP) in its seeds is a major deterrent in its adoption, which has been associated with neurolathyrism, a non-reversible neurological disorder in humans. Evaluation of grasspea germplasm in the past has shown that presence of low-ODAP or ODAP-free accessions are nascent in all collections world-wide, although considerable variability exists for ODAP content within the cultivated germplasm. With successful tissue culture techniques and regeneration protocol, somaclonal variation has emerged as a novel source of genetic variability towards low-ODAP contents for grass-pea improvement. At ICARDA, we evaluated 260 somaclones ($R_4$) generated from 19 high-ODAP genotypes using internodes as initial source of explant for callus induction during 2009-10 and 2010-11. The results showed significant somaclonal variation for ODAP content and yield related traits except for seeds per plant and protein content. The ODAP content ranged from 0.06 to 0.38% among the somaclones. Sel435 recorded the lowest ODAP (0.06%) content and holds promise in terms of adaptation and productivity.

***Key words:*** Grasspea, ODAP, somaclonal variation, tissue culture.

# DEVELOPMENTAL ACCUMULATION OF ODAP (Β-N-OXALYL-L-Α, Β-DIAMINO PROPIONIC ACID) AT DIFFERENT GROWTH STAGES IN GRASSPEA (*LATHYRUS SATIVUS* L.)

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Grasspea (*Lathyrus sativus* L.) is a climate resilient crop for adaptation to fragile agro-ecosystems. In drought years, grasspea assumes the role of survival foods for poor masses and the only source of feed and fodder for animals in rural areas of South Asia and Sub-Saharan Africa. In such years, people consumes higher quantities of grass pea in their daily diets as a staple food, and this makes low-income people vulnerable to a disease called 'neurolathyrism' due to a plant toxin called β-N-oxalyl-L-α, β-diaminopropionic acid (ODAP) present in its seeds and vegetative parts. Since grass pea plant is used as green fodder for animals and twigs as leafy vegetable for humans, and dry seeds for human food and animal feed, it is imperative to assess ODAP concentration in different plant parts at various growth stages. In the present study, we evaluated five genotypes of grass pea (387, B222, 390, Bio 520, and 587) with different ODAP levels in their seeds for two growing seasons (2009-10 and 2010-11) to understand the developmental changes in ODAP accumulation in different plant parts. The results indicated significant differences in ODAP accumulation at various growth stages across the genotypes. The ODAP content was highest (1.13 to 1.47%) at early vegetative phase in all the genotypes which, on an average, gradually declined to 0.19% in seeds and 0.69% in dry leaves at maturity.

**Key words:** β-ODAP, Grasspea*, Lathyrus sativus*, neurolathyrism

# GENOTYPES X ENVIRONMENT INTERACTION EFFECT ON NUTRITIONAL QUALITY OF SORGHUM LINES IN INDONESIA

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The adoption of sorghum as alternative source of food in Indonesia depends on consummer acceptance of sorghum grain which is determined by the nutritional and anti-nutirtional values and quality of sorghum grain. The objectives of this study is to obtain information of genetic variability of nutritional and antinutritional content of sorghum lines and the effect of genetic x environment on the variablity in sorghum grain nutritional vaues. The study was conducted on 24 sorghum lines with diverse genetic diversity consisted of breeding lines, introduced lines and a local variety. The lines were planted in a randomized complete block design with tree replications in two locations differing in soil fertility. The results showed that protein, fat, amylose and tannin contents of these genotypes are effected by the interaction of genotype x environment with different magnitutes. The G X E interaction qualitatively changed the rank of genotypes for protein and tannin contents in the two locations. The presence of G X E interaction caused an upward biased of the genetic variances and estimates of heritability of the characters for a single location.

***Keywords*** : *sorghum grain, protein content, tannin content, genetic variance, heritability*

# LINKAGE BETWEEN *SR2* AND *LM1* AND ITS EFFECT ON PHENOTYPIC EXPRESSION OF LESION MIMIC IN WHEAT

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Adult plant resistance gene *Sr2* conferred durable Stem rust resistance in wheat. PBC is the phenotypic marker of *Sr2* gene and stm559tgag is the genotypic marker for *Sr2* gene. Lesion mimic mutants (LMM) express HR in the absence of pathogens and also confer resistance to biotrophic pathogens, including leaf rust (Tao et al., 2012). LMM expressed on leaf, stem, glumes and awns. Three genes have been reported for LMM viz., *lm* (Xwmc85.1 and Xgwm264) on 1B**,** *lm1* (Xbarc147 and Xwmc674) on 3BS, and *lm2* (Xgwm513 and Xgwm149) on 4BL. Association between *lm1* and *Sr2* has not yet reported. 500 diverse lines of spring wheat were screened for *Sr2* and LMM both phenotypic and genotypic. The genotypes which have *Sr2* and *lm1* showed very high expression of lesion mimic. Genotyping reveals that *Sr2* and *lm1* were present together in 86 % lines in combination with other lesion mimic genes. The *Sr2* and *lm1*genes both are on chromosome 3BS of wheat genome. The genetic distance of *Sr2* and *lm1* genes is ~2cM) and 1.2 cM, respectively. Hence, the distance between *lm1* and *Sr2* is < 1cM (~0.8cM). It indicates the linkage of *lm1* and *Sr2*. So association of *Sr2 and lm1* enhance the lesions production and reduce rust infection*.* *lm1* was present in various combination with *lm* and *lm2* in the population screened and resulted in increase lesion mimic expression.

# MARKER-ASSISTED IDENTIFICATION AND TRANSFERRING NEW RESISTANCE GENE FROM *AEGILOPS SPELTOIDES* TO BREAD WHEAT

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A number of *Lr* genes (*Lr28, Lr35, Lr36, Lr47, Lr51,* and *Lr66*) were transferred into the wheat genome from *Aegilops speltoides* Tausch. However, this wild species and their hybrids with common wheat are still useful as a source of new resistance genes. Line 73/00i, carrying durable resistance to leaf rust, was chosen from collection of *Triticum aestivum* × *Ae. speltoides* hybrids. Three translocations—T1SS-1BS.1BL, T5BS.5BL-5SL, and T6BS.6BL-6SL—were identified in line 73/00i using *in situ* hybridization and SSR analysis. Marker-assisted backcross was used for developing the lines carrying a single *Ae. speltoides* translocation. It was shown that the line 16-9 carrying the T5BS.5BL-5SL translocation were resistant to leaf rust. The new gene that determined resistance to leaf rust from the long arm of *Ae. speltoides* chromosome 5S was preliminarily designated as *LrAsp5*. The T5BS.5BL-5SL translocation carrying *LrAsp5* was transferred from the line 16-9 to Novosibirskaya 29, Lutescens 29, Lutescens 307, Lutescens 716 by cross. The Xcgi15 marker was developed for fast screening of wheat BC1F2 populations and discrimination genotypes resistant and susceptible to leaf rust. Resistance of the BC1F3 plants was evaluated at an adult stage at two locations of West Siberia (Russia) during two years. All wheat lines carrying the T5BS.5BL-5SL translocation were resistant to leaf rust. The impact of T5BS.5BL-5SL on some quantitative traits was assessed. No negative effects of the alien genetic material on yield and other quantitative traits were noted.

# MOLECULAR MAPPING FOR GRAIN PROTEIN CONTENT IN A *TRITICUM AESTIVUM* AND *TRITICUM SPELTA* CROSS

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Grain Protein Content (GPC) is an important nutritional parameter of wheat significantly influenced by environmental factors. The present study was undertaken to detect QTLs for GPC using 185 *Triticum spelta* ($H^{+}$26) × *Triticum aestivum* (cv. HUW 234) Recombinant Inbred Lines (RILs) under three locations in India viz., Banaras Hindu University (B.H.U.) Varanasi, Rajiv Gandhi South Campus (R.G.S.C.), B.H.U., Mirjapur and Indian Agriculture Research Institute (I.A.R.I.) New Delhi for two consecutive crop cycles 2010-11 and 2011-12. The whole grains of RIL population were evaluated for GPC (FOSS Infratec 1241 Grain Analyser) which ranged from 10.6% to 17.7%. A total of five QTLs were identified for GPC on four chromosomes 1B, 2B, 5A and 6A across environments of which three were consistent explaining 25% of variation. QTL on chromosome 2B was more consistent ($QEI_{LOD} < 2.5$ and $QEI_{R}^{2} = 0.01$) and was detected in four environments, with $R^2$ and *LOD* ranging 5.31%-7.17% and 2.88-3.36 respectively. However, the QTL *QPro.bhu-6B* explained maximum (10.89%) phenotypic variance with *LOD* of 5.91. Only QTL *QPro.bhu-1B* had its high protein allele from the low protein *T. aestivum* parent HUW 234 and the remaining four QTLs were favoured by alleles from the protein rich *T. spelta* parent $H^{+}$26. All the QTLs detected were tightly linked to one of the flanking makers. Among those, QTL on 2B (at 511cM, *1089780|F|0 - 1278607|F|0*) was tightly linked (0.26 cM) to the marker 1278607|F|0 followed by the QTL *QPro.bhu-6B* (0.34cM) to the marker *100003574|F|0*. The two consistent QTLs (QPro.bhu-5A.2 and QPro.bhu-6B) with around 10% phenotypic contribution each may be useful for marker assisted breeding to get enhanced level of GPC due to their tight linkage with the one of the flanking makers.

# OPTIMIZATION OF *IN-VITRO* CULTURE CONDITION FOR GENETIC TRANSFORMATION OF COTTON (*GOSSYPIUM HIRSUTUM* L)

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Cotton (*Gossypium hirsutum* L.) is one of the most important fiber and oil crops with a great economic value worldwide. Recent, trends in the development of agricultural crops with agronomic traits is inclined towards development of resistance to pests, herbicides, insecticides, pathogens and fiber-quality modification using genetic transformation techniques. Different varieties of cotton have evolved by hybridization that is why every regeneration protocol is cultivar specific and the researchers have to develop new protocols for each cultivar. Moreover, cotton is highly recalcitrant plant under *in vitro* conditions. Therefore, regeneration protocol was optimized for two cultivars SG-125 (Turkish cultivar) and Coker-310 to study the effects of media (MS, $B_5$ & MS salt with B5 vitamin), PGRs (BAP, Kin singly or in combination with NAA), other supplements (activated charcoal, PVP & ascorbic acid with citric acid) on shoot regeneration from shoot meristem explants. Bialaphos (1, 2, 3, 5 and 10 mg/l), Phosphinotricin (1, 3, 5, 10 & 15 mg/l) and pre-hardening conditions peat moss:perlite (1:1, 2:1 & 4:1) were also optimized for genetic transformation. The optimal culture medium for shoot organogenesis consisted of MS macro and micro salts with $B_5$ vitamins containing 0.5 mg/l 6-benzylamino purine (BAP), 0.1 mg/l Kinetin (Kin), 0.1 mg/l α-naphthalene acetic acid (NAA) and 2 g/l activated charcoal. The maximum herbicide tolerance capacity of non-transgenic plants for selection purpose was 10 mg/l PPT and 5 mg/l Bialaphos identified. The pots containing peat moss-perlite (4:1) mixture were best substrate for acclimatization in greenhouse. These findings indicate that regeneration protocol must be carefully selected for useful and higher expression of transgenes in developing cotton tissues for improving through genetic engineering.

**Key words:** Cotton, *Gossypium hirsutum* L., Genetic transformation, *In-vitro,* regeneration.

# PHENOTYPIC AND GENETIC IDENTITIES OF FINGER MILLET (*ELEUSINE CORACANA* (L.) GAERTN) LANDRACES IN NIGERIA

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A study was conducted to characterize the morphological diversity of 10 germplasm accessions of Finger millet (*Eleusinecoracana* (L) Gaertn) collected from diverse locations spread across the geographic Northern Nigeria during the 2008, 2009 and 2010 cropping seasons. The seeds of the accessions were planted in a randomized complete block design (RCBD) with three replications in each of two locations- Keffi and Gwagwalada, during the three cropping seasons. The field studies for the three seasons in the two locations followed uniform agricultural practices. Evaluation of phenotypic and genotypic characters of the different accessions revealed that the genotypes expressed significant genetic diversity for plant height, 1000seed weight, leaf length and number of tillers than all the other traits assessed at $p<0.05$ level of significance. These results tend to suggest a high variability existing among the selected morphological traits. Specifically, 87% of the variations were explained by the ANOVA model leaving only 13% unexplained. The cluster analysis based on morphological traits revealed six major distinct groups with one landrace forming independent cluster for the pooled analysis for the three years. The genetic identities were carried out using the molecular marker RFLP (Restriction Fragment Length Polymorphism), and *EcoR1* and *HindIII*restriction enzymes were used to cut the genomic DNA. The results using RFLP generated four clear bands of molecular weights 10000KDA, 8500KDA, 1000KDA and 200KDA. This suggests the existence of polymorphism among the accessions. These results demonstrate high variability existing among the genetic traits for these germplasm accessions. This information is very useful in unraveling the pedigree genetic relationships, as well as, in designing breeding and selection experiments for this crop.

# THE EFFECTS OF SEED PRIMING ON SEED YIELD İN CHICKPEA (*Cicer arietinum* L.)

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The study was conducted during 2009-2010 and 2010-2011 at the experimental fields of the Department of Agronomy, Faculty of Agriculture, Ankara University. The study, aimed to find the effects of different priming pretreatments and doses on seed yield of chickpea cv. Gökçe. The priming treatments consisted of no chemical treatment (control), priming with 50 & 100 mg / L $GA_3$, 15% & 20%PEG, 4%, & 6% mannitol for 24 hours and 18 ve 24 hours distilled water priming.Thereafter, the the seeds were rubbed with drying paper and allowedto dry for 24 hours. In this study; plant height, first pod height, number of branches per plant, number of pods per plant, number of pods per plant filled, number of empty pods per plant, weight of pods per plant, number, number of hundredweights, grain yield, and yield per hectare was optained. In terms of two years average, the maximum average grain yield of 165.70 kg / da was obtained after priming with 1% PEG, followed closely by a yield of 163.90 kg / da on seeds primed for 24 hours with distilled water. Minimum average gtrain yield of 85.82 kg/da was obtained on control seeds.It is concluded that priming the seeds of cv. Gökçe of chickpea results in early germination and initial growth by providing a rapid, enzyme activity with increased nodulation and increased yield.

**Key Words**: Chickpea, Priming, Polyethylene Glycol, Mannitol, Distilled water, Gibberallic Acid, Yield

# YELLOW RUST RESISTANT, NEW IMPROVED WINTER WHEAT GENOTYPES FOR CENTRAL ASIA AND THE CAUCASUS

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Yellow (stripe) rust is the most important disease constraint of winter wheat in Central Asia and the Caucasus (CAC). There were severe epidemics of yellow rust in many parts of the CAC in 2013. A few widely grown varieties, which were moderately resistant during 2009 and 2010 epidemics, became highly susceptible to yellow rust in 2013. A few varieties ready for release by the State Variety Testing Commission (SVTC) showed susceptibility to yellow rust in 2013. However, several advanced breeding lines evaluated in the nurseries originating from International Winter Wheat Improvement Program showed high level of resistance to yellow rust. A few winter wheat lines, selected for high yield, and satisfactory quality and agronomic characters in the previous years were resistant to yellow rust across the region in 2013. One superior line (Ymh/Hys//Hys/Tur3055/3/Dga/4/Vpm/Mos/5/5/TAM200/Kauz, TCI-02-138: -0AP-0AP-7AP-0AP-5A-0AP), resistant to yellow rust will be submitted to the SVTC in Tajikistan in 2013. Another resistant line (Attila/2*Pastor//Bulk Seln 00F5-43-11, OCW02S557S: -0OK-0E-6E-0E -1E -0E) is going to be submitted to the SVTC in Uzbekistan in 2013. In Georgia, one line (Burbot-6/Cardinal, TCI-01-13: -0AP-0AP-8AP-0AP-2AP-0AP) resistant to yellow rust and leaf rust will be submitted for registration by the State Agency. The findings of this study provide valuable information on yellow rust resistance and performance of the internationally important winter wheat genotypes. This information could be useful for the national and international winter wheat improvement programs in either further evaluation of the resistant lines for varietal identification or using them as parents in the crossing.

# ASSOCIATION MAPPING FOR FIBER TRAITS AND DROUGHT TOLERANCE IN TURKISH COTTON GERMPLASM

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Cotton has an important position in the textile, pharmaceutical, oil and food industries. Turkey, with its unique ecology and soil, ranks eighth in worldwide cotton production. Turkey's textile industry is largely based on cotton fiber. Drought stress causes seriously yield losses up to 70-80%. We aim to develop cotton cultivars with drought stress resistance and high quality fiber. To achieve our aim we used 73 SSRs providing 340 markers in a natural population composed of 105 different cultivars. The population was subjected to drought stress by growth under limited irrigation conditions. Phenotypic measurements were carried out under both drought and control conditions. We examined seven important agronomic characters including total number of bolls, boll set at second position, yield of unginned cotton, ginning efficiency, fiber yield, water-use efficiency and yield under limited water. Phenotypic and genotypic data were associated using TASSEL to find associated markers. As a result, we found 15 SSR markers significantly associated ($p<0,01$) with the phenotypic traits. Structure of the population was determined with STRUCTURE. Thus, the population was found to be clustered into 4 groups (13 individuals in Group 1, 18 individuals in Group 2, 12 individuals in Group 3, 23 individuals in Group 4 and 39 individuals of intermixed ancestry). The identified markers will be used in marker assisted selection screening of an F2 population generated for breeding of drought resistant, high quality cotton cultivars.

# BREEDING AND PERFORMANCE OF BATEM TATLI (SU) SWEET CORN HYBRID

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Sweet corn production is getting increasing in Turkey and there is need to develop new hybrids which are suitable for local markets. To meet grower demands studies have been going on at Bati Akdeniz Agriculture Research Institute (BATEM) since 2000. BATEM TATLI is a standart sweet corn (su) type and is a first local hybrid of Turkey developed and released by BATEM in 2013 . The hybrid developed from Mediterranean Region Maize Breeding Project that is supported by the General Directorate of Agricultural Research and Policy of Turkey. Pedigree breeding procedures applied to develop BATEM TATLI. Mean fresh ear yield of the variety was 15.2 t ha $^{-1}$ and dry ear yield was 5,9 t ha $^{-1}$. Crude protein was 10,7 %, oil 6,7 %, Starch 53,3 % and total sugar in mature seeds was 4,8 %. When the two years data analysed for stability parameters it was shown that the variety's yield performance was in the middle for both bad and good environmental conditions. In the present study, breeding and performance of the hybrid was discussed.

# BREEDING VALUE OF AN INITIAL MATERIAL OF WINTER WHEAT IN AZERBAIJAN

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Wheat is the basic crop and increase of production is considered a priority direction in the country. By long term researches is revealed that correct selection of an initial material, make possible creation of high-yielding and high-quality varieties with high adaptability, which have great importance in conditions of global climate change. The purpose of the carried out investigation was selection of an initial material for realization of resistant to biotic and abiotic stress factors of varieties with high productivity and quality of grain. During 2008-2010 years on Apsheron EBS in irrigation conditions have been investigated 1327 local and introduced from CIMMYT and ICARDA, varietysamples of bread and durum wheat. At various on morphophysiological features and origin varietysamples duration of heading, maturing, number of days at heading-maturing and vegetative period has been investigated and observed that duration of each stages and vegetative period along with influence of various factors of cultivation also depends on biological features of variety. By this research varietysamples of bread wheat Parzivan-1, Aran, Taraggi etc., (Azerbaijan), Donetskaya Yubileynaya, Tanya, etc., (Russia), AWYBGOP$_{00-01}$ KN 12, 11th FAWWON KN 149-193, SG.4.7063 (CIMMYT) and durum wheat Agbugda-13, Karagilchig-2, Алтун (Azerbaijan), Local-549 (Morocco), Radj-91 (India), Vezio (France), Zedon-3D-56 (Algeria), Bereket (Dagestan), Bezenchucskaya-65 (Russia) on positive economic, technologically-qualitative features and revealed high donor abilities is involved to crossings in 90 combinations as a valuable initial material.

# EFFICIENT SELECTION ON QUALITY TRAITS IN ALGERIAN DURUM WHEAT CULTIVARS

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Durum wheat value chain is organized through the production exclusively oriented to human food mainly for couscous and pasta making. Quality is becoming now very important and a priority objective to feed our population. In this study, we wanted to assess and appreciate the quality of ten new durum wheat genotypes cultivated in Algeria in two contrasting environments (sub-littoral and semi arid area). Several important wheat quality traits (physico-chemicals) i.e grain humidity, yellow berry, black points, total crude proteins, thousand kernel weight and and grain yield have been undertaken. Results revealed a large variability for each quality trait among all genotypes and within sites, this confirms the quantitatively genetic control of these traits where the environment has a large effect and reflects this fluctuating data. Some good results are noticed mainly for yellow berry, level of black points, mainly crude total proteins (12.75- 16.77%) and grain yield; it has been observed a high vitrosity level (exceeding 95 to 99%) in most of the selected varieties in the study. The Constantine site showed better quality traits values than the Oum el bouaghi one ; the same conclusion goes for grain yield where the favorable site (Constantine) exceeded the semi arid one by almost 9q/ha.

**Key words** : Durum wheat, Quality, physico-chemical traits, total crude Proteins, Constantine, Oum el bouaghi.

# CANOPY DIAMETER AS SELECTION CRITERIA FOR YIELD IMPROVEMENT OF BAMBARA GROUNDNUT (*VIGNA SUBTERRANEA* (L.) VERDC.)

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Bambara groundnut is future food crop because of its nutrition content as well as drought tolerant. The aim of the research was determining the selection criteria for bambara yield improvement. Field experiments was conducted during March-August 2011 at BAU experimental station Cikabayan located in Bogor, Indonesia. The experiment consisted of two separate parts that were distinguished by genotype used i.e. landraces from Sukabumi and Parung in the first experiment and 'plant-to-row' families selected from Sukabumi landrace in the second one. Planting arrangements in the field for the first experiments was based on landrace origin, while in the second experiment used augmented design with repeated families as controls. Seeds were space-planted 60x60 cm apart, using usual cultivation method. Characters observed were canopy diameter, number of branch and node per plant, number of total and filled pod per plant, and dry weight of total and filled pod per plant. Statistical analyses used was correlation and variance component for appropriate experiments. The results showed that canopy diameter was positively correlated with all of the pod characters in landraces from Sukabumi and Parung (r = 0.72** - 0.82**). On the 'plant-to-row' families landrace of Sukabumi origin, canopy diameter was also positively correlated with all of the pod characters (r = 0.36** - 0.60**). Therefore canopy diameter can be used as selection criteria to improve bambara yield. This was strenghtened by moderate broad-sense heritability ($h^2_{bs}$ = 0.41) of the character, and a non-destructive way in observation.

**Keywords:** canopy diameter, correlation, broad sense heritability, non-destructive character

# CEREAL MIXTURES — SOURCE OF PROTEIN IN ANIMAL FODDER

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High protein content of animal fodder produced in the farm itself has a great importance in the biological farming system. According to different research results around the world the growing of two and more species together increases their productivity. In years 2007 and 2008 the State Stende Cereal Breeding Institute carried out research on how to ensure protein content in fodder produced in biological farming system, by growing wheat (*Triticum aestivum* L.) variety *Uffo*, barley (*Hordeum vulgare* L.): hull barley variety *Abava*, hulless barley line IC- 364 both separately and a mixture of both species as well as cereal mixture together with the pea (*Pisum sativum* L.) variety *Vitra*. The results were analysed, determining the yield at the humidity level of 14 % (t ha$^{-1}$), the crude protein (g kg$^{-1}$), the yield of crude protein in the dry matter (t ha$^{-1}$). It was found that by growing a mixture of barley and wheat, the yield increased: in a wheat mixture with the hulless barley— by 0.30 t ha$^{-1}$, in a mixture with hull barley — by 0.57 t ha$^{-1}$, in comparison to the barley sown separately. By analysing the acquired protein yield from one hectare it was concluded that the highest protein yield was gained from the mixture of three species. By sowing a mixture of the wheat, hull barley, and pea, it was found that the protein yield had increased (by 64 kg ha$^{-1}$), the increase of the protein yield (by 59 kg ha$^{-1}$) was found also in the mixture of wheat, hulless barley and pea varieties in comparison to the barley that was sown separately.

This study is performed with financial support of Practical Applied Research Projects from the Ministry of Agriculture of Latvia, project No. 100413/76.

# COMPARATIVELY DETERMINATION OF AGRONOMIC PERFORMANCES OF ALFALFA (*MEDICAGO SATIVA* L.) GENOTYPES UNDER ERZURUM ECOLOGICAL CONDITIONS

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This study was conducted for devoloping resistant, high yield and high-quality hay-type alfalfa in Eastern Anatolia Region agro-ecological conditions and determining the agronomic performances of strain developed in alfalfa breeding studies in two location of Erzurum during 2003-2004. There were used X-1312/15 strain, X-1312 alfalfa varieties and Savaş alfalfa as study material in this study. It was planned "Randomized Complete Block Design" with three replications and 8 $m^2$ of each plot. Yield and yield components and quality of used varieties and strains were investigated. According to the plant height, stem thickness and dry matter yield, X-1312/15 and X-1312 were significantly different from Savaş alfalfa variety but quality analyzes weren't different among to varieties and strains. While X-1312/15 (69,5cm, 2,97mm, 1553,1kg/da) and X-1312 (69,1cm, 2,97mm, 1462,1kg/da) with respectively highest plant height, stem thickness and dry matter yield taken places in the same group, Savaş alfalfa variety had lowest ( 60,7 cm, 2,70mm, 1258,1kg/da). According to quality (NDF and ADF), there was no difference among the varieties and strains statistically. Savaş alfalfa variety had highest crude protein (19.01%) and it were followed by X-1312 (17.81%), X-1312/15 (16.78%) respectively. According to the data obtained from this study, it was applicated for registration of X-1312/15 in 2004 and the strain was registered in the name of Ömerbey in 2009.

**Keywords:** Savaş Alfalfa, yield, yield components, quality

# COMPARISON OF DIFFERENT LEAF TYPES OF CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES FOR YIELD AND YIELD COMPONENTS

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The research was carried out to compare the effect on the yield and yield compenent ofcompound and simple leaved chickpea (C*icer arietinum* L.) genotypes. The study was conducted in 2010 and 2011 under Ankara condition. In the study, 20 cultivars and lines which are consists of 10 to each leaf type was used as materials. Experiment was conducted in a randomized comlete block design with split plot and with three replications. Biological yield per plant (g/plant), number of pods per plant (number/ plant), number of seeds per plant ( number/ plant), seed yield per plant (g), yield of unit area (kg da$^{-1}$), biological yield of unit area (kg da$^{-1}$) and harvest index (%) of lines and cultivars were compared according to two types of chickpea leaf. There were no statistically significant differences in biological yield, number of pods per plant, number of seeds per plant, seed yield per plant and harvestindex among the leaf types. However, significant differences were found in seed yield, biological yield among the leaf types at 0.01 level statisticly. The yields of compound and simple leaved chickpea cultivars and lines were 203 kg da$^{-1}$ and 156 kg da$^{-1}$ respectively. Biological yields were 258 kg da$^{-1}$ in simple leaf and 575 kg da$^{-1}$ in compound leaf.

**Key Words**:Chickpea,Simple leaf, compound leaf, yield

# CURRENT STATUS OF DISEASES AND PEST MONITORING AND CEREAL GRAINS' BREEDING IN UZBEKISTAN

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Cereal grains are the main food crops in Uzbekistan as in most other countries. The main cereals of Uzbekistan are wheat, barley, corn, and also rice, which are grown in intensively irrigated oases. Biotic stress factors such as diseases, pests and weeds in wheat fields of Uzbekistan also have been aggravating and causing great economical losses. Releasing of the resistant varieties of the cereal grains to them is the requirement of the time and plays important role in the national food security. By the support of the FAO-SEC and IWWIP (CIMMYT-ICARDA), within the fields of the cereal grains of Uzbekistan, every year conducting monitoring of cereal grains fields on biotic and abiotic stress factors, which also plays important role in determining of priority breeding programs for the current real situations of the cereal grains fields of the country. According to our 2 yearly surveillance results it was determined that in cereal grains fields of Uzbekistan main disease which causing to economical losses is wheat yellow rust in wheat fields, Spot blotch in barley fields. Septoria and powdery mildew diseases have less importance and lower than economical risk. It was fixed that in 2013 year in Uzbekistan first time observed incidence of take all disease in the 3 wheat fields with high damage to the grain yield destroying by whole harvest in Kitab district and crown root rot in Karshi district of Kashkadarya region. Screening of the wheat materials to this disease will ensure yield stability at the presence of this disease. The most fixed pests were Sunn pest, Cereal leaf beetle and Greenbug in wheat fields. Sawfly damage first time fixed at the field Namangan branch of Andijan Research Institutute of Cereal grains. Breeding works on resistance to above mentioned pests and diseases will decrease pesticides application and yield losses.

# CYTOLOGICAL STUDY OF THE EFFECTIVENESS OF SEEDLING LEAF NUMBER IN RAPESEED (*BRASSICA NAPUS* L.) FOR THE COLD PERCEPTION DURING VERNALIZATION USING EPI-ILLUMINATION LIGHT MICROSCOPY

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Vernalization, a process required for transition of the vegetative meristem into the reproductive one is promoted through exposure of plants to long periods of cold temperature. Different studies have shown that the apical meristem is the site of cold perception during vernalization. In this study, the transition of vegetative meristem into the flowering state through the different stages of plant development (3,5 and 7 leaf seedlings)and different durations of cold (4$^{\circ c}$) exposure (15,30,40,50 and 60 days) was studied in two winter cultivars of rapeseed (Okapi and Licord) using Epi-illumination light microscopy. Results indicated that the developmental stage of plants as measured by seedling stage and the duration of exposure time are crucial in vernalization effectiveness. The 3 leaf seedlings cold treated for periods of 15,30,40,50 and more days did not show any changes in vegetative meristem feature. In the case of 5 leaf seedling exposed at 4ºC after 15 and 30 days transition was not observed, but after 40, 50 and 60 days of cold exposure the transition into the flowering meristem have been occurred. In the 7 leaf seedlings, transition occurred after only 30 days of cold exposure and remarkable changes in the developmental pattern of apical meristem was observed, followed by the apparition of inflorescence and floral buds after 30, 40, 50 and 60 days at 4ºC. It seems that seedling developmental stage of rapeseed as characterized by leaf number play a more important role in cold perception during vernalization as compared with the duration of cold exposure.

***Key words***: Development, Floral apex, Rapeseed, Vegetative apex, Vernalization

# DETERMINATION OF DURUM WHEAT GENOTYPES HAVING SUITABLE QUALITY TRAITS

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In Turkey, it is considerably important to develop and spread new varieties which have high quality, good yield and are adaptable to different climates and soil conditions. In the study 2011-2012 yield trials and regional yield trials of Transitional Zone Agricultural Research Institute were used. 112 durum wheat lines including checks were evaluated in terms of technological quality properties. For this purpose; 1000 kernel weight, test weight, protein content, CIMMYT-SDS sedimentation value, b* and karotenoid pigment value were measured. The lines which have good pasta quality were selected to the next breeding level or crossing block. Besides of these researches, the relationships between some quality characteristics were also investigated.

**Keywords:** Wheat, pasta, quality, breeding.

# DETERMINATION OF GRAIN MOISTURE CHANGES IN SOME CORN HYBRIDS IN KONYA ECOLOGICAL CONDITIONS

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This study was carried out to determine moisture changes in corn kernels in Konya conditions. A total of 15 corn hybrids, 3 hybrids from FAO 400, 5 hybrids from FAO 500 and 7 hybrids from FAO 600, was used as a material in this study. Experiment was conducted in a randomized block design with 3 replicates in 2004. Until the harvest in the last 42 days, starting from September 20 to November 1, in 6 different dates kernel moisture in each plot was measured. In order to show daily numeric moisture changes, regression analysis were applied to obtained data. Analysis of data showed that all moisture changes were linear in all FAO groups and corn hybrids. Daily moisture changes showed apparent changes from hybrid to hybrid. Average moisture reduction in FAO 400 group was 0.73 %, 0.67 % in FAO 500 and 0.70 % in FAO 600 group. While among FAO maturity groups the differences were not very clear, within the groups or among hybrids obtained daily moisture changes showed more clear cut values. Daily moisture reduction within FAO 400 group changed from 0.63 % to 0.86 %. While this change was from 0.57 to 0.85 % in FAO 500, hybrids in FAO 600 showed changes from 0.63 to 0.77 %. Moisture level of kernels in price formation due to drying costs is a very important trait and it is a second important trait after yield in present time. In order to give opportunities corn breeders to select material for this trait, breeders should know correlated responses related to daily moisture reduction and heredity of this trait must be enlightened. When the traits related or correlated with daily moisture content were known, breeders would be more effective to improve fast drying inbred lines and hybrids. The parameters obtained in this study can be used to estimate harvest time which can be useful for planning of works in any farm.

**Key words**: Corn hybrids, kernel moisture content, daily moisture change

# DETERMINATION OF INFECTION RATES OF EUROPEAN WHEAT STEM SAWFLY (*CEPHUS PYGMEUS* L., HYMENOPTERA: CEPHIDAE) IN BREAD WHEAT CULTIVARS IN TURKEY

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European wheat stem sawfly *Cephus pygmeus* L. (Hymenoptera: Cephidae) is the important and prevalent pest in the wheat growing areas of Turkey. The pest is very common and dangerous especially in Thrace, Central Anatolia and Southeastern Anatolia regions. It can seriously reduce yield and quality of grain. In this study, the pest infection rates and relations between cultivars and their chlorophyll contents were determined. Totally 133 bread wheat cultivars were tested against the pest. Field studies were carried out in test stations of Thrace Agricultural Research Institute. All saw fly larvae in the wheat stems were identified as *C. pygmeus*. It was seem that there was a large variation of infection between the cultivars. The ratios of the cultivars infected with the pest were determined as minimum for Menemen cultivar with 0.0% and maximum for Nenehatun cultivar with 27.6%. Infection rates were determined as less than 5.0% for nine cultivars, 5.1-10.0% for 40 cultivars, 10.1-20.0% for 73 cultivars and more than 20.1% for 11 cultivars. The relation between infected wheat cultivars and their chlorophyll contents was found as statistically insignificant.

**Keywords:** Wheat stem sawfly, *Cephus pygmeus,* cultivar, infection, chlorophyll content

# DETERMINATION OF RELIABLE SELECTION CRITERIA FOR EARLY GENERATIONS IN POTATO BREEDING

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This study was conducted to evaluate the effectiveness of some visual selection criteria; and, to determine the reliable selection criteria for seedling and the first clonal generations in potato breeding programs aiming to develop of high yielding cultivars. The hybrid true potato seeds from eleven crossing combinations were obtained with crossing in Nevsehir during summer season in 2010. The seedlings from true seeds were grown in greenhouse in Hatay from December 2010 to March 2011 to obtain seedling generations. Then, one tuber of each seedling was planted into field in Kayseri in June 2011 to obtain the first clonal generation. In each generation, some morphological and agronomic traits, which can be used as selection criteria, were measured on each plant. A Breeder Preference Score (BPS) on 1-9 scale (1 the worst-9 the best) were also given to each plant based on their visual appearance before and after harvest. Then, the correlation coefficients were calculated between measured traits and given BPS in each generation. The correlation coefficients between BPS of seedling and the first clonal generation for each hybrid plant were also calculated. The results indicated that morphological characteristics of same plant could significantly vary between seedling and field generations. The selections for even tuber shape and eye depth may be misleading when the tuber size is very small in the seedling stage. It was concluded that the threshold level for BPS should be lower in the seedling stage due to weak correlation between BPS values of seedling and field generations.

# DETERMINATION OF THERMOTOLERANCE IN TWO WHEAT VARIETIES BY PHOTOSYNTHETIC RESPONSES

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The effects of heat stress at 37°C and 45°C for 8 h on the seedlings of Karacadağ and Fırat wheat cultivars differing in sensitivity was investigated by means of chlorophyll a fluorescence, photosynthetic pigment content and 2-D SDS polyacrylamide gel electrophoresis of the thylakoid membrane. Heat stress inhibited chlorophyll accumulation at 45°C for 8 h and caused marked alterations in the chlorophyll a fluorescence and photosynthesis in the primary leaves of the wheat cultivars at 37°C and 45°C for 8 h. Examination of the 2-D SDS polyacrylamide gel electrophoresis analysis of the thylakoid membrane proteins from the two wheat cultivars showed that while a heat treatment at 37°C and 45°C did not induce or enhance the synthesis of any protein. While the synthesis of some proteins were repressed when compared to the control temperature cultivars, the photosynthetic responses of Karacadağ were less altered than Fırat to the effect that; Karacadağ showed lower reduction in the chlorophyll content, FV and FV/FM parameters where the F0 parameter only increased in the Firat cultivar at 45°C. Therefore, Karacadağ was determined to be a heat tolerant cultivar that can be used for cultivation in warmer regions.

# EFFECTIVE SELECTION CRITERIA FOR ASSESSING DROUGHT STRESS TOLERANCE IN WINTER WHEAT (*TRITICUM AESTIVUM* L.)

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The objective of this study was to assess the selection criteria for identifying drought tolerance in wheat genotypes, so that suitable genotypes can be recommended for cultivation in different environments and regions. Twenty Bulgarian winter wheat varieties were grown in two successive years – 2005/2006 and 2006/2007 at two locations: Dobrudzha Agricultural Institute (DAI), General Toshevo and Institute of Agriculture (OCH), Ruse. The trial was designed by the Latin square method in 5 replications. The following drought resistance indices were calculated: mean productivity (MP); geometric mean productivity (GMP); stress tolerance index (STI); stress susceptibility index (SSI); tolerance index (TOL); yield index (YI); yield stability index (YSI). The most effective indices in identifying high yielding cultivars under different moisture conditions (MP, GMP, STI) showed that wheat varieties Kristi, Zlatitsa, Aglika, Preslav, Milena, Demetra had best performance in stress and non-stress conditions at DAI and varieties Pliska, Boryana, Demetra, Pryaspa were the best for Obraztsov chiflik. Wheat breeders should focus on incorporating drought tolerance mechanisms into germplasm with high yielding capacity to develop both high yielding and drought tolerant varieties.

**Key words:** wheat, drought tolerance, selection criteria

# EFFECTS OF SEED PRIMING ON GLUMED AND GLUMELESS BARLEY CULTIVARS

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Barley is an important crop that is grown all over the world for feed and to produce beer. Generally, high protein barley is used as feed, whereas, low protein barley is preferred for beer production. The seeds of Turkish glumed barley cultivar Aydanhanım and glumeless cultivar Özen were primed with $ZnSO_4$ to improve seed germination speed, germination vigor and important components that affect yield. The results showed positve effect of osmopriming compared to control on seedling growth. The early and maximum germination was achieved on osmoprimed seeds.The results showed that the osmopriming could effect germination ratio of *Hordeum vulgar* L. positively under arid Central Anadolu conditions and could be positively manipulated for increased yields of *Hordeum vulgare* L.

**Key words:** *Hordeum vulgare* L., $ZnSO_4$ , Seed, Germination speed, Germination vigor

# EFFECTS OF SEED PRIMING ON TURKISH COTTON CULTIVARS

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Cotton is an immensely important crop for the sustainable economy of world and livelihood of the farming community. It is cultivated in about 33.0 M hectares across the world. Turkey is one of the eight biggest countries which produce the 80% of cotton in the world. From the Turkey's side, cotton as a raw material is really important for Turkey main industries especially for the textile and ready-to-wear clothing sectors. The seeds of Turkish cotton cultivar Özbek and Ayhan 107 were primed with, 4, 6, 8, 10, 12 mM $ZnSO_4$ to improve seed germination speed, germination vigor and important components that affect yield. The results showed that priming was helpful in improving seed germination speed, germination vigor, root shoot ratio, fresh and dry weight over control (unprimed seed). The best results of the study suggest that $ZnSO_4$ priming could be recommended to the farmers for improved yield and performance of the two cultivars in the dry land farming systems for significant improvement in yield and performance.

**Key words:** *Gossypium hirsutum* L., $ZnSO_4$ , Seed, Germination speed, Germination vigor

# ELABORATION OF MONITORING TOOLS FOR SUNFLOWER BREEDING

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The breeding monitoring process, especially the evaluation of the initial material is one of the major components in improvement programs. The designs of the instruments which facilitate the sunflower breeding and elaboration of the breeding program along with data stock and processing should become a priority. Economic situation in Black Sea region stimulates seed producers to accelerate the obtaining of high quality hybrids and their implementation in production. Thus, the effective tools of seed quality monitoring based on laboratory tests are needed. These consist of molecular biology research methods that may give a rapid answer regard of the quality of plant material. As informational technologies have a great impact in modern science, its success may increase the outcomes of plant breeders. Monitoring tools can be realized by test results processing using a computer soft. They contain a database, data processing module and prognosis or modeling application. Its goal is to stock various data, to process it and, finally, to give an answer regarding a biological process or phenomenon such as productivity, resistance, the effect of heterosis, etc. Elaboration of monitoring tools such as register is important for to integrate the morphological and genetic data. To study allow correlation the phenotypic features of the genetic substrate with reference to the important trait for the study of the association of these types of biological data. Generally, it may be adopted for other crops (depends on their biological particularities) or aims (statistics, modeling, prognosis), as, e.g., testing of genetic modified plants etc.

# ESTIMATION OF HYBRID YIELD PERFORMANCE BY THE SELECTION OF HETEROTIC GROUPS ON DENT TYPE MAIZE INBRED LINES USING SSRs

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Dent type 48 maize inbred lines were assayed for microsatellite-simple sequence repeats (SSR) with 35 primer-combinations to investigate genetic distances among maize material and their relationship to heterotic groups for hybrid performance. The parents selected from heterotic groups by SSRs as addition to their effective morphological traits were crossed with half diallel method for field experiments. The hybrids from these crosses were tested in two field experiments for their yield performances with two control hybrids named Bora and Ada523. The coefficient of genetic similarity among genotypes changed from 0.557 to 0.959. The average number of alleles per SSR locus was 2.37 with a range of 1 to 5. The polymorphism information content (PIC) value for the SSR loci varied from 0.0 to 0.66 with a mean of 0.364. The cluster analysis of the lines resulted in a clear separation of eight main heterotic groups. According to observed results, heterotic grouping of inbred lines based on SSR markers, generally agrees with their yield performances. The correlation between SSR data and hybrid yield was found to be significant(r=0,631). It can be suggested that the relationships for the selection of parents by SSR molecular markers can be used to control the yield performance which has some limitations.

**Key Words :** Maize, SSR, yield, heterotic groups

# AGRO-MORPHOLOGIC VARIATION IN A LARGE BARLEY GERMPLASM COLLECTION UNDER CENTRAL ANATOLIAN HIGHLANDS -THE FIRST YEAR (2005-06)

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The aim of this study was to determine agromorphologic variation among a global set of barley germplasm collected from different countries and international research centers during three successive years under field conditions of Central Anatolian highlands. In the first year of the experiment, totally 1039 barley entries from 40 countries and 5 Turkish check were winter planted and the germplasm were observed by 21 quantitative and qualitative parameters based on IBPGR (1982). Germplasm from USA, Turkey, Italy and unknown group consisted of majority of the first year barley populations with 215, 186, 174 and 95 entries, respectively. In terms of qualitative traits; 98.2 % of the germplasm was hulled and 88.3 % white grain colored; 51.3 % of germplasm was two-rowed while 37.4% six-rowed; 24.5% of germplasm was erect type habitus while 65.3% semi- prostrate habitus. Quantitatively, a large variation was observed among continents and regions of the world for some agro-morphological traits. Standart deviations at continent and regional levels changed between 10.7-16.3 for plant height; 0.8-2,1 for number of tillering; 0.9-2.7 for flag leaf width and 3.4-8.2 for heading date. Correlation analysis among quantitative charters showed that there was a statistically significant and positive relation between flag leaf width and length (0.79) and maturity date (0.71) and maturity date and heading date (0.64). Fourty countries were grouped into 13 main groups based on hierarchic cluster analysis and Turkish, American and Italian germplasm consisted of a separate sub-group within the first main group. Cumulative percentage of the first two main components explained 69.5% of the total variation in general , and then bi-plot graph showed that Turkish, Western Europe and North American germplasm can be selected for number of tillering while Asian, South American and Australian germplasm for heading an maturity date further breeding studies as a new genetic sources.

**Key words:** barley germplasm, characterization, quantitative and qualitative traits, variation, principal components.

# EVALUATION OF GRAIN YIELD AND SOME AGRICULTURAL CHARACTERS OF SOME BARLEY (*HORDEUM VULGARE* L.) GENOTYPES

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This research was carried out to determine of yield and some agricultural characters of some barley genotypes which was developed by Trakya Agricultural Research Institute and Bulgaria Karnobat Research Institute. The experiments were set up with 25 barley genotypes in completely randomized blocks design with four replications during 2006-2007 and 2007-2008 growing years in the experimental field of Trakya Agricultural Research Institute. The characters such as grain yield, plant height, spike length, heading and maturating days and grain number on spike and correlation among these traits were investigated. The results of the study showed that there were significant differences among the genotypes based on investigated characters. The mean grain yield of the genotypes was 647,4 kg/da. The highest grain yield (764,9 kg/da) was computed for TEA1500-22 line. In Trakya region, earliness is very important to production second crops in one growing season. The early heading genotype was TEA1525-25 line and, DRT136 was the latest heading line. Plant height is another important traits especially for lodging resistance in barley, and plant height ranged between 91,8 cm and 101,4 cm in the genotypes. The shortest plant height was measured in Veslets, TEA1535-21 and Sladoran. The spike length ranged between 8,90 cm and 4,31 cm in genotypes. Grain number in spike was 57,8 in the genotypes with 6 rows and, 27,7 grain genotypes with 2 rows. The significant and positive correlation coefficient was determined between grain yield and plant height (r=0,624). It was found that the genotypes with early maturing and tall plant high gave higher grain yield than the others.

**Keywords:** Barley, variety, yield, correlation, yield components

# EVALUATION OF GRAIN YIELD AND SOME PHYSIOLOGICAL AND AGRICULTURAL CHARACTERS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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This study was carried out to determine of yield, some agricultural and physiological characters of the some bread wheat varieties in 2009-2010 growing years in Edirne. Experiment was established with 25 cultivars in completely randomized blocks design with four replications. The characters such as grain yield, flag leaf area, canopy temperature, chlorophyll content of flag leaf, water content and dry matter of flag leaf, plant height, heading days and maturating days were investigated. According to the results, it was found significant differences among genotypes in terms of studied the characters except canopy temperature and dry matter. General mean grain yield of varieties was 734,2 kg/da. The highest grain yield was determined with 826,9 kg/da for Trakya BVD7 line and 800,0 kg/da for Bereket cultivar. The widest flag leaf was measured with 35,62 cm$^2$ in Tina variety and, the lowest leaf area with 17,78 cm$^2$ from Kate A-1 variety. Canopy temperature and chlorophyll content in flag leaf was measured at heading stage. Canopy temperature changed between 18,7 $^{o}$C and 20,5 $^{o}$C and, the highest canopy temperature was measured from ÖVD1-51 line and, the lowest from Yunak cultivar. The highest and lowest chlorophyll contents were measured with 54,13 in Gelibolu and with 46,33 in Yunak cultivars, respectively. The highest leaf water content and dry matter value were measured in Golia and Nina varieties, respectively. Milena and Kate A-1 cultivars, Trakya BVD12 line were the highest plant height, and Golia was the shortest plant height. In this research, Trakya BVD7, Bereket, Trakya BVD12 and Gelibolu have been prominent genotypes with their highest yielding capacities.

**Keywords:** Bread wheat, genotypes, yield, wheat quality.

# EVALUATION OF PROMISING SPRING BREAD WHEAT (*TRITICUM AESTIVUM* L.) BREEDING LINES UNDER IRRIGATED MULTI-ENVIRONMENT CONDITIONS IN ZIMBABWE

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The trials were set up to identify breeding lines that combine high yields with stability across environments via GGE bi-plot methodology. In addition, we intended to identify the best test environments. The studies were conducted across seven locations during the 2008, 2010 and 2011 wheat growing seasons. The experiments were laid out in a RCBD with three replications. Grain yield and agronomic traits were analyzed in Genstat Discovery Version 14 software. The GGE bi-plot in Genstat Discovery Version 14 was used to identify best test environments, stable and high yielding genotypes across locations. Environment, genotype and genotype x environment interaction main effects were highly significant ($P < 0.001$) for grain yield. Environment main effect accounted for 95.22% of the total variation. S02147-7H-ON-2H-ON, INSIZA, S02006-5H-ON-1H-ON and S01214-3H-ON-2H-ON were high yielding and stable across three years and could be proposed for release. Mutare was the best test environment.

**Key words:** Stability, *Triticum aestivum* L., multi environment trials, GGE bi-plot

# FORAGE OAT BREEDING IN MOROCCO: MOST ACHIEVEMENTS AND FUTURE CHALLENGES

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Oats (*Avena sativa*) was introduced to Morocco by the French at the beginning of the twentieth century. It was a crop that French farmers knew well, and yielded several products, such as grain, forage or could be mixed with vetch. It was also particularly immune to the Hessian fly *Mayetiola destructor* which caused serious damage to other cereals. In Morocco, oats are grown essentially in rainfed areas, almost exclusively for forage, mainly for hay; alone or as a mixture with annual legumes, mainly vetch. The first varieties from Europe were of little interest to Morocco. Thereafter, Grillot (1938), the first oat breeder in Morocco, introduced the *byzantina* types from Algeria, which constituted the genetic basis of the first Moroccan selected varieties. Some of these varieties are still grown such as cv. Roummani, Zhiliga and Tiddes. These varieties are now very susceptible to the common diseases and cannot cover all the potential ecological zones for oats. Local oat seeds are mainly a mixture of these varieties with some imported ones. The oats breeding program initiated by INRA in the eighty's resulted in the selection of some new varieties which were registered in the national catalogue. Most varieties are selected from the Quaker Oat nursery, dominated by North American genetic material, more adapted to biotic and abiotic stresses than the European one. Breeding methods and the genetic gain of the selected varieties will be presented. Cnstraints to transfer these new varieties will be also analyzed. Furthermore and taking into consideration the climatic change and the new Moroccan agriculture strategy (Morocco green plan), the future orientation of the oat breeding program will be discussed.

Key words: forage oats, breeding methods, selection criteria's.

# GENES EXPRESSION ON SUNFLOWER MICROSPOREGENESIS AND MICROGAMETOGENESIS

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Male sterility is one of several gibberellin responses. In an effort to understand the involvements of GAs in sunflower male reproductive development, male sterility was induced by exogenous application of gibberellic acid ($GA_3$) to the apex of 2 isogenic lines (A and B) in early reproductive development. Using different experimental approaches: hormonal quantitative analyses, protein profiles and transcripts assays have been revealed a similarity in expression of both male sterility types. Our results provide the first evidence that expression of CMS-specific *orfH522* gene can be induced by $GA_3$ in plant with original fertile cytoplasm. In addition, it has been shown that another *orf* from mitochondrial rearranged area (*orfH873)* is expressed in fertile and sterile inflorescence tissues of sunflower. To establish the sequence of events that occur during differentiated expression and phenotypic manifestation of hereditary factors causing male sterility/male fertility, using bioinformatics methods, the genes that exhibit affinity for $GA_3$ and are involved in nucleus-mitochondria interaction through different gene networks have been selected. These groups of genes related to cell signaling, oxidative systems, mtDNA repair and recombination, apoptosis, signal transduction, hormone metabolism, etc., were included in study to detect molecular processes that initiate and conduct microsporogenesis that is reflected in the final by androsterility/androfertility.

# GENETIC ANALYSIS OF AGRONOMIC CHARACTERS OF SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH]) UNDER ACID SOIL CONDITION

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The objective of this study was to conduct genetic analysis of the inheritance of agronomic characters of sorghum under acid soil condition. The genetic material used in this study was six sorghum populations, consisted of the parental lines B69 ( P1/sensitive), Numbu (P2/tolerant), F1 and F1R , BCP1 (back cross of F1 to B69) and BCP2 (backcross of F1 to Numbu), and the F2 generation. The materials were planted in acid soil at Bogor Regency, Indonesia. The agronomic data were tested for the adequacy of simple additive-dominance model to explain the gene action of characters using the joint scaling test. The results of the analysis showed that the genetic model for the characters of days to flowering, plant height, stem diameter, stem weight, seed weight / panicle was additive- dominant with interaction effect of additive x additive [i] and dominance x dominance [l]. The genetic model for panicle length was additive dominant with the interaction effect of additive x additive [i] and additive x dominance [j]. Additive genetic component value [d] greater than the value of the genetic component of dominant [h], indicating that additive gene has a greater contribution than dominant genes in the characters except grain weight / panicle. All characters have medium to high broad sense heritability and narrow sense heritability.

*Keywords : geneti analysis, addivie dominant, epistasis, sorghum,*

# GENETIC INTRASPECIFIC POLYMORPHISM ANALYSIS FOR THE ELABORATION OF MOLECULAR MARKERS OF SOME MEDICINAL AND AROMATIC PLANTS (MAP) CHEMOTYPES

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Most of the MAPs are described in terms of macroscopic level indicators such as the plant form, size, color, organoleptic properties and so on, does not give a complete description of the substances of interest in the plant data. Chemical profiling characterizes the quality and quantity of plant material performance using techniques such as GC, HPLC, MS and other analytical methods. The diversity of plant secondary metabolites analysis provides description in terms of chemotaxonomy, and using specific markers - distinguish plant varieties. These studies generate data for plants chemotyping. Being influenced by environmental factors, biochemical composition of plants can serve as a unique criterion in the selection of MAPs. The genetic diversity of these plants is estimated by evaluating the level of DNA polymorphism in molecular techniques. In R. Moldova in medicinal plants research are involved eight research institutions and universities. Core focus is on creating and maintaining germplasm collections of MAPs, the study of spontaneous plant diversity, design and development of growth and processing technologies of MAPs. PCR-based methods are most useful in creating molecular markers and assessment of economic interest. They can be applied to poorly studied species at the genetic level (RAPD, AP -PCR, DAF, RFLP), and those with genome sequencing techniques (AFLP, SSR specific primers). Sequencing-based methods are used to identify genetic variation at nucleotide level, variations in the type and indelibly sites. These methods allow the phylogenetic studies based on ribosomal gene characterization, eg., 18S - 26S rDNA, tRNA genes, etc.

# GRAIN PROTEIN QUANTITY AND STABILITY FOR LATVIAN BARLEY VARIETIES

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Grain protein content is an important grain quality criteria in barley breeding program. In Latvia barley is of outmost importance for livestock feeding. As pig and poultry production are protein-demanding in feed concentrates barley are often combined with grain legumes. One of the strategies to produce high protein yields could achieve by high crude protein concentration of each component in intercrops. The objective of this research is to determine grain protein quantity and stability for spring barley varieties under growing conditions of West Latvia with respect to their potential usage as a intercrop component. Phenotypic stability analysis was performed on results for crude protein (CP) and protein yield (PY) of 11 barley varieties of Latvian origin grown from 2006 to 2012. Stability parameters were estimated using regression coefficient ($b_1$), coefficient of variation (V%) and the nonparametric rank-based test. Year effect was significant ($p<0.05$) for CP and PY variability explained by 65 and 63% of the total variance. As showed rank-based test hulless genotype 'Kornelija' (154.0 g $kg^{-1}$) had the highest and the most stable CP. Protein yield for varieties varied from 0.53 to 0.61 t $ha^{-1}$. The highest PY provided covered variety 'Austris' characterized with grain yield stability ($b_1$=1.09) and average protein content (130.0 g $kg^{-1}$).

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# IDENTIFICATION OF NEW RUST RESISTANT SOURCES OF WHEAT BY MOLECULAR TOOLS AND FIELD EVALUATION

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Around 4000 wheat lines were evaluated for yield and agronomic traits at Obregon, Mexico during 2008-2009. 670 diverse lines were selected as potential germplasm for Pakistan and were evaluated for leaf rust at Elbatan, yellow rust at Toluca, and stem rust (Ug99) at Njoro, Kenya. The best 184 lines with 0-30% disease severity were selected and screened at CIMMYT with DNA markers for resistance genes. Durable rust resistance was identified due to presence of *Lr34/Yr18* and *Lr46/Yr29*. Resistance to Ug99 was due to presence of *Sr2, Sr25, Sr26, SrSha7, SrHuw234, SrTmp*. These lines were evaluated for yield at Wheat Research Institute, Faisalabad during 2009-11, and 14 lines having rust resistance and better yield than Seher-06 and Lasani-08 were selected for further evaluation and seed multiplication. The *Sr2* gene was in high frequency in current Pakistani varieties, while 1B-1R was absent based on DNA marker and quality analysis.

# IMPACT OF *Orobanche Cumana* Wallr. ON SUNFLOWER CULTIVARS ON NATURAL INFESTED FELDS IN REPUBLIC OF MOLDOVA

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*Orobanche cumana* Wallr. is responsible for severe infestations of cultivated sunflower in many countries. During last two decades, the aggressiveness of the parasite increased significantly. The new physiological races appeared fast enough after a relative stable period of time on race E, F and G of broomrape, especially around Black Sea. Thus, the virulence explosion has been identified in Trakia from Turkey, extending further in south-eastern part of Bulgaria and Romania, Republic of Moldova, Ukraine and Russia. The objective of this study was to evaluate the effect of natural broomrape infection on grain yield of sunflower and some agronomical important parameters. Eleven commercial sunflower hybrids have been tested in fields (naturally infestation with broomrape). Broomrape occurrence is depending on genotype and was evaluated by frequency, intensity and attacking rate based on Pustovoit method. The attacking rate was from 0.21 to 26.43, intensity: 1,6 – 26,43 and frequency – from 12.5% to 100%. The bigger number of broomrape flower-bearing stems per one infected host plant was 53 parasite plants. The highest influence was on the total achene weight per head (-37.7%) and head diameter (-20.4%), comparing with plant height (-1.7%). Linear dimensions, thousand grain mass, geometric mean diameter, sphericity, surface and projected area, volume, shape parameters (such as flakiness ratio and elongation ratio) were statistically affected. Taken together, the results from the present study demonstrated that *O. cumana* had statistically negative effect on sunflower and its agronomical important parameters.

# INTROGRESSION OF RESISTANCE TO POWDERY MILDEW (*BLUMERIA GRAMINIS* DC. F. *TRITICI*) FROM *T. TIMOPHEEVII* ZHUK. INTO THE GENOME OF *T. DURUM* DESF.

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Common wheat sample n.1678B-21 (Alibidum 653*2/IT-3) was used in breeding program as a donor of resistance to powdery mildew (*Blumeria graminis* DC. F. *tritici*). Resistance trait was inherited from IT-3 created in Vavilov Research Institute of Plant Industry by introduction of powdery mildew resistance from *T. timopheevii* Zhuk. The first stage of hybridization of 1678B-21 with durum drought-resistant wheat varieties Saratovskaya zolotistaya and Gordeiforme 740 led to development of durum wheat line 9D-5-2 possessing resistance to powdery mildew. Resistant trait from line 9D-5-2 was transferred to commercial wheat cultivar Bezenchukskaya Niva and to a number of breeding lines (Leukurum 1751, Leukurum 1753, 495d-22, 495d-14) adapted for environmental condition of Volga-Ural region of Russia. Genetic analysis of three lines (Leukurum 1751, Leukurum 1753, 499d-22) performed on $F_1$-$F_3$ populations obtaining on the base of susceptible wheat cultivar Pamyati Chehovicha has shown that resistance of the lines is determined by one semi-dominant gene. To determine chromosomal localization of the fragments introgressed from the *T. timopheevii* genome in line Leukurum 1753 there were used 90 microsatellite (SSR) markers with known map positions in the genomes of *T. aestivum* and *T. timopheevii*. Molecular analysis revealed a single translocation in chromosome 6B, located in the range of microsatellite markers *Xgwm518* и *Xgwm1076*. The newly developed breeding material is also characterized by resistance to leaf rust, leaf spots, drought tolerance and grain and pasta quality. The developed lines can be used in durum wheat breeding program as donors of resistance to fungal diseases and drought tolerance.

# INVESTIGATION OF SOME AGRICULTURAL TRAITS AND STABILITY OF THE BARLEY (*HORDEUM VULGARE* L.) GENOTYPES

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The study was carried out to determine grain yield and yield stabilities and some agricultural and physiological characters of the some barley genotypes. This study was established with 20 lines and 5 checks, in completely randomized blocks design with four replications in 3 locations in 2011-2012 growing years. The characters such as grain yield, plant height, heading days, canopy temperature, thousand kernel weight and test weight were investigated in the study. Adaptation abilities and stability of the genotypes were determined. It was determined that there were significant differences among genotypes for investigated characters. The highest yield mean was determined in Tekirdağ location. General mean of grain yield was 647,4 kg/da. Among the genotypes, highest grain yield (848,6 kg/da) was weighed in TEA1765-22 line. Martı and Harman varieties was medium adaptable across to various environmental conditions. It was determined that Sladoran and Bolayır had positive and high intercept value indicating their performance will not decrease even in bad environmental conditions. Earliness is very important trait to grow second crops within one growing year for barley in Trakya region. Martı and TEA1619-2 were the early genotypes and Lord variety was the latest heading. Short plant height is considerable traits for lodging resistance in the region. The shortest plant height was measured in Lord variety  with 63,5 cm. Canopy temperature was measured at heading stage and changed between 23,8 °C and 26,7 °C. The highest canopy temperature was measured in TEA1765-8 line and the lowest in TEA1676-12 line. It was determined significant differences among genotypes according to thousand kernel weight and test weight in this study. It was seen that Harman variety and four sister lines with TEA1765 pedigree number had good adaptation across to good environmental conditions.

**Keywords:** Barley, genotypes, yield, stability, agrıcultural traits

# MINING AND FUNCTIONAL CHARACTERIZATION OF SIMPLE SEQUENCE REPEATS IN GENES OF *PUCCINIA TRITICINA*

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*Puccinia triticina*, the causative agent of wheat leaf rust (brown rust of wheat), is one of the most serious diseases of wheat throughout the world. The genome size of *P.triticina* is 162.95 Mb and the genome sequences are available at Broad Institute of MIT and Harvard was used for the study. Gene sequences were searched to identify SSRs using Simple Sequence Repeat Identification Tool (SSRIT) which is available at GRAMENE ebsitehttp://www.gramene.org/db/. It was found that out of 11,638 available genes; Hypothetical proteins were maximum in number (8220), followed by predicted protein (2584), and conserved hypothetical protein (187), unknown proteins (32) and 615 well known proteins (Fig.1)**.** The purpose of present study was to understand the organization and abundance of SSRs in the well known proteins of *P.triticina* and its functional characterization. Only 30% well known protein showed SSR repeats. Dinucleotides repeats were the most abundant repeats in the genome accounting 50.5% of SSRs followed by trinucleotides SSRs (44.2%). Tetra-and penta- repeats were the least frequent repeats accounting 5.3% of SSRs. Out of 615 well known genes, SSR were identified in 217 genes. Genes were annotated under the Gene Ontology system. Results showed that for cellular component, most of the genes coding for proteins localized in large ribosomal subunit, cytosol & nucleoplasm. In the molecular function category, most of the genes encoding proteins involved in structural constituent of ribosome, ATP binding and protein serine/threonine kinase activity. In the biological process category, genes involved in signal transduction and translation were frequently observed. The results provide general source of SSRs which are highly polymorphic in nature and could be useful for strain typing, population genetics, phylogenetics, genetic mapping and evolutionary studies of fungal organisms.

# MONITORING OF DISTRIBUTION OF THE BASIC DISEASES AND BREEDING ON RESISTANCE TO THEM IN NORTHERN KAZAKHSTAN

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Spring wheat is the basic export crop in Kazakhstan. The area under this crop is about 12 million hectares, 80% of which are concentrated in the north of Kazakhstan. In the result of monitoring spreading of basic diseases, which was being conducted in 2002-2013 years it is revealed that the major diseases of wheat in the Northern Kazakhstan are brown, stem rusts and *Septoria*. Epiphytotic progress of a brown rust occurred in 2002, 2005, 2007 years; weak progress in 2003, 2004, 2006, 2008, 2009, 2010, 2011, 2012, 2013 years. The progress of *Septoria* was marked in all years of observation: weak progress in 2003 and 2010 years, moderate in 2002, 2004, 2005, 2006, 2008, 2012 years; severe in 2007, 2009, 2011, 2013 years. Moderate progress of stem rust occurred in 2007 but it was weak in other years. The samples of spring bread wheat were identified from the number of 1747 collection samples on the severe infectious background from 2002 to 2012 years, among them 300 samples of wheat resistant to brown rust; 198 samples resistant to stem rust, besides 20 samples of wheat had group resistance to brown and stem rusts. A new original material was created resistant to leaf and stem rust on the basis of the selected sources and varieties of local origin. It was done about 180 targeted crosses. During the screening of 910 breeding lines it was identified the samples on artificial infectious backgrounds which are resistant to brown rust - 10 samples, to stem rust - 7 samples and one sample which had group resistance to these diseases. One sample resistant to brown rust is in the final stage of breeding.

# MORPHOLOGICAL AND SEED YIELD CHARACTERISTICS OF ORCHARDGRASS ECOTYPES OF EASTERN ANATOLIA REGION

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Present research was carried out to assess the genetic diversity in orchard grass ecotypes of Eastern Anatolia region and to determine the genotypes available for breeding. Morphological and seed yield characteristics of 25 orchard grass ecotypes collected from natural vegetations of Ağrı, Aradahan, Artvin, Bayburt, Bingöl, Erzurum, Kars and Muş provinces of the region were determined. Plant height, stem thickness, number of nodes, node spacing, leaf length, leaf width, length of panicle axis, seed yield parameters of orchard grass (*Dactylis glomerata* L.) were investigated. The parameters of seed yield (g) and plant height (cm) exhibited a great variation than the other investigated parameters. Based on principle components analysis, orchard grass genotypes were separated into 3 principle groups. Specified parameters were able to explain 72,666 % of current variation. The first component representing 34,611 % of total variation was composed of leaf length, leaf width; the second component representing 21,101% of total variation was plant height, and third component representing 16,953% of total variation was number of nodes.

**Key Words:** Orchardgrass, Eastern Anatolia, Morphological Biodiversity

# PARTICULARITIES OF SUNFLOWER – DOWNY MILDEW INTERACTION

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Sunflower downy mildew (*Plasmopara halstedii* (Farl.) Berl et de Toni) is one of the most devastating pathogens which affects sunflower in Europe, including Republic of Moldova. The disease causes significant yield losses and it is extremely difficult or impossible to eliminate once it established in an area, because the pathogen spores have long lasting durability, being able to survive in soil up to 10 years. The rapid evolution of downy mildew populations in recent years needs identification of new resistance sources. An efficient solution for obtaining resistant hybrids is combination of both resistance sources: specific (Pl genes) and quantitative non-specific resistance. Actual study aimed understanding of particularities in relationship sunflower – downy mildew through analysis of sunflower resistance potential in genotypes cultivated in Republic of Moldova. In this context, research was conducted in two directions – genetic and physiological. Genetic studies included molecular screening of Pl genes, responsible for specific resistance, and estimation of the expression of genes associated with non-specific resistance (encoding antioxidant enzymes, defensin, phenilalanin-amonia-lyase, PR proteins and other), using quantitative PCR technique; those physiological allowed estimation of hydrogen peroxide and superoxide levels in healthy and infected plants. Thus, some relevant aspects were revealed during research, however further investigation is needed for a better understanding of the resistance mechanisms and all types of interactions in this pathosystem.

# PHONOLOGICAL, NUTRITIONAL AND MOLECULAR DIVERSITY ASSESSMENT AMONG 35 INTRODUCED LENTIL (*LENS CULINARIS* MEDIK.) GENOTYPES GROWN IN SAUDI ARABIA

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Morphological, nutritional and molecular analyses were carried out to assess genetic diversity among 35 introduced lentil genotypes (*Lens culinaris* Medik.*).* The genotypes exhibited significant differences for their field parameters and noticeable superiority were detected in some genotypes. The nutritional and proximate analysis showed that some genotypes were excellent sources of proteins, essential amino acids, minerals, anti-oxidants, total phenolic contents (TPC) and total flavonoid contents (TFC) and hence, highlights lentil nutritional and medicinal potential. Sequence-related amplified polymorphism (SRAP) and amplified fragments length polymorphism (AFLP) markers were used to estimate the genetic variability at the molecular level. The existence of considerable amount of genetic diversity among the tested lentil genotypes were also proven at molecular level. A total of 2894 polymorphic SRAP and 1625 AFLP loci were successfully amplified using six SRAP and four AFLP primer pair combinations. Polymorphism information content (PIC) values for SRAP and AFLP markers were higher than 0.8, indicating the power and higher resolution of those marker systems in detecting molecular diversity. UPGMA cluster analysis based on molecular data revealed large number of sub clusters among genotypes, indicating high diversity levels. The data presented here, showed that FLIP2007-122L and FLIP2008-8L could be as a significant source of yield, total protein, essential amino acids, and antioxidant properties. The results suggest potential lentil cultivation in Central region of Saudi Arabia for its nutritional and medicinal properties, as well as sustainable soil fertility crop.

**Key words:** lentil, nutritional value, molecular markers, genetic diversity.

# QTL ANALYSIS OF GRAIN YIELD AND YIELD -RELATED TRAITS USING RECOMBINANT INBRED LINES IN WHEAT UNDER DROUGHT STRESS

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Quantitative trait locus (QTL) analysis of yield and yield -related traits in common wheat was conducted using a set of 75 recombinant inbred lines (RIL) derived from Roshan × Superhead in drought stress. The Diversity Array Technology (DArT) approach was employed for genotyping the population. The skeleton map consisted of 347 markers with a total length of 641 cM and average distance of 1.84 cM between adjacent markers. The length of individual chromosomes ranged between 8 cM for chromosome 7Ato 62 cM for chromosome 3B. Twenty nine QTL were located on 8 chromosomes, 1A, 1B, 2D, 2A, 4A, 5B, 6A and 7B. Four (main spike harvest index, biological yield, number of tillers per plant and number of fertile tillers), Three (grain Number per spike), two (plant height and spike length), one(biological yield of main stem , plant harvest index, length of internode, flag leaf length, grain yield and grain weight per main spike) QTL were detected. These results will provide important information for further functional analysis of drought-tolerance-related genes in wheat. DArT markers linked with QTLs for grain yield-related traits may be useful for marker assisted selection to enhance drought tolerance.

**Keywords**: Wheat, Drought stress, Quantitative trait locus, Recombinant inbred line

# RANDOM AMPLIFIED POLYMORPHIC DNA ANALYSIS OF PLANT GENETIC POLYMORPHISM

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The research on the variability of characteristics determined by genetic polymorphism may contribute to the elucidation of spontaneous and crop plants genetic fund potential. The polymorphism can be detected at different levels of plant organization by morphological, physiological, biochemical, cytogenetic or molecular analysis. More recently, the random amplified polymorphic DNA (RAPD), restriction fragment length polymorphisms (RFLP), amplified fragment length polymorphisms (AFLP) or other techniques have been used to identify genetic variability. The RAPD method has been very little explored in crop plants in Republic of Moldova, thus, the aim of the present study was to assess genetic variability in different homo and heterozygous genotypes of sunflower (*Helianthus annuus L.*), cucumber (*Cucumis sativus L.*), sage *(Salvia sclarea L.),* various local populations of mint (*Mentha piperita* L.) and medicinal plants from spontaneous flora. The highest variability level (78.5 %) was observed in sunflowers, compared to cucumbers (57.6 %) and mint (9.3 %). The RAPD analysis of various sunflowers' parental lines and their hybrids indicated the presence of 69 loci. Depending the primer, the number of amplified DNA fragments varied from 3 to 11, and ranged in length from 90 to 3000 pb. A number of 5-20 polymorphic loci for different primers and genotypes have been identified.

# RESEARCH ON THE POSSIBILITIES OF CULTIVATION OF THE FODDER CROPS ON PASTURE AND MEADOW AREAS OF EASTERN ANATOLIA

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To answer the questions of ''how negative effects will influence the future situation of biodiversity'', scientists calculated from the estimated researches that the potential of biodiversity will have decreased from 45 % to 32-42 % between the years of 2000-2030. Since 1950, more than 12-13 million ha pasture have been converted into arable land by ploughing in Turkey. Because of inadvisable and continuously usage of natural resources by human impact, 20% lost of global biologic diversity have been thought till 2020. East Anatolia region's grasslands are gene resources for many forage plants. The desirable forage plants both grass and fabacea family species, which can found on natural fauna, have a great potential to rehabilitate abundant and degraded areas. The aim of this study was evaluated and collected to the forage plants which can naturally found in East Anatolia grasslands. It was attention that species seed which was determined in previous studies, found more frequently in region and had high feed value was collected. Totally 235 forage plants included 180 fabaceae, 55 graminaceae were collected in 2009-2012 period of this project.157 seed material (33 greminea, 124 fabacea) were transferred to National gene bank in 2011-2012. 2 alfalfa varieties (Savaş, Ömerbey), 1 sainfoin variety (Lütfibey), 2 red clover varieties (Tavlaş, Dadaş), 2 white clover varieties (Arife, Karbeyazı) from the plants which were passed to breeding step from previous years were registered. 3 different candidate cock's foot variety in advanced breeding level is on registration process. Crown vetch (Coronillavaria) in evaulated process will be regestreted in coming years. Also grazing type alfalfa and sainfoin lines determined in observing field were consigned to breeders for advenced breeding stages. In 2012, 76 Festuca ovina, 47 Phleum montanum, 16 Agropyron cristatum, 37 Koeleria cristata and 9 Dactilis glomerata were passed to post breeding process.

**Key words:** Meadow breeding, variety improvement, forage plant, gene resource protection.

# THE ALLELIC STATE IDENTIFICATION OF THE NON-RACE-SPECIFIC DISEASE RESISTANCE *LR34/YR18/PM38* LOCUS IN UKRAINIAN POLISSIA WINTER WHEAT (*TRITICUM AESTIVUM* L.) CULTIVARS

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Resistance against rusts and powdery mildew is one of the most important characteristic of modern wheat cultivars, because in some years these diseases can significantly reduce yields. The basis of many breeding programs is resistance genes that confer durable or non-race-specific resistance. One of these genes is *Lr34/Yr18/Pm38.* This multiple resistance locus associated with partial and durable resistance to rust diseases, powdery mildew and, possibly, tolerance to barley yellow dwarf virus. We used the allele-specific marker *caISBP1* (insertion site-based polymorphism marker) for identification. It is codominant marker situated between the ABC-transporter and cytochrome P450 in region involved in resistance expression. A collection of 28 winter wheat cultivars of NSC ‘’Institute of Agriculture NAAS Ukraine’’ developed in different periods was the object of our investigation. The “resistant” allelic state of the *Lr34/Yr18/Pm38* locus (*Lr34+)* was identified in 11 cultivars (39% of the total number): Stolychna, Artemida, Analog, Benefis, Polesskaya-70, Polesskaya bezostaya, Kievskaya-73, Kievskaya polukarlicovaya, Polesskaya-80, Zhuravka, IZ15-12. The “susceptible” allelic state of *Lr34* was identified in 9 wheat cultivars (32%) and 8 (29%) cultivars were heterogeneous at the *Lr34* locus. The investigation confirmed the presence of allele *Lr34+* in genotypes of Ukrainian Polissia winter wheat cultivars (derived possibly from cultivar Bezostaya-1) which can be used as donors of this resistance gene.

# THE ANALYSIS OF YIELD STABILITY OF MAIZE HYBRIDS

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Information on agricultural yield stability is very important for breeders and maize producer because it helps in the choice of cultivars giving high and stable yields in different environmental conditions. Parameters were calculated for yield stability of maize test hybrids grown in six locations. The research material consisted of 22 test hybrids and three control cultivars (NK Ravello, ES-Paroli and Ronaldinio). In order to assess the biological stability the following methods were used: the method of multivariate analysis of variance; univariate methods: regression coefficient ($b_i$) and the deviation from the regression line $S^2_{di\ (}$Eberhardt and Russell), the Shukla's stability variance. For agriculture stability two non-parametric methods were used: the method of Kang and the modified method of $R_D$ homogeneous groups ranks. Nine hybrids yielded higher than the control cultivars (SL12114, SMH1813-1216, SL10096, SL10324, SMH1806-1209, SL20127, SL10066, SMH1810-1213, SMH1792-1141) and among them there were three early maturing genotypes. According to the Shukla's stability statistic the most stable and high yielding were hybrids SMH1778-1127 and SMH1808-1211 which had low values of stability variance. Calculated regression coefficients were not different from one, indicating average response of the hybrids to changing environmental conditions. According to Kang's measure, the highest yielding and stable hybrids were SL10066, SL20114, SMH1810-1213. Agricultural yield stability was assessed using non-parametric method of homogeneous groups rank and the coefficient of variation. The hybrids SL20114 and SL10066 were characterized by the highest agricultural stability as they had high yields in all environments. Hybrid SL20114 showed high stability and had the highest yields in all experiments.

# THE COMPARISON OF ADAPTIVE CAPABILITY OF TWO WILD SPECIES OF *ONOBRYCHIS* PLANTS

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The comparative analysis of adaptable capability of legumes of two species of *Onobryshis Adans ciucium* - *Onobrychis cyri A. Grossh* and *Onobrychis vaginalis C.A.M. Vesr. Pfl. Camc.* - has been carried out. Plants were collected in the Shemaha area of Azerbaijan located 800 metres above the sea level. It was revealed that the population of *Onobrychis vaginalis* is smaller than *Onobrychis cyri* in the area. With the use of cytogenetic and biochemical methods of analysis, the level of adaptation of these species to the environment was studied. The analysis of frequency of chromosomal aberrations in cells of the seedlings demonstrated that the level of spontaneous mutability in the species of *Onobrychis cyri* was within the standard data, while the same indication was almost 2 times higher in *Onobrychis vaginalis*. At the same time, there were chromosomal aberrations of the same types in cells of both the species: chromosomal and chromatid bridges, rings and fragments. In leaves of the plants, the amount of malonic dialdehyde, as the basic product of peroxide lipid oxidation, and the activity of protective peroxidase enzyme were measured. As it is known, these metabolites of plant cells are most sensitive to changes of the environment and reflect the level of adaptive reactions of a plant. It was found out that the amount of malonic dialdehyde in *Onobrychis vaginalis* is almost 3 times higher that of *Onobrychis cyri*, while the activity of peroxidase demonstrated inverse results. The data of the researches made during 3 years has revealed a dynamics of increasing the spontaneous mutability and strengthening the processes of lipid peroxidation in *Onobrychis vaginalis*. The conclusion on the liability of this species to risks of genetic erosion has been drawn.

# THE CONTRIBUTION OF ASHES OF WASTE OF THE PLANTS TO *IN VITRO* REGENERATION OF POTATO (*SOLANUM TUBEROSUM* L.)

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The present study has allowed to us, to achieve the main aim that we fixed ourselves at the beginning, namely the possibility of regenerating in vitro a whole plant of two varieties of potato to knowing Désirée and Spunta via the caulogenesis and the rooting environments in mediums made starting from ashes of vegetation wastes. It enabled us to know the effect of the mineral composition of the mediums of induction on the processes primordia of the two studied varieties. In addition, this study enabled us to conclude that the meristem constitute explants have good primordia aptitudes. This first generation represents the phase of micropropagation the purpose of which is obtaining of a sufficient quantity of vitro healthy seedlings. We thereafter studied the microtuberization of these two varieties according to two types of mediums MS to knowing MS without hormones and MS with ANA under three photoperiods: total darkness, 8 hours and 16 hours. Medium MS presented a growth of the roots and stems very high compared to medium MS with ANA, at time that medium MS with ANA showed a significant effect for the rate and the duration of microtuberization. Generally, the photoperiod influenced the microtuberization with an effect strongly observed on the weights and the diameters of the microtubers. However, the 8 hours photoperiods and 16 hours gave weights and diameters higher by contribution than those obtained to the total darkness.

**Key words:** *Solanum tuberosum* L, Ashes, Medium MS, Micropropagation, Microtubérization.

# THE DETERMINATION OF SOYBEAN (*Glycine max* L. Merr.) GENOTYPES ON KONYA ECOLOGICAL CONDITIONS FOR YIELD AND QUALITY

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Soybean is one of the most important crops for animal consumption and Turkey imports almost 95% of soybean used. For this purpose, this study conducted to determine the soybean cultivars for Konya region. It was carried out in 2009 and 2010 the production year at the Selcuk University Sarayönü Vocational School experiment field. Six varieties (Defiance, Nova, NE 3399, Arısoy, and Atakişi A 3935) was used in the trials with three replications under irrigated conditions. The varieties are evaluated plant height, number of branches per plant, number of pods per plant, first pod height, number of grains per pod, pod length, height of the first branch, thousand grain weight, yield with protein, ash and fat ratios in terms of quality characters. The varieties were significantly different ($p < 0.01$) from each other in terms of plant height, number of branches per plant, number of pods per plant and grain yield. Arısoy was most high yielding variety with 5920 kg ha$^{-1}$ whereas Defiance was the lowest yielding varieties with 3650 kg ha$^{-1}$. Varieties Arısoy, NE 3399, Atakişi and Nova were in the first groups in terms of yield. The highest protein content (40.2%) and the highest oil content (14.2%) were obtained from Defiance and A3935 varieties, respectively. According to results Arısoy for grain yield and Atakişi for yield and protein can be recommended to Konya region.

**Keywords:** soybean, cultivar, yield, quality

# THE DEVELOPMENT RESISTANT MATERIAL TO YELLOW RUST AND STEM RUST BY USING ANTHER CULTURE IN WHEAT BREEDING PROGRAM

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The aim of this study is to develop Turkish doubled haploid bread wheat lines resistant to local rust races both stripe/yellow rust (*Puccinia striiformis* f.sp. *tritici*) and stem/black rust (*Puccinia graminis* f.sp. *tritici*) and especially to stem rust race Ug99 in the shortest time possible. The lines used in this study are derived from the crosses made in wheat breeding program of Central Research Institute for Field Crops-Ankara (CRIFC). Doubled haploid lines, 242 lines in total, have been obtained throughout Anther Culture in the Tissue Culture laboratory of CRIFC in 2011. Field tests have been carried out in the fields of CRIFC at İkizce (Ankara) locations in 2011-2012 growing season. The material artificially inoculated with the inoculum collected from İkizce location. By using the scores collected through field observation, Coefficients of infection (CI) were calculated and values below 20 were considered resistant. Among the material tested, 72 genotypes have been found resistant to local yellow rust race/races, 112 genotypes resistant to local stem rust race/races and 49 genotype resistant to both local yellow rust and stem rust race/races. The material resistant to both disease will be tested for Ug99 Stem rust race/races in Njoro/Kenya under artificial conditions. The results obtained from this study, indicate that doubled haploid wheat lines derived from anther culture could be used for speeding up the process to produce new yellow rust and stem rust resistant bread wheat lines.

**Keywords**: Wheat, doubled haploid lines, yellow rust (*Puccinia striiformis*), Stem rust (*Puccinia graminis*), resistance

# THE EFFECT OF DIFFERENT POLLEN DEVELOPMENT STAGES AND MEDIUM ON ANTHER CULTURE IN WHEAT HYBRID POPULATIONS

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The objectives of this study were to determine the effects of two different pollen development periods to the anther culture in three bread wheat hybrid populations and to determine the effects of two different induction mediums to the anther culture in four durum wheat hybrids. In the study, the numbers of callus which developed from anthers, albino plantlets, green plantlets and the plants which transferred to the greenhouse were determined. Based on the results of the study, the effects of two different mediums ($W_{14}F$ and $C_{17}F$) on numbers of callus were statistically significant. However, the effects of two different mediums on number of albino plantlets, green plantles and the plants which transferred to the greenhouse were not statistically significant. When examined the effect of pollen development stages on anther culture, anther culture with pollens in their early-mid uninucleate period were obtained higher numbers of green plantlets and plants which transferred to the greenhouse comparing to mid-late uninucleate period. Based on the analysis of LSD, the differences between numbers of green plantlets in hybrid populations were found statistically significant. Regarding the effect of basal plant medium, the highest numbers of plantlet were obtained from Svevo/Zenit combination with three plant, in $W_{14}F$ medium. The lowest numbers of plantlet were provided from Gediz 75/Yavaros and 79//IDSN 209 hybrid combination in $C_{17}F$ medium. The highest numbers of plantlet were obtained from Krasunia/Sana combination with 131 plants in early-mid uninucleate period. But, the lowest numbers of plantlet were found from Pehlivan/F-85 combination with 28 plants mid-late uninucleate period.

**Keywords:** Wheat hybrid population, callus, green plantlets, medium, pollen development stages, albino plantlets

# THE PROCESS WILD CROSSING ANALYSIS OF RYE WITH MAIZE BASED ON THE OBSERVATION OF CYTOLOGICAL POLLEN TUBES BEHAVIOR

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Efforts were made to induce the development of haploid embryos of rye and to trace the maize pollen behavior to determine the prezygotic barriers role in this process. Distant crosses with a pollen mixture of two varieties of sweet maize hybrids were carried out for five spring rye hybrids on previously castrated spikes. In addition, the samples were sprayed with 2.4 D and Dicamba. The testing material was rye pistils collected and fixed for observation after 1, 3, 7, 14 days after pollination and/or growth regulators spraying. Observations were conducted to determine the degree of deposition of maize pollen, the stigma germination, the overgrowth of pollen tubes in the pistil and into the ovules. The highest percentage of pollen germination and overgrowth of pollen tubes in the pistil were reported for the method based on maize pollination and 2.4 D spraying. The germination of pollen on the stigma of studied genotypes was on average 79%. One of the genotypes, which recorded the best germination of pollen on the stigma 89.8%, at the same time had the lowest percentage of germinating pollen grains in the pistil 3.1%. A significant reduction in the percentage of germinating pollen maize grains was found in the pistil 6% and in pollen tubes reaching the ovules 4%. In conclusion, the low efficiency of pollen tubes reaching the ovules may have a decisive impact on the use of remote crossing for inducing haploid plants.

# THE SEARCH FOR MARKERS CONNECTED WITH GENES OF RESISTANCE TO POWDERY MILDEW IN WHEAT

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Winter rye (*Secale cereale* L.) is widely grown in Poland. Powdery mildew (*Blumeria graminis* f. sp. *secalis*) is one of the most serious diseases of rye and it may cause yield losses of up to 20%. In rye there are numerous described genes controlling for resistance to powdery mildew infection, but resistance adjustment has not been as thoroughly studied as in the other cereals. This paper attempts to demonstrate the potential application of molecular markers developed for wheat in the identification of resistance genes to powdery mildew in winter rye. Inbred lines of winter rye were studied in terms of susceptibility to infection by *Blumeria graminis* f.sp. *secalis* under artificial inoculation. The studied genotypes were not completely resistant to this pathogen. The most and the least infected lines were selected for further study. The lines were tested for the presence of molecular markers connected with the sixteen powdery mildew resistance genes. The studied winter rye genotypes showed the presence of eight markers linked to resistance genes to powdery mildew in wheat [Xcfd81-5D (Pm2), specific for Pm3a, Xgwmc356 (Pm4a), ResPm4 (Pm4), Xgwm159 (Pm16), IAG95 (Pm17), Xbarc144 (Pm34), Xwmc41 (Pm43)]. Among these markers only ResPm4 marker was found only in resistant genotypes (UP77, UP84) and was absent in the genotypes susceptible to infection with *Blumeria graminis* f. sp. *secalis*. Therefore, the relation of this marker with the resistance to powdery mildew in winter rye was determined, and thus created the possibility of using the ResPm4 marker in rye breeding programs using marker assisted selection (MAS).

# YIELD AND YIELD COMPONENT PERFORMANCE, MORPHOLOGICAL AND QUALITY CHARACTERISTICS OF AROMATIK-1 RICE VARIETY WHICH IS THE FIRST AROMATIC RICE REGISTERED IN TURKEY

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Aromatic rice studies were started in 1999 with introduction of nurseries from IRRI (International Rice Research Institute). Some more material were continued to introduce later years. Introduced materials were tested at observation nurseries, primary yield, yield and regional yield trials, crossing program was initiated and mutation breeding was started to obtain aromatic rice adapted to Turkey conditions. As a result of these studies, YRF-204 Australian line obtained from IRRI IRFAON (International Rice Fine Grain Aromatic Observation Nurseries) nurseries was given to registration trial and registered with Aromatik-1 name in Turkey in 2007. Aromatik-1 variety has high yield and aromatic characteristics. In this study, yield and yield components, morphological and quality characteristics of Aromatik-1 which is first aromatic rice registered in Turkey was given.

# ASSESSMENT OF PROTEIC POTENTIAL OF IMPROVED OAT HEXAPLOID LINES DERIVATIVE OF INTERSPECIFIC CROSSES WITH THE TETRAPLOID OAT SPECIES

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Oats are known recently to be a healing plant because of their beneficial nutritional, health and physiological effects engendering a good impact on some diseases such as obesity, diabetes, hypertension and blood cholesterol. INRA breeding programme has been directed to produce lines with high nutritional value. Therefore, eight hexaploid lines derivative from interspecific crosses realised between four hexaploid Moroccan common oat cultivars and the tetraploid oat *A. magna* were subjected to study their profile for total protein using SDS-PAGE technique, in comparison to their common oat parents, respectively. Results revealed that over 90% of stabilised lines maintained interesting protein quality of the tetraploid parent A. *magna* compared to their hexaploid parents. The SDS–PAGE profile of total prolamin fractions from oat groat protein showed most protein bands with MWs related to globulin (avenalin). Furthermore, analysis of total groat protein revealed an improved of 2 to 3% for the derivatives hexaploid lines than that of their common oat parents, respectively.

**Keywords**: Hexaploid oat (*Avena sativa* L.); tetraploid oat *A. magna* Murphy and Terrell*;* SDS-PAGE; Seed proteins storage; groat protein content.

# MOLECULAR ANALYSIS OF FLORAL TRANSITION IN SOYBEAN

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The control of flowering time is one of the key features governing adaptation of crop plants to different geographic regions. Soybean [*Glycine max* (L.) Merr.] is a photoperiod sensitive crop whose floral transition is triggered by exposure to short-day conditions. Photoperiodic response is a major factor determining the latitude at which soybean cultivars are grown. Most soybean varieties have intense photoperiodic sensitivity, such that soybean is usually cultivated as different ‘‘maturity groups,’’ each adapted to a narrow latitudinal range. Our understanding of the molecular and genetic basis of flower initiation in legumes is limited. Accordingly we have used an integrated bioinformatic and experimental approach to addresses this gap in our knowledge. Initially we used computational approach to reveal repertoire of flowering regulatory genes in the soybean genome. Our study identified key flowering genes in soybean and indicates that the vernalisation and the ambient-temperature pathways seem to be the most variant in soybean. Subsequently we conducted whole genome transcriptome analysis to uncover the dynamic transcription and regulation after short-day treatment. We obtained ~240 million paired-end sequences from 9 samples of leaves and shoot apical meristems at different time-points after short-day treatment and identified over 90,000 transcripts from ~50,000 loci. Furthermore, a comparison with the, *Glycine soja*, a wild ancestor of soybean revealed SNPs and structural variants of genes associated with putative soybean flowering genes. Our study provides molecular tools for further investigations of flowering pathway and insights into the relationship and evolution of flowering genes in soybean, a major crop legume.

# CROSS-COMPATIBILITIES OF DURUM WHEAT WITH *AEGILOPS TAUSCHII* ACCESSIONS SCREENED UNDER WATER-DEFICIT STRESS

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With the aim of developing new, synthetic hexaploid wheats having enhanced drought adaptation, a total of 400 accessions of *Aegilops tauschii* Coss. (goat grass) collected from western Asia and the Caucasus were screened for the productive tillering capacity under rain-fed field conditions. Of these, 23 *Ae. tauschii* accessions were selected for interspecific crossing with two durum wheat varieties 'Belikh-2' and 'Jennah Khetifa'. Fifteen of the selected accessions were of Pakistani origin and exhibited early ear-emergence and low cross-compatibility, and five accessions were from Iran and Turkmenistan and exhibited high cross-compatibility. A wide variation among accessions in cross-compatibility might be related to their region of origin. Successful hybridization resulted in the formation of immature embryos, which are capable of regenerating to plants on culture medium. The *Ae. tauschii* accession ig 47219, of Turkmenistan origin, gave the highest frequency of embryos in crosses with both wheat varieties, but regeneration from the crosses with 'Belikh-2' failed due to the occurrence of hybrid necrosis. Thus, a high frequency of embryo production did not always result in the satisfactory development of hybrid plants. Treatment of the hybrid plants with colchicine was essential for the successful set of hexaploid seeds on the newly-synthesized plants. These constraints were discussed for the efficient development of new, synthetic hexaploid wheats.

# DETERMINATION OF THE CONVENIENT METHOD TO BE USED IN TESTING COLD HARDINESS IN SOME CEREAL GENOTYPES

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Among the factors limiting cereal yield cold damage has an important place. However, development of cold hardy varieties take a long time in classical breeding methods. Also, non-occurrence of unfavorable climatic conditions every year emerges as another limitation in terms of selection. The aim of this study was to determine the best method in testing the cold hardiness under controlled conditions to be used to shorten the time required in the development of the cold hardy varieties. For this purpose, two different medium was compared in this study, Houghland solution and the soil prepared with sand, peat and field soil at equal proportions. Study was conducted in both mediums to determine the degree of cold hardiness by applying the same acclimation period and temperatures.2 triticale, 3 barleyand 37wheatgenotypes were used in the study.10 plants from each genotype were tested at each temperature (-7, -9, -11, -13 and -15 $^0$C)and study was established with three replications. Cold acclimation (CA) temperatures were determined according to the long year averages of climatic data of Erzurum province. In total of 42 genotypes were exposed to 49 days of cold acclimation period and pre-determined CA temperatures in both solution and soil mediums. At the end of this period, the plants were frozen by cutting at various temperatures. After a certain time plants were taken from deep freeze to the acclimation chamber at room temperature and kept there for 3 weeks. At the end of this period the live plants were counted. Statistical analysis revealed significant interactions of medium x temperature, medium x genotype, temperature x genotype, medium x temperature x genotype ($p<0.01$). The most and least live plants were obtained at -7 and -15°C as the highest and lowest stamina were obtained from KrasuniaO'deska bread wheat and Betadur durum wheat respectively. It was concluded that soil medium was more user friendly and the number of live plants obtained was morewhen compared to Houghland solution.

**Keywords:** Cold hardiness, Houghland solution, soil medium, cereal genotypes, acclimation period

# EFFECTS OF SALICYLIC ACID AND GA3 PRECONDITIONING TREATMENTS ON REGENERATION FROM COTYLEDON EXPLANT OF CV. KARAELCI

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Common vetch is an important forage legume crop plant of Turkey that ıs cultıvated over large areas in the central Anatolia. Common vetch is largely self- pollinated plant and it is difficult to induce variability. Therefore, there is need to increase variability using biotechnological techniques. The study made use of common vetch cultivar Karaelci cotyledon explants that were initially primed with water for 24 h. Thereafter, the explants were divided into two lots; one lot was given treatment with 200 mg/ l salicylic acid and the other was treated with GA3 for 24 h each. Each of the explant was cultured with abaxial side touching the MS culture medium containing 0.25, 0.50, 0.75, and 1 mg/l BAP. Comparing the two, it was noted that the explants treated with GA3 were more potent to shoot regeneration compared to those treated with salicylic acid. Maximum shoot regeneration frequency of 47% was noted on 0.25 mg/l BAP previously treated with salicylic acid with 5 shoots per explant, with shoot length of 0.82 cm and variable rooting. Whereas, maximum shoot regeneration frequency of 40% was noted on 1.00 mg/l BAP previously treated with GA3 with 9 shoots per explant, wıth shoot length of 0.89 cm, cm and variable rooting. The plantlets obtained from both applications were acclimatized and transferred to field conditions for flowering and seed set. All of them flowered and set seeds. The results show that the biotechnological tools have high potential for breeding common vetch.

**Key words:** Common vetch, Micropropagation , regeneration, Salicylic acid,GA3, rooting,

# GENETIC ANALYSIS AND RESPONSE TO SELECTION OF SOME PHYSIOLOGICAL TRAITS IN RELATION TO PRODUCTIVITY IN BREAD WHEAT UNDER SANDY SOIL CONDITIONS

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Non-allelic interaction scaling tests combined with three and six parameter genetic models were used to determine the adequacy of genetic model, types of gene action, heritability and response to selection for some physiological traits and grain yield/plant. Breeding parameters were assessed using the six populations (P1, P2, F1, F2, BC1 and BC2) of four bread wheat crosses grown under sandy soil conditions. Results revealed the presence of non-allelic interaction in controlling grain yield/plant in all crosses. The simple genetic model as well as the non-allelic interaction was adequate for explaining the inheritance of the physiological traits in different crosses. Additive gene effect was the main type controlling the inheritance of flag leaf chlorophyll content, osmotic pressure and relative water content in some crosses whereas additive, dominance and their digenic interaction were involved in the inheritance of these traits in others. Furthermore, additive gene effect and the digenic model have been reported in thegenetics of proline content while dominance gene effect and the digenic model were detected in the inheritance of transpiration rate and grain yield in most of the crosses. The narrow sense heritability was high (>50%) for the studied physiological traits in most of the crosses and varied from low (27.82%) to moderate (48.89%) for grain yield/plant. Response to selection in F2 generation provide evidence that substantial genetic progress in grain yield/plant has been occurred when selection was imposed to higher flag leaf chlorophyll content, osmotic pressure, relative water content, proline content and lower transpiration rate.

# GENETIC RESILIENCE IN WHEAT FOR TOLERANCE TO HEAT STRESS IN RELATION TO CLIMATE CHANGE

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Wheat (*Triticum aestivum* L. em. Thell) is one of the most important cereal crops and staple food for 35% world population. Wheat is grown under subtropical environment during mild winter, which warms up towards the grain filling stage of the crop. High temperature during tillering, spike differentiation and grain filling phases could be major constraints in increasing productivity of wheat. IPCC has recognized that global mean temperatures will rise 0.3°C per decade and it could be 1°C above the present values by 2025. This implies need to identify genes that impart genetic plasticity for optimization of phasic development of wheat plant under varied climatic conditions. Thus, it would be important to recombine candidate genes through introgression to incorporate *Vrn, Ppd*, and *Eps* genes, increase partitioning of photo-assimilates, ability to maintain green leaf area duration (stay green), starch accumulation in grains for a longer duration and grain yield. Our results have revealed that developmental mutants can be evolved for heat tolerance at vegetative stages by altering Vrn and Ppd genes. Also for terminal heat stress tolerance genotypes like WH 542, WH1021, WH1025, WH1105, Raj 3765, and PBW 373 have considerable genetic plasticity as demonstrated by their segregating populations from their crosses. Increase in grain growth rate and AGPase activities resulted in increase in grain yield. Genotype PBW 435 and the cross PBW 343 x PBW 435 exhibited less cell membrane injury and greater thermo- tolerance under high temperature stress. Likewise, chlorophyll fluorescence enabled to identify heat tolerant genotypes. An integrated approach would be useful to combine resilience, heat stress tolerance and grain yield.

# *IN VITRO* CULTURE USE FOR DURUM WHEAT (*TRITICUM DURUM* DESF.) REGENERANT PRODUCTION UNDER SALT STRESS

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The genetic variability is considered as the major principle of plant breeding for durum wheat. This variability can be induced *in vitro* by selection pressure exerted by stress factors such as salinity and promoting regeneration of vitroplantlets tolerant. This study aims in the first step the regeneration of plantlets tolerant to salinity from mature embryos culture derived from two Tunisian durum wheat varieties : improved (Razzek) and local (Jenah Khotifa JK) varieties. The tolerance evaluation to salt stress was applied *in vitro* (100 mmol $l^{-1}$NaCl) and is based on various parameters. Our results showed that JK variety is distinguished by a stable response for all parameters tested : average weight of callus (368.1 mg for control, 307mg under salt stress), callus regenerated percentage (36.6% for control and 35.7% under salt stress); and green shoots number /callus (17 for control and 17 under salt stress). This stability of response translates the adaptability of this variety to salt stress. In order to fix regenerated JK plantlets in single generation and obtain HDs homozygous stable lines, *in vitro* gynogenesis technical is tested for this genotype. The Evaluation of gynogenetic capacity focused on about 1200 unfertilized ovaries of JK and is based on its ability to induction, differentiation, development of green shoots, haploid plantlets regeneration and HDs production lines. JK showed a relatively good response to gynogenesis with a rate of regenerated lines HDs / total haploid plantlets of 60%.

# INHERITANCE OF DROUGHT RESISTANCE, YIELD AND QUALITY PARAMETERS IN COTTON (*Gossypium hirsutum* L.)

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This study was done between 2009-2010 at Department of Field Crops, Institute of Natural and Applied Sciences of Çukurova University for investigation of $F_1$ hybrid vigor, determination of the best parents and hybrid combinations and investigation genetic behavior under stress, optimum and combined conditions of 6 populations belonged to *Gossypium hirsutum* L. cotton genotypes (Beyaz Altın Mig 119, Sure Grow 125, Beyaz Altın 151, TamCot 22, TamCot Sphinx and Siokra L-22) which are distinguished by obtained by the half-diallel mating design and selected for adaptation ability and drought tolerance at our previos studies. Based on the ratio of general combining ability's variance to specific combining ability's variance, additive gene effects on seed cotton yield, leaf water content, stomatal conductance, fiber length, fiber strength and micronaire under stress; optimum and combined conditions. From the inspected 6 characteristics, 2 for BA 119xSG 125 hybrid was showed positive specific combining ability effects under stress conditions, 4 for under optimum and combined conditions; BA 119xTC 22 hybrid was showed positive specific combining ability effects for 4 traits under stress conditions, 6 traits under optimum and 5 traits combined conditions; SG 125xTC Sphinx hybrid was showed positive specific combining ability effects for 2 traits under stress conditions, 4 traits under optimum and 3 traits combined conditions; BA 151xTC Sphinx hybrid was showed positive specific combining ability effects for 3 traits under stress conditions, 2 traits under optimum contions and 5 traits under combined conditions. Therefore, the mentioned hybrids were determined as the potential combinations that can be used at breeding studies for improvement of these traits.

**Keywords**: Cotton, drought, combining ability.

# MAIZE BREEDING STUDIES in TURKEY; PAST, PRESENT and FUTURE

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Corn is still one of six grains which are feeding the world population. Corn is the most over-produced cereals in the world due to multi-usage, adaptability and efficiency. Although corn production increased 4.4 million tons in 2012, however the ratio of production to consumption is around 80% in Turkey. Grain corn produced in our country use 70% feed industry and 20% in the starch industry. In recent years, the cultivation of corn for silage widespread as second crop. Hybrid maize breeding in our country started in 1950. Through breeding programs carried out to present have been developed valuable populations, a large number of varieties and inbred lines. Seed production rights of varieties were transferred to the private sector with the aim to reach more farmers. Territorial Maize Integrated Crop Management Project was initiated in 2004, maize breeding, agronomy, biotechnology, crop protection, grain and silage quality and physiology research projects in various institutes that conduct studies were collected under a single project. National project includes increase of productivity, improve the quality of grain and silage, development of abiotic and biotic stress tolerant or resistant varieties, and enrich the country's maize germplasm resources development using advanced breeding techniques, cultivation techniques and biotechnological methods. Inbred lines have got different levels of resistant to *Fusarium moniliforme* were determined as inoculated to ear and stem. Identification resistant inbred lines to *Maize dwarf mosaic potyvirus* (MDMV) and *Sugarcane mosaic potyvirus* (SCMV) studies were conducted using molecular markers and inoculation. Determination of high temperature and drought tolerance of inbred lines are also conducted. In recent years, 256 inbred lines were determined genetic distance by SSR markers.

# PEDIGREE AND SSR DATA ANALYSIS REVEAL DOMINANT PREVALENCE OF FEW PARENTS IN PEDIGREES OF PAKISTANI WHEAT VARIETIES

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A randomly selected set of 62 Pakistani wheat varieties developed during 1934 to 2010 was evaluated on the basis of pedigree and SSR data. Average contribution ofaa parent per variety was 2.5. The dominating parents included BLUEBIRD, KALYANSONA, CIANO-67 and SIETE-CERROS-66 which were present in the pedigrees of 35.48, 32.25, 20.5 and 13.20% varieties. The COP value for varieties IQLAB-91 and KIRAN-95 was P=0 which indicated that these varieties had same pedigree and were genetically identical. Similarly, varieties PAVON-76 and SOGHAT-90 had also P=0. This genetic similarity was also confirmed by SSR base cluster. The SSR cluster showed that about 75% of selected varieties were genetically 60% similar. The results emphasize the inclusion of novel and genetically diverse parents in Pakistani wheat programs to maintain broader genetic base of varieties/cultivars.

# PRINCIPAL COMPONENT ANALYSIS (PCA) AND EXAMINATION OF DROUGHT INDICES IN DURUM WHEAT LINES

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Drought is one of the most important environmental stress factors in many countries that limit the production of wheat plant. Thereby, it is possible to increase the yield of wheat by development of drought-resistant plants by regions showing stable efficiency. This study, made use of normal and drought stress conditions to select drought-resistant wheat lines using and two replications of 49 durum wheat lines in simple Lattice (7x7) experimental design. Irrigation development was normal until the end of the first experiment, while physiological, stress was applied at four major physiological developmental stages in wheat (tillering, stem growth, flowering and seed filling stage) applied to drought stress. The study reports data obtained under normal conditions and the stress pertaining to drought-resistant grain yield indices*: Average Productivity (MP), Geometric Mean Productivity (GMP), Tolerance (TOL), Harmonic Average Yield (HAR), drought susceptibility index (SSI),* and *Stress Tolerance Index* ( STI). Principal components analysis (PCA) showed that the first two components of data variation of 97.47% in total. Consequently, the first was identified as tolerant to drought stress and the second component was identified as sensitive to stress. Under normal and drought conditions, the correlation was noted between grain yield and drought tolerance indices. STI, HAR, GMP and MP with maximum index of Looking at the conclusion, tolerant line index was identified as the best choice. According to the statement of biplot lines 27, 44 and 47 were identified as tolerant to drought stress.

**Keywords:** biplot, Durum wheat, drought-tolerant Index

# RUST OCCURRENCE, EPIDEMIC DEVELOPMENT AND RESISTANCE OF WHEAT CULTIVARS DEPLOYED IN NORTHWEST OF PAKISTAN

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Both yellow and leaf rusts are the key biotic stresses of wheat in Pakistan and around the world. Fifteen wheat growing districts of Khyber Pakhtunkhaw Province were studied during 2012 under the surveillance component of “Pakistan Wheat Productivity Enhancement Program” supported by the United States Department of Agricuture and other international partners to get real time information regarding disease status and epidemic development of both yellow and leaf rust along with resistance and trend of deployed cultivars. Surveillance program covered around 4670 acre of farmer fields. Results of wheat landscape covering 700 acres of district Peshawar and Nowshara indicated that yellow rust damage was sever in Maghdarzai (Peshawar) and Azakhel Bala (Nowshara) areas respectively while in case of leaf rust, damage was high in Utozai (Peshawar) and Aman Garh (Nowshara) areas respectively. Yellow rust epidemic developed fastest at Maghdarzai (Peshawar) and Mian Gul Village (Nowshara) while for leaf rust it was maximum at Utozai (Peshawar) and Miskeen Abad (Nowshara). Number of unknown and known wheat cultivars including Atta Habib, Auqab-2000, Bahkhar-2002, Bathoor-08, Janbaz, Pirsabak-04, Pirsabak-05 and Sehar-2006 were deployed and have displayed variable susceptibility levels. Both “Sehar-2006” and “Pirsabak-04” emerged as the major cultivars and have occupied 71% and 12% of the wheat landscape respectively. Yellow rust resistance of “Sehar-2006” and “Pirsabak-04” is based on *Yr9* and *Yr9+27* respectively while for leaf rust, it is based on *Lr1+26* and *Lr26* respectively. Additionally both these cultivars are susceptible to stem rust race Ug99 and its variants. Cultivation of these cultivars should be strongly discouraged for avoiding rust epidemics in the region as resistance of both these cultivars is narrow and based on defeated genes.

# THE DETERMINATION OF GENETIC PROGRESS FOR YIELD AND QUALITY TRAITS AT WINTER BREAD WHEAT

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This study was conducted in 2007-08 and 2008-09 growing seasons, in Konya and Eskisehir locations, by 30 registered winter bread wheat varieties of which 15 were developed for rainfed and the others for irrigated conditions on the randomized block design with 3 replications. The main objective of the study is numerically to demonstrate genetic progress for grain yield and quality of the varieties developed since 1931. In terms of grain yield on rainfed conditions Sönmez-2001, Seval and Harmankaya-99 varieties, on irrigated conditions Ahmetağa, Alpu-2001, Harmankaya-99, Ekiz, Yıldız-98 and Çetinel-2000 varieties took place in the first group of the experiment. In both irrigated and rainfed conditions, considering grain yield and quality characteristics Harmankaya-99 ranked as the first cultivar. Genetic progress for grain yield was identified as 40.9 kg per year per hectare for under irrigated conditions, while it was 9 kg per year per hectare under rainfed conditions. Genetic progress for content of wet gluten in both experiments over the years was found on negative direction (on irrigated $R^2$=0.3397*, on rainfed $R^2$=0.5477**) and statistically significant. In fact, under this reduction is %0.15 every year irrigated conditions whole, this value was found %0.08 under rainfed conditions.

**Key Words:** Bread wheat, grain yield, genetic progress, quality

# YIELD STABILITY OF SOME BREAD WHEAT VARIETIES RELEASED TO DRY AREAS OF CENTRAL ANATOLIA

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This research was carried out to determine yield performance and stability in dry conditions of some bread wheat cultivars which was developed through four years (from 2005 to 2008). As a research material of 12 registered bread wheat cultivars (Bayraktar 2000, Bezostaja 1, Dağdaş 94, Demir 2000, Gerek 79, Gün-91, Harmankaya-99, İkizce 96, Kınacı-97, Pehlivan, Tosunbey, Zencirci-2002) were used. The research was carried out on a randomized complete block design with four replications for a period. According to years the yield varied, in the good conditions Tosunbey, Kınacı-97, Pehlivan, Demir 2000; the worst conditions Zencirci-2002, Bayraktar 2000, Gerek 79, Harmankaya-99 and İkizce 96 come to the fore. According to the 4 years result and stability characters Tosunbey maintained to be the best cultivar.

**Key Words:** Bread wheat, yield, stability

# EFFECTS OF SALINITY STRESS ON WHEAT GRAIN QUALITY AND SCREENING FOR TOLERANCE BY MOLECULAR MARKERS

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High soil salinity affects on growth, yield and grain quality of wheat worldwide. To solve this problem it is necessary to develop tolerant varieties through selection and breeding techniques. At the present study we examined the effect of salinity on grain quality characteristics, such as thousand kernel weight (TKW), protein content, wet gluten, gluten index and SDS sedimentation volume. Screenings of wheat genotypes for salt tolerance were also conducted by molecular markers. *Triticum durum* Desf genotypes, such as Garagylchyg-2 and Barakatli-95 and *Triticum aestivum* L. genotypes - Giymatli-2/17, Nurlu-99 and Azamatli-95 developed by the Institute of Crop Husbandry (Baku) were the subjects of the study. Plants were grown in the field under low and high salinity. It was found out that salinity reduce the grain quality in all cultivars, but did not significantly affect the protein content. Thousand kernel weight and wet gluten content decreased more in the cultivars Giymatli-2/17 and Garagilchig-2, but the decline was less than in cultivar Barakatli-95. Soil salinity reduces of sedimentation volume in bread wheat. Gluten index did not change significantly (from 0.1-10). 14 bread and durum wheat genotypes have been analyzed using RAPD (OPZ 09) and SSR (gwm312 for Nax1 and Nax2 marker cslinkNaz2) markers. PCR amplification of OPZ 09 marker produced a band of 590 bp in resistant cultivars-Azamatli, Giymatli-2/17, Gobustan, Nurlu-99 and Saratovskaya-29. Nax1 and Nax2 genes absent in these modern wheat cultivars and the results of screening correspond to the literature data.

**Key words:** salinity, grain, *Nax* genes, wheat

# EFFECTS OF SALT STRESS (NACL) ON PLANT GROWTH AND YIELD OF RICE (ORYZA SATIVA L.) VARIETIES

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In order to survey salinity tolerance of 10 rice varieties including: Dorfak, Tabesh, Amol3, Gharib siyah reyhani, Hasan saraie atashgah, Tarom, Pakutah, Dom sepid, Tarom amiri, Pokkali and IR29 tow separate farm experiments (salinity and non salinity conditions) were carried out under randomized complete block design in three replications in Iran-Astara,2008. The traits of panicle weight, grain1000 weight, number of seed in panicle, biomass, straw weight and paddy yield were measured in tow conditions of the farm. The result showed that there was a significant difference between varieties for any traits, and salinity condition in comparison to non salinity condition, reduced every trait. Paddy yield had a positive meaningful correlation with every trait at 1% probability. Among the studied varieties, the Gharib siyah reyhani and Pokkali due to high resistance to salinity stress have highest yield.

**Keywords**: Rice, Salinity Stress, Yield, Yield Components

# ADAPTIVE CHANGES OF PHYSIOLOGICAL SIGNS OF WHEAT GENOTYPES UNDER SOIL DROUGHT CONDITIONS

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Drought is the most important unfavorable environmental stress that limits wheat production in drought-prone and rainfed areas of Azerbaijan. Study of physiological characteristics of wheat has an important role in the understanding of drought adaptation mechanism and for identification of the tolerant genotypes. The aim of the present study was to analyze gas exchange parameters, the content of photosynthetic pigments and relative water content, as well as dynamics of the assimilation surface area and dry biomass of leaves from 6 durum (Garagilchig-2, Vugar, Shiraslan 23, Barakatli-95, Alinja-84, Tartar) and 7 bread wheat (Gobustan, Giymatli-2/17, Gyrmyzy gul 1, Azamatli-95, Tale-38, 12nd FAWWON№97, 4thFEFWSNN№50) genotypes grown in field conditions under water deficit. Drought stress caused a decrease of RWC in flag leaves of these genotypes. A slight decrease was observed in genotype Tartar. The flag leaf assimilation surface area decreased approximately 8-44%, dry biomass - 7-43%. Specific leaf density ($mg \cdot mm^{-2}$) increased in all genotypes. Number of spikes, weight of sheaves yield in $1m^2$, yield components, 1000 kernel weight decreased under the influence of drought. The rate of photosynthesis was equal to 11.3-20.6 $\mu mol\ CO_2 \cdot m^{-2} \cdot s^{-1}$ in flag leaves of wheat genotypes. At the same time photosynthesis rate, stomatal conductance, intercellular $CO_2$ concentration, transpiration rate were also reduced significantly under the influence of drought. The rate of photosynthesis strictly correlated with stomatal conductance, especially with mesophyll conductance. Contents of chlorophyll *a* and *b*, total carotenoids ($mg \cdot g^{-1}dw$) decreased under the influence of drought. Lower values of the ratio (a+b)/ car were found in stressed plants. The obtained results may be useful for selection of drought tolerant wheat genotypes in breeding programs.

**Key words:** drought, photosynthesis rate, transpiration, wheat

# AGRONOMIC PERFORMANCE OF SOYBEAN WITH RESISTANCE POTENTIAL TO STINK BUGS

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Soybean [Glycine max (L.) Merrill] is the most important legume cultivated around the world, due to its high protein and edible oil contents. One of the main objectives of genetic breeding programs is increasing the yield and other agronomic characteristics. Thus, the main objective of this study was to evaluate F5 progenies (originated from IAC100 and CD215 cultivars crossing), from the “Luiz de Queiroz” College of Agriculture (ESALQ/USP, Brazilian acronym) breeding program for resistance to soybean stink bugs complex. Progenies evaluations were carried out during 2012-2013 harvest, in experimental fields of the Genetics Department of ESALQ/USP and in the Anhembi Experimental Station, located respectively, in the municipalities of Piracicaba and Anhumas, both in Sao Paulo state. It was used the augmented block design with 504 progenies and five mixed check plots, namely IAC100, CD215, Potência, LQ1402 and LQ1519. Experimental plots were constituted of a five-meter line, each with 18 plants by linear meter. The evaluation of agronomic performance was measured according to grain production (GP): obtained as grams after plant threshing and grain drying. Mean values of GP were 1,200 g for Piracicaba, and 900 g for Anhumas, with general maximum value of 1,800 g and general minimum value of 280 g. Amongst the progenies, 24 showed GP higher than 1,400 g in both municipalities, and will be evaluated for their resistance to soybean stink bug complex during the next harvest period, aiming the launching of new soybean cultivars resistant to stink bugs and with high yields.

# AGRONOMY AND BREEDING OF RAPESEED (*Brassica napus* L.) IN TURKEY

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Used as lamp oil in the middle age, rapeseed (*Brassica napus* L.) evolved to the most important oil crop in Europe due to the intensive breeding work in the beginning of 1970' s and forthcoming years. Turkey acquantained with this plant also in 1970's, but it's cultivation was later forbidden; because canola was imported from Canada - turnip rape (*B. rapa*) – and erucic acid content increases after seed multiplication. İn the middle of 2000 rapeseed (*B. napus* L.) become the main topic of conversation regarding closing the deficit of edible oil in Turkey. Rapeseed (*B. napus* L.) cultivation begun with the support of the government, but in spite of suitable climate conditions it does not ranged the value it deserved; the reasons fort his are lacking information regarding the cultivation of this plant form side the farmers, wrong cultivar choice, applicational difficulties and harvest losses etc. Rapeseed (*B. napus* L.) breeding work were done by Research İnstitutes and by related departments of universities mainly as adaptation trials using genetic material provided form gene banks or breeding companies. The main reason for this is that we don't have a broad rapeseed (*B. napus* L.) genetic material. One local rapeseed (*B. napus* L.) cultivar was developed by limited breeding studies far now. This review focusses on the problems and solutions regarding rapeseed (*B. napus* L.) cultivation and breeding in Turkey.

**Key words:** rapeseed, breeding

# AN OUTLOOK TO A PRIVATE POTATO BREEDING PROGRAM IN TURKEY

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The potato is one of the most important agricultural crops in Turkey with annual production of 4.8 million tonnes. Despite the magnitude of potato sector in the country, potato breeding efforts are very limited. Hence, potato production still totally depends on foreign cultivars, mainly from European countries. However, some governmental and private institutes were started potato cultivar breeding programs in recent years. Doğa Seed Inc. is one of the biggest private companies dealing with seed and ware potato production in Turkey. The company has started the largest cultivar breeding program for potato in Turkey in 2010. The main aim of their breeding program is development of high yielding ware and processing cultivars resistant to wart (*Synchytrium endobioticum*) and PVY. The company also invested to molecular genetic laboratory to integrate the marker assisted selection into breeding program. Currently, thousands of breeding lines from different generations are on the way of registration. The general outlines, aims and achievements of this breeding program will be introduced in this presentation.

# BREEDING FOR WHEAT RUST DISEASES IN ALGERIA AND STRATEGIES FOR PATHOGENICITY REDUCTION

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Yellow rust and leaf rust are predominating in Algeria, stem rust is seldom found but Septoria leaf blotch is important over different wheat growing areas. Epidemics of stripe rust continue to cause sometimes severe losses as in many parts of the world and threatening the food security and livelihood of resource-poor farmers and their communities. It is mainly due during this last decade to the outbreak of Yr27. Aggressive new strain of yellow rust have decimated wheat yields (80% loss in 2005) over the most growing bread wheat variety (Hidhab) that became highly susceptible in both high rainfall and semi arid regions with losses of 20 to 80% being recorded almost annually. Most of the varieties grown at farmer level have susceptible reactions to stripe rust (cham8, Inquilab 91, Attila, veery, bobwhite or Kauz). Strategies conducted in these late years aim to reduce the risk of wheat rust (yellow and leaf) targets a continuous efforts in surveillance from all parts of northern Algeria and neighboring countries (Tunisia and Morocco), research on breeding for rusts resistance has higher priority, diversified cropping is now used (reducing planting of mega-varieties across large areas), multiply and use new developed resistant varieties such as Tiddis, Boumerzoug, Akhamokh and Massine for yellow rust and the new cv.Yacine which is resistant to *Pgt* race Ug99 (*Sr2*, *Sr25*).

**Key words**: wheat rusts, susceptibility, strategies, surveillance, breeding, seed multiplication.

# BREEDING STRATEGIES AND PROGRESS TOWARDS IMPROVEMENT OF YELLOW RUST AND STEM RUST RESISTANCES IN TAJIK WHEAT BREEDING PROGRAM

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Wheat is the staple food and main source of caloric intake for 8 million people in Tajikistan. Therefore, it's high importance to have an in-country breeding program in collaboration with International Centers, in order to maintain food security for growing population in country. The breeding activities carried out by the national wheat breeding program, and it has resulted in a number of high yielding, yellow rust and stem rust resistances facultative/winter and spring bread wheat lines being identified through multi-location yield trials. Yellow rust and stem rust of wheat continues to cause severe damage locally and globally. In this context the identification of yellow rust and stem rust resistance genes present in cultivars currently cultivated, advanced lines and landraces are important information for national wheat breeding program. The objective of this study was to postulate, using filed screening and seedling resistance tests. We evaluated materials for yellow rust response in the field in Tajikistan, and seedling reactions to a worldwide panel of isolates were assayed at the Global Rust Reference Center in Denmark. Stem rust response in the field at Njoro, Kenya, and seedling reactions to *Pgt* races TTKSK, TTKST, TTTSK, TRTTF, TPMKC, TTTTF, QTJHC and RKQQC at the USDA-ARS Cereal Disease Laboratory were evaluated. Gene postulation and adult stage testing indicated that resistance genes *Yr1*, *Yr2*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, and *Yr27* for yellow rust, and the *Sr10* and *Sr31* for stem rust were identified. Moreover, several lines were highly resistant and likely possess novel genes for yellow rust and stem rust resistances.

# CAMELINA (*CAMELİNA SATIVA* (L.) CRANTZ) BREEDING OPPORTUNITIES AND GOALS IN TURKEY

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*Camelina sativa* (L.) Crantz in Brassicaceae familia which known commonly as false flax is an alternative oilseed plant. Cameline is natural plant of Northern Europe and Central Asia. It is a plant be grown in summer and winter, annual, autogamy. One of the most important properties is having around 40 % fat ratio in the seed. Camelina oil is used in human nutrition as well as traditionally and also at cosmetics industry, obtaining cleaning products, making lamp oil and candle. It may substitute for the fish oil due to their similar fatty acids. Pomace remaining after pressed and obtained oil from the seed is used as protein enrichment in fodder mixtures. Camelina seeds are used as snack and its stems are used as raw material for fiber pulp and paper. Also it is used as an ornamental plant in landscaping areas. This plant is not grown at large scale today. However, camelina deserves great attention due to not effected environmental factors much, be grown in marginal areas, drought- tolerance, early maturing, requirement of less input from the other oilseed plants, well adaptation ability, high oil content and oil yield per hectare, oil composition. In recent years, researches on biodiesel in our country reveal the need of searching plants can be used for this purpose and planning of adaptation, cultivation technique packages and breeding studies in the future.

**Key words:** Camelina, oil plant

# CELL VIABILITY AND MEMBRANE FLUIDITY IN RELATION TO DROUGHT TOLERANCE OF WHEAT: GENETIC OPTIONS FOR IMPROVEMENT

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Drought stress is an important production constraint of wheat during grain-fill period in India and in other parts of the world where the moisture stress become high during anthesis to maturity stage of plant growth. Drought induced damage of plasma membrane was assayed by membrane thermo-stability (MTS), which measure electrolyte leakage from leaf tissues after exposure to high moisture stress. Cell membrane stability (CMS) and tetrazolium triphenyl chloride (TTC) test, drought susceptibility index (DSI), drought response index (DRI) and grain yield were used to evaluate these genotypes under normal and drought stress conditions for two years. This revealed that high grain yield under drought stress in these genotypes might have been contributed by the other traits other than the TTC and CMS. Correlation coefficients revealed that the genotypes having high cell viability (TTC) also had high CMS high grain yield under drought stress and high value of DRI. CMS was also significantly positively related with DRI. Significant positive association of TTC and CMS with DRI revealed that these characters appeared to contribute towards drought tolerance. High grain yield under normal environment was associated with early heading (r= -0.46*) and susceptibility to drought stress (DSI), while high grain yield under drought stress was contributed by drought escape and combination of both, i.e., high grain yield potential and drought escape, and drought tolerance (DRI, r= 0.49*). The varieties ‘Seri’ and ‘Raj 3765’ had a desirable combination of cellular drought tolerance (TTC and CMS), drought tolerance (DRI) and high grain yield potential under drought stress, while ‘WH 730’ and ‘WH 533’ were better in cellular drought tolerance and drought tolerance. The varieties ‘PBW 373’ and ‘Kauz’ also performed better under drought stress in terms of grain yield and DSI/ DRI. The varieties ‘Kanchan’, ‘PBW 373’, ‘NIAW 34’ and ‘GW 173’ were avoiders/ escapers, ‘Seri’ and ‘HUW 234’ were tolerant to drought stress, while ‘WH 730’, ‘WH 533’, ‘Nesser’, ‘Raj 3765’ and ‘Kauz’ showed the combination of both. Correlation coefficients revealed that DRI was the most important trait followed by TTC because the genotypes having high DRI also had high grain yield and better in mitochondrial viability and membrane stability under drought stress. Results suggested that the selection for drought tolerant genotypes based on MTS in this material may be more effective by reducing the dominance variance after a few generation of selfing. The varieties, Hindi 62 was the best general as well as specific combiner followed by NIAW 34 in drought tolerant group, while WH 542, HD2329 and HD 2687 were good specific combiners in drought sensitive group. For improvement of MTS in this material selection after a few generations of selfing is suggested to contain dominance type gene action/ interaction.

**Key words:** cell viability, membrane fluidity, drought tolerance, wheat, genetic

# COMPUTATIONAL EXTRACTION AND COMPREHENSIVE MOTIF ANALYSIS OF EST BASED SSRS IN THREE DIFFERENT *PUCCINIA* SPECIES

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Cereal rust pathogens have flexible genomes and tend to develop new resistance mechanisms. Hence, an exact identification of rust species carries significance for pathogen specific resistant crop development. On the other hand, EST based microsatellites are one of the feasible switches to make comparisons between species and they enable an effective genome wide screening. In this study, motif structures and frequencies of Class I and II microsatellites were identified using computational pipeline. To achieve this, a total of 47.532 EST sequences derived from *Puccinia triticina* (leaf rust-*Pt*), *Puccina striiformis* (stripe rust-*Pst*) and *Puccinia graminis* (stem rust-*Pg*) were used. Over 18.2 million bases condensed using DNA Star software and tracking of perfect and imperfect repeats in assembled ESTs processed by eTRA1.0. According to overall statistical calculations, the lowest rate for average number of repeat strings per sequence found as 0.176 and 0.167 in contig and singleton sequences of Pg, while the highest rate obtained as 1.108 and 0.824 in Pst respectively. The most abundant imperfect repeat distribution found as 38.3% in Pst sequences. Additionally, Class I microsatellites prominently clustered as 33.7% in *Pst* ESTs. Interestingly, there were any penta and hexa-nucleotide repeats both Pg and Pst species. In the contrary, (TTCTT) was the most repeated motif among four types of penta-nucleotides in *Pt*. A set of 104 tri-nucleotide repeats presented only in *Pt* and di-nucleotide repeats covered the vast majority of assembled ESTs for all *Puccinia* species. These candidate EST-SSRs would be used to estimate of diversity testing in *Puccinia* species

# DETERMINATION OF AGRONOMIC CHARACTERISTICS OF SOME SOYBEAN GENOTYPES AS A SECOND CROP UNDER CUKUROVA CONDITIONS

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This study was conducted to determine yield and agricultural characters of some F6-F7 soybeans lines and varieties as a second crop in the Cukurova region conditions. Türksoy, ÇU04-74, ÇU04-53, ÇU04a-45, ÇU04-34, ÇU03-75-2, ÇU04-122, Nazlıcan and ÇU04-78, ÇU04-75-1 were used as a material. This study was conducted in the East Mediterranean Agricultural Research Institute's experimental area in the randomized complete block design with three replications in 2010. In this study, seed yield, plant height, first pod height, days to maturity, days to flowering, 1000 seed weight, lodging, charcoal root, green stem syndrome were observed. According to the results, plant height ranged from 94.9 to 129.8 cm, first pod height ranged from 2.3 to 5.1cm, 1000 seed weight ranged from 142,5 to 199,1 g, lodging ranged from 1.0 to 3.2, charcoal rot ranged from 1.0 to 2.7, days to maturity ranged from 106 to 109 day, green stem syndrome ranged from 1.7 to 3.7, seed yield ranged from 155.8 to 355 kg/da. According to the seed yield, the results indicated that ÇU04-53,ÇU04-45,ÇU03-75-2 and ÇU04-122 lines can be grown as a second crop in the Çukurova region conditions at the future.

**Key words:** soybean, yield, agricultural characters.

# WINTER BARLEY BREEDING HISTORY OF TURKEY

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Turkey is one of the gene centers for cereals including barley so that reason has great genetic diversity among landraces collected trough the country. Barley breeding activities was commenced in 1925 by collecting, characterization and evaluation of barley landraces from all over the Turkey. These studies resulted in selection of the first winter facultative feed barley cultivars such as Tokak 157/37 , Güzak and Yeşilköy and then barley acreage was doubled in 1960 after adoption of these cultivars by Turkish farmers. Tokak 157 /37 was the most common cultivar especially under Turkish highlands till 2000 and used as genitor in almost all crossing programs for development of new winter facultative barley genotypes. The cultivar was replaced by its progenitors and then the second break-trough was realized when these new cultivars have been adopted by Turkish farmers especially for rain-fed conditions. Today, public and private feed and malting barley breeding programs have been making some crosses to improve new cultivars by using modern breeding techniques including marker assisted characterization and microspore culture in Turkey.

**Key words:** Barley breeding, landraces, rain-fed conditions, genitor, modern breeding techniques.

# MAPPING OF QUANTITATIVE TRAIT LOCI FOR GRAIN ZN CONCENTRATION IN WHEAT IN EASTERN GANGETIC PLAINS OF INDIA

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The terminal heat stress is serious threat for wheat in Eastern Gangetic Plains (EGP) of India. Malnutrition in women and children is another serious social and health concern. Both of these, if addressed together, would resolve the food and nutritional insecurity issue to large extent. 140 double haploid wheat lines including parent Krichauff and Berkut were evaluated (4.5m$^2$ x 3 replication in 2011-12, 2012-13) in two locations of EGP, Banaras Hindu University (Varanasi) and Jamalpur (Mirzapur) to find out QTLs for high Zinc concentration (measured by X-ray fluorescence**)** in grain. Consequent to genotyping through 233 SSRs, 311 DArT and 1 *Vrn* gene linked marker by Composite Interval mapping 1 major loci, *QZn.bhu*-1B is detected (flanking markers *wmc036*c and *cfa2129*, interval size 2cM, mean LOD 5.04 and phenotypic Variance 23.14) consistently throughout the experimental period. The low QTL × Environment interaction and high heritability reflected less environmental effect. This QTL appears to be useful for use in marker assisted breeding for enhancing grain zinc concentration Of the 140 DH lines, 3 were found superior for high zinc as well as grain yield, leaf rust resistance and protein content under late sown conditions. The identified lines are being further evaluated for their direct deployment as variety or as a prebreeding material in the ongoing breeding program.

# OVER-EXPRESSION OF A SPECIFIC SOYBEAN *GM*GSTU4 ISOENZYME IMPROVES CHLOROACETANILIDE HERBICIDE TOLERANCE OF TRANSGENIC TOBACCO PLANTS

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Plant glutathione transferases (GSTs) have a major role in the plants herbicide detoxification. Soybean (*Glycine max* L.) *Gm*GSTs have been well studied for their correlation in herbicides selectivity towards diphenyl ether, chloroacetanilide and sulfonylurea herbicides. Chloroacetanilide herbicide tolerance was assayed *in vitro* by measuring the growth inhibition of wild type (wt) and transgenic tobacco seedlings from cultivars (Basmas, Virginia, Burley) in the presence of 7.5 and 15 mg/L of alachlor and metolachlor. Alachlor caused strong inhibition of shoot and root growth of wt tobacco plants. All the transgenic Basmas lines showed significantly higher shoot and root elongation at 7.5 mg/L alachlor, with line BAGST-3 exhibiting the greatest tolerance. However, at 15 mg/L alachlor, growth was highly reduced in transgenic and wt plants. In Burley, only line BUGST-2 has statistically significant greater mean of root and shoot length compared to wt under the two doses. On the contrary, Virginia has reduced growth which was similar to the wt. Metolachlor toxicity was less severe compared to alachlor. Growth of the transgenic lines of the three cultivars was not significantly greater in either metolachlor concentrations tested, compared to wt plants, except line BAGST-3 which exhibited significantly greater mean of shoot and root elongation at 7.5 mg/L. Transgene expression was determined quantitatively using Real Time qPCR, lines BAGST-3 and BUGST-2 showed consistently greater expression of *Gmgstu4* compared to actin gene. These results confirm that overexpression of GmGSTU4 in tobacco provides higher catalytic activities towards xenobiotics, resulting for future use in environmental cleanup of alachlor.

# MORPHOLOGICAL, PHYSIOLOGICAL AND METABOLOMIC RESPONSE OF TRANSGENIC TOBACCO PLANTS (*N. TABACUM* L.) OVEREXPRESSING *GM*GSTU4 UNDER DROUGHT STRESS

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GSTs appear to have a significant role in plants' adaptation under abiotic stress as many isoenzymes are found to be differentially expressed under these conditions yet, little is known about the regulatory functions of GSTs. Wild type and transgenic tobacco plants over-expressing the soybean *Gm*GSTU4 of cultivars Basmas, Burley and Virginia were grown *in vitro* under 100 and 200mM mannitol or in soil (plant pots) by withholding watering for 15 days. However, *Gm*GSTU4 plants did not exhibit significant differences in drought tolerance compared to wild-type plants. Morphological (shoot length, total and root fresh weight) and physiological (chlorophyll content, relative water content and photosynthetic capacity) parameters of transgenic plants did not differ from the wild-type in the presence of 100 or 200mM mannitol or in the soil when watering was halted. Metabolite profiling was used to understand the dynamics between the wild-type and transgenic tobacco response to drought stress. Different metabolic pathways are involved in production of osmoprotectants. These molecules accumulate in plants under stress conditions as adaptive mechanism, which can provide stress tolerance. GmGSTU4 plants did not exhibit difference in drought tolerance compared to wild-type plants, however metabolomics analysis indicated alterations in metabolite profile and increased concentration of sorbitol, glycerol and pyruvic acid. In conclusion, overexpression of GmGSTU4 in transgenic plants did not affect their drought stress tolerance although it has altered their metabolite profile possible because of diverse effects on plant stress tolerance mechanism.

# MOLECULAR PATHOGENICITY OF WHEAT – *FUSARIUM GRAMINEARUM* INTERACTION

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The *Fusarium graminearum* is responsible for Fusarium head blight (FHB) disease in wheat which makes unsuitable for end-use quality of wheat. Global gene expression study was undertaken to analize and identify wheat disease reaction mechanism and fungus disease causing mechanism. The study was conducted using three genotype of wheat, Japanese landrace Nobeoka-bouzu (Highly resistant), cv. Sumai 3 (Resistant) and cv. Gamenya (Susceptible) which florets were inoculated 10 µl ( $10^5$ conidia / ml) of *Fusarium graminearum* "H-3" strain during the flowering stage. Microarray analysis was carried out by extracting RNA from 3 DAI (days after inoculation) and 7 DAI. Wheat custom array 4x38k and 8x15k *F. graminearum* array was used. The expression of defense-related genes were more up-regulated in highly resistant landrace Nobeoka-bouzu followed by cultivar Sumai 3 and finally by susceptible cultivar Gamenya. Comparison between the genotypes, in highly resistant Nobeoka-bouzu the expression of up-regulated genes at 3 DAI was more than 7 DAI, while in resistant cultivar Sumai 3 the expression pattern was opposite, this could be due to the different resistant mechanism. Moreover in susceptible cultivar Gamenya the expression was minimum at both time points. The most highly expressed genes in resistant wheats were UDP-glycosyltransferase and Multidrug resistance genes, both are genes which encode protein involved in detoxification process. The *F. graminearum* genes expression was more up-regulated in susceptible cultivar Gamenya than in highly resistant landrace Nobeoka-bouzu and resistant cultivar Sumai 3 at 3 and 7 DAI. Comparative gene expression map was developed for wheat-*Fusarium* molecular pathogenicity.

# THE USE OF RELATIVE WATER CONTENT AND LEAF WATER POTENTIAL FOR THE SELECTION OF MAIZE INBRED LINES UNDER DROUGHT STRESS

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Maize plants can cope with drought stress by manipulating key physiological processes like photosynthesis, respiration, water relations, antioxidant and hormonal metabolism. We investigated whether single-plant selection can be made on Relative Water Content (RWC) and Leaf Water Potential (LWP). It was asserted that relative crop yield (CY) potential of a genotype can be predicted from plants grown in the absence of competition through a novel equation that incorporates two components into a single value (value B), the first based on plant yield (PY) potential and the second based on the coefficient of variation (CV) of individual plants. During the 2012 season, R-31 honeycomb experiments were established in two different areas in northern Greece at normal and water-stressed conditions, including ultra-spaced individual plants (0.74 plants/m$^2$) of thirty inbred lines. The LWP values varied from 9.80 up to 18.06 bars, while the RWC averaged from 92.02 up to 94.93%. The overall CVs were 0.26 and 0.04 for LWP and RWC, respectively. Moreover, genotype and water treatment affected significant both RWC and LWP. As expected, at normal and water limited treatments the rates of RWC and LWP were reverse. Grain Yield was strongly correlated with B values (0.93) and a significant correlation between LWP and Grain Yield (0.38) was measured. However, RWC and LWP did not correlate significantly (-0.23). The conclusions were that these measurements and especially LWP could be used in the selection of maize inbred lines tolerant to water stress under low density conditions.

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# ISOLATION OF GST ISOENZYMES FROM *PHASEOLUS VULGARIS* L. AND CHARACTERIZATION OF DETOXIFYING MECHANISM UNDER BIOTIC AND ABIOTIC STRESS

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Three Glutathione transferase (GSTs) isoenzymes have been isolated from *P. vulgaris* leaves after *in vivo* treatment with 1/250 fluazifop-p-butyl herbicide. The inducible GST isoenzymes were identified and separated by affinity chromatography. They found to belong to phi and tau classes. Moreover, the fluazifop-inducible glutathione transferases from *P. vulgaris* (PvGSTs, termed PvGSTU2-2, PvGSTF1-1 and PvGSTU3-3) were found to catalyze a broad range of reactions and exhibit quite varied substrate specificity. Another GST isoenzyme was isolated from *P. vulgaris* (PvGST, termed PvGSTU3-3), after its induction with biotic stress treatment (*Uromyces appendiculatus* infection). PvGSTU3-3 shares high homology the tau class plant and catalyzes several different reactions and exhibits wide substrate specificity. Of particular importance are the high antioxidant catalytic function and hydroperoxidase, thioltransferase, and dehydroascorbate reductase action of Pv-GSTU3-3. Transgenic tobacco plants over-expressing PvGSTU2-2 isoenzyme have been developed via *Agrobacteriun tumefaciens* in order to study their *in planta* potential to confer biotic and abiotic resistance as a means of plant breeding. Our results provide new insights into catalytic and structural diversity of GSTs and the detoxifying mechanism used by *P. vulgaris*. Moreover, highlight the functional and catalytic diversity of plant GSTs and demonstrate their pivotal role for addressing biotic stresses in *P. vulgaris.*

# POTATO BREEDING IN THE CZECH REPUBLIC

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The breeding system of continuous material development in individual years is used in the Czech Republic. Selection of suitable partners is always the background. Usually, parental components with excellent agronomic characteristics are selected for given breeding intention. When possible, the breeders also work with materials possessing increased resistances to individual pests and diseases. Last but not least they are also focused on resistance to abiotic factors (drought, high summer temperatures etc.). During several years the offer has substantially been enlarged with varieties possessing new characteristics. The development was especially done in consumer quality of varieties, where varieties representing all cooking types are available – waxy, fairly firm and mealy with various growing period duration. Further, breeders fulfilled increasing requirements for varieties for production of various special products. We can expect that the trend of breeding especially focused on quality of potatoes for consumption and processing raw stuff will continue also in the future. Topical consumer's requirements will be taken into account. In addition to the emphasis on internal potato quality under conditions of our republic, varieties with improved resistance to viral diseases will be further bred. Selection for resistance to potato nematode and wart disease will still have an important position in resistant breeding. In varieties of all utility types growers require resistance to potato late blight and storage diseases. Growing potatoes resistant to late blight will be a quality guarantee of ware potatoes containing low pesticide residues and metabolites of secondary pathogens.

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# BREEDING FOR GRAIN ZINC DENSITY IN TALL AND SEMI-DWARF INDIAN BREAD WHEAT (*TRITICUM AESTIVUM* L.) VARIETIES

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The objectives of our study was to analyze the impact of *rht* genes on yield and grain zinc concentration and to access the molecular diversity in 15 Indian bread wheat cultivars released before and after green revolution. There is a strong positive correlation between grain yield and year of release in the experimental material. However, small but statistically significant negative relationships exist between the time of release and the concentrations of grain zinc, and total phosphorus. Genotyping of the wheat varieties was performed by using 54 wheat microsatellite (SSR) markers, derived from each wheat chromosome. The value of average polymorphic information content for these SSR markers was estimated to be 0.36. The Genetic Similarity (GS) coefficient for all possible pairs of varieties ranged from 0.34 to 0.90, indicating the presence of considerable range of genetic diversity at molecular level. The dendogram prepared on the basis of unweighted pair-group method of arithmetic average algorithm grouped the 15 wheat varieties into three major clusters. Clustering and sub clustering of the accessions does not coincide with the grain zinc assimilation and year of varietal release.

# PLANT REGENERATION AND MICRO PROPAGATION STUDIES USING TWO TURKISH BROAD BEAN CULTIVARS FOR BREEDING

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Broad bean plant *( Viciafaba L.)* is a leguminous plant that is an excellent source of protein for human consumption and is used in the development of animal feed. It can also play an important role in enrichment of soil with nitrogen fixation. Likewise , the challenges of pollination ,limited genetic pool, has resulted in limitations to develop a reliable system for the regeneration has resulted in slow progress in breeding new varieties. Development of an efficient gene delivery technology and the development of a suitable regeneration system is needed to supplement conventional breeding programs*. This can be accelerated by direct or indirect organogenesis and* embryogenesis using direct or indirect tissues like like callus, depending on internal and external factors of plant. Due to release of high amounts of phenolic compounds, broad bean is known as recalcitrant, tenacious and difficult due to regenerate. In order to solve the above- mentioned issues, the study made use of embryonic axis of two cultivars raised in Turkey namely Filiz 99 and Eresen 87 for micro propagation. The embryos were cultured on MS medium containing 7 different concentrations 0 , 0.05 , 0.15, 0.25 , 0.35 , 0.45 , 0.55mg /l TDZ. Maximum number of 5.33 and 3 shoots per explant were obtained on cv. Filiz99 and Eresen87 on MS medium containing 0.15 mg / l TDZ. . Three weeks after the shoots were rooted on MS medium containing 1 mg/l IAA. Thereby, the rooted plants were transferred to pots containing peat under controlled conditions in the greenhouse to acclimatize the plants. Acclimatized plants flowered and set seeds under external conditions.

**Keywords :** Broad bean, embryo, Regeneration

# OBTAINING NEW MAINTAINER LINES FROM CMS PLANTS WITH TRADITIONAL BREEDING METHODS IN SUNFLOWER

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Today, hybrid sunflower varieties are used in order to take advantage of heterosis in sunflower seed business. The quickest and easiest way of having the desired these features in a single plant (hybrid) is, collecting these traits on CMS and Restorer lines separately and merge by the crossing of that selected lines. Initial (introduction) materials are obtains from in various research organizations, local varieties and public lines. But, resulting in the use of these materials is mostly hard to provide a wanted hybrid combinations to cover present market requirements. In that reason, usage of the commercial hybrids to enrichment present genetic materials (germplasm), for the components of yield, quality and resistance to biotic and abiotic stress factors, is very common issue in plant breeders. Although existence of cytoplasmic male sterility factors in commercial sunflower varieties, plants are becoming fertile by the suppression of dominant Rf genes in cell nucleus. Only restorer (male) lines can be developed from selected plants of the populations because of the CMS factors in cell and dominant Rf gene in nucleus. In this study, shows how to transfer features of the cytoplasmic male sterile plants to the new maintainer lines with traditional breeding methods.

# NEW WAY TO DEVELOP AN ECONOMIC HEALTHY FOOD BASED ON OATS EXPLOITATION IN MOROCCO

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Knowing that Morocco does not have data about the healthy food or a food guide to estimate the value of daily food, and to contribute to built healthy population, the main goal will be the development of a food-based health natural resources of Moroccan origin. Continuous development of new functional foods is the response of science and technology to consolidate consumer awareness regarding health and the role of foods for improving life quality. Long known for its benefits on blood cholesterol, diabetes, hypertension as well as obesity, while promoting the growth and balance of the gut microflora, Oats is becoming popular as part of a healthy diet and new oat products emerge at the functional food market. The large distribution and important nutritive value of cereals have focused the attention on their use as raw materials for the development of new economic healthy foods. It is also noticed that Oats and barley are known as major sources of beta-glucan, which are considered as the main functional component of cereal fibbers. The objective of this study is to act scrupulously through the development of a food product meets the allegation healthy nutrition. The laboratory model for the development of oat drink was based on estimation and modelling to predict the conditions for performing this product.

**Keywords:** Oats, formulation, health food.

# DETERMINATION OF YIELD AND AGRICULTURAL CHARACTERS OF SOME F6 SOYBEAN LINES AS A MAIN CROP UNDER CUKUROVA REGION CONDITIONS

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This study was conducted to determine yield and agricultural characters of some F6 soybeans lines and varieties as a main crop in the Cukurova region conditions. ÇU04-07, Adasoy, ÇU04-74, ÇU04-53, ÇU04-45, ÇU04-34, ÇU04-01, ÇU04-67, Nazlıcan and ÇU04-08 were used as a material. This study was conducted in the East Mediterranean Agricultural Research İnstitute's experimental area in the randomized complete block design with three replications in 2010. In this study, seed yield, planth height, first pod height, days to maturity, 1000 seed weight, lodging, charcoal rot, oil content and protein content were observed. According to the results , plant height ranged from 101.5 to 137.7cm, first pod height ranged from 2.9 to 5.2 cm, 1000 seed weight ranged from 142,5 to 199,1 g, lodging ranged from 1.2 to 3.2, charcoal rot ranged from 1.7 to 2.3, days to maturity ranged from 132 to 136 day, seed yield ranged from 395.9 to 538.1 kg/da, oil content ranged from %21.4 to %23.0 and protein content ranged from %33.7 to %38. According to the seed yield, the results indicated that ÇU04-07 can be grown as a main crop in the Çukurova region conditions at the future.

**Key words:** soybean, yield, oil content, protein content.

# DETERMINATION OF HETEROTIC EFFECTS FOR SIGNIFICANT AGRONOMICAL AND TECHNOLOGICAL PLANT CHARACTERS IN ST 468 X DP 388 COTTON CROSS COMBINATION

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This investigation was conducted to determine heterotic effects and combination suitability for significant agro-morphological and technological plant characters in East Mediterranean Research Institute, in 2011. In this study ST 468 and DP 388 cotton varieties which were commonly grown  Southeast Anatolian Region and Mediterranean Regions respectively and their $F_1$ cross combination were investigated. While pozitive heterotic effects determined for number of sympodial branch and number of boll, negative heterotic effects were determined for number of nodes first sympodial branch, height of first sympodial branch and lint yield. No heterotic effect was determined for the remained plant characters. DP 388 cotton variety was superior for plant height, first sympodial branch, number of  bolls and lint yield compared to the ST 468 and ST 468 was superior for number of sympodial branch,  node number of first sympodial and ginning turnout to DP 388.

# S1 RECURRENT SELECTION METHOD IN THE POPULATION OF ADAPOP 11 SILAGE CORN

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It has been indicated in the literature of corn breeding that the most important phase of the hybrid corn improvement programs is "To Obtain Inbred Line", and that inbred lines are derived from the improved populations which were selected as baseline (materials exposed to dust in the open air, $F_2$ generations of the synthetic, composite and hybrid varieties). Consequently, one of the most significant steps of the breeding programs is to develop source material. Therefore, Adapop 11 population for silage has been composed in the year 2008 in order to procure $S_1$ source material for "Breeding Researches for Silage Corn for Marmara Region" implemented by Directorate of Sakarya Corn Research Station. "$S_1$ Repetitive Selection Method" has been used in said population. In order to see the progression, "Yield Test for Silage Population" (t test) has been set up in İzmir and Sakarya in 2012 which consist of Adapop 11 $C_0$ and Adapop 11 $(S_1)$ $C_{1.}$ In İzmir, the results for Adapop 11 $C_0$ were detected as follows: green plant yield 4163 kg.da$^{-1}$ , dry substance yield 1821 kg.da$^{-1}$ , ear plant ratio 11 %, plant height 234 cm, leaf stem ratio 17 %, while the results for the Adapop 11 $(S_1)$ $C_1$ were as follows: green plant yield 4116 kg.da$^{-1}$, dry substance yield 1996 kg.da$^{-1}$, corncob plant ratio 13 %, plant height 239 cm, leaf stem ratio 14 % . In Sakarya, the results for Adapop 11 $C_0$ were detected as follows: green plant yield 7266 kg.da$^{-1}$ , dry substance yield 2577 kg.da$^{-1}$ , earplant ratio 22 %, plant height 234 cm, leaf stem ratio 97 %, while the results for the Adapop 11 $(S_1)$ $C_1$ were as follows: green plant yield 6957 kg.da$^{-1}$, dry substance yield 2464 kg.da$^{-1}$, corncob plant ratio 25 %, leaf stem ratio 113 %.

**Key words:** Corn for silage, Adapop 11 population, S1 recurrent selection.

# SAFFLOWER (*Carthamus tinctorius L.*) BREEDING ACTIVITIES AT TRAKYA AGRICULTURAL RESEARCH INSTITUTE

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Safflower is an alternative oil crop in Turkey. Safflower planted area is about 50-60 thousands hectares in Turkey. Some of the main obstructions in safflower production in Turkey are low oil content, diseases and insects. The varieties in production have an oil content of about 28-32 %. They also are susceptible to safflower rust (*Puccinia carthami*), alternaria leaf blight (*Alternaria spp*.) and safflower fly (*Accanthiophilus helianthi*). In safflower, the breeding programme was started in 2000 and has been executed in two different oil types, oleic and linoleic. Each year, about 35 materials in oleic types and 250 materials in linoleic types introduced from around the world are observed in observation-crossing blocks. Among the materials found promising, about 15 crossing combinations in total are made each year both in oleic and linoleic type safflowers. The main objectives of the safflower breeding programme at Trakya Agricultural Research Institute are to develop new varieties which have high yielding capacity, yield stability, high oil content, wide adaptation capacity, resistance to diseases and insects prevalent in the region. Pedigree method was utilized in segregating populations getting after hybridization. Each year about 500 single plants are selected. The preliminary yield and yield trials were set up only in Edirne (headquarters) location. Three different locations (Edirne, Kırklareli and Tekirdag) were utilized for safflower regional yield trials. As a result of safflower breeding programme, two lines (TRE-ASL09/14 and TRE-ASO12/08) have been developed so far. Both of them were put in the state registration trials after evaluation of their performance in the regional yield trials. They both had higher oil content and yield than the check varieties in 2012. One of them was registered in 2013 and named as “LINAS”. This variety is linoleic type and has an oil content of 37-38 % at dry basis (at 0 % moisture). The second line developed is an oleic type variety which has an oil content of 40 %. It also has an oleic fatty acid content of 73-75 %. When this line is registered it will be named as “OLAS”. The performance of both varieties are also acceptable in terms of the results of regional yield trials in 2013. Besides these two lines, bulk harvested many new lines in F7 also have been developed both in oleic and linoleic types. Their oil contents are near 40 %. In oleic types, oleic fatty acid contents are also near 80 %. These lines are at preliminary yield trials in 2013 growing season. Some of them will be suggested for registration if their performance are better than the check varieties in coming years (2013 and 2014 growing season).

# FAST AND EASILY APPLICABLE QUALITY PARAMETERS FOR SOFT WHEAT BREEDING

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In soft wheat using industry that is fast-growing and has a large export potential, unavailabilty of wheat required for appropriate flour production is one of the most important problem in Turkey. Wheat developing studies are very important to eliminate this problem. Soft wheat developing studies demanded by industry in bread wheat breeding material have been continued in Transitional Zone Agricultural Research Institute since 2003. This study was done to determine some quality parameters which can be helpful to breeding studies in terms of soft wheat quality evaluation. 24 material, consist of 19 advanced lines and 5 varieties and planted both irrigated and rainfed conditions, were used in the study. Physical quality properties, whole meal, milling and flour properties, starch gelatinization and thermal properties, proportions of protein fractions, dough rheological properties, biscuit physical and sensory properties were evaluated. According to the results of the study pearling index, PSI hardness, breaking flour yield, damaged starch, Zeleny sedimentation value, solvent retention capacity-water, sucrose, sodium carbonate and alkali water retention capacity analyses were determined as fast and easily applicable quality parameters for soft wheat quality evaluation in breeding.

**Key Words:** Breeding, soft wheat, quality parameters, Transitional Zone

# NEW SOURCES OF RESISTANCE TO THE COWPEA WEEVIL (CALLOSOBRUCHUS MACULATUS *F.*) IN CHICKPEA (*CICER ARIETINUM* L.) ACCESSIONS

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The cowpea weevil (**Callosobruchus maculatus *F.***) is one of the most damaging insect pests on chickpea (*Cicer arietinum* L.) seeds. The pest is capable of damaging 50-60% chickpea seeds in a 6-month storage period. The aim of the current study was to compare resistance characteristics of new sources of chickpea accessions for cowpea weevil seed damage. The number of eggs laid (TNE), emerging adults (EA) and percent seed weight loss (SWL) parameters were measured under choice and no-choice conditions for eight accessions of chickpea. Under no-choice conditions, two new sources (AWC 304; **Cicer echinospermum** and AWC 603; **Cicer echinospermum****reticulatum*) showed minimal egg laying without emerging adults and did not suffer from SWL. On the other hand, susceptible accession CA2969 (*Cicer arietinum* L.) suffered 52% SWL with highest TNE and EA. Furthermore, a previously reported resistant accession, ICC4969 (*Cicer arietinum* L; a desi type) displayed 16.9% SWL with moderate TNE and EA. Under choice conditions, while AWC304 and AWC603 were not preferred for egg laying at all, CA2969 and YAR (*Cicer arietinum* L) were the most preferred seeds after, AWC602 (**Cicer** *reticulatum),* AWC999 (**Cicer isauricum)**, ICC4969 and AWC 613 (**Cicer** *reticulatum*) accessions. Given the fact **Cicer echinospermum** is cross compatible with cultivated chickpea, the immunity level resistance in AWC 304 and AWC 603 accessions for cowpea weevil can be utilized in chickpea breeding programs.

**Keywords: Callosobruchus maculatus,** chickpea, resistance, choice, no-choice.

# POLYMORPHISM STUDY IN RILS CREATED BY TOSUNBEY X TAHIROVA 2000 CROSS

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Abiotic and biotic stresses direct plant breeders to identify new traits and genes for wheat improvement. In this study, we created 245 RIL lines using Turkish bread wheat cultivars Tahirova 2000 and Tosunbey. They both have relatively higher drought tolerance and also are rust and powdery mildew resistance. Hence we screened these parents with molecular markers, such as SSR, ISBP, COS, and SRAPs to identify polymorphism. A total of 483 diverse molecular markers were used for the polymorphism study. Out of the 99 (29 of them were from 1AL wheat chromosome and 24 of them were from 5D wheat chromosome) SSR markers, 19 was found to be polymorphic among the parents. Out of the 77 different combinations of SRAP markers, only 3 of them were polymorphic. The least polymorphism was seen for the ISBP and COS markers. A total of the 295 1AL wheat chromosome ISBP primers were used to screen parents and only two of them were found to be polymorphic. A total of 11 5D COS markers was also used and two of them showed polymorphism between parents. We are currently working on screening RILs using these polymorphic markers. These markers will be used for marker assisted selection in wheat breeding programs.

# DEVELOPMENT OF COTTON LINES WITH SUPERIOR YIELD AND FIBER PROPERTIES THROUGH CROSSING OF PARTIAL INTERSPECIFIC LINES WITH COMMERCIAL CULTIVARS

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Cotton (*Gossypium* spp.) is one of the most important crops worldwide providing natural fiber for the textile industry and cottonseed. The main objective of the specific project was the improvement of stability of partial interspecific cotton lines (PIL) with increased lint production and enhanced fiber quality traits through crossing with commercial varieties. The PIL were produced through pollination of $F_1$ hybrid (*G. barbadense* x *G. hirsutum*) with *Hibiscus cannabinus,* followed by selection for high yield and superior fiber quality properties until the 6th parthenogenetic generation ($Pa_6$). The application of this specific methodology had as a result the production of high yielding cotton lines with outstanding fiber qualitative characteristics but with unstable performance. For this reason, a 3-year backcross scheme was applied, using four PIL ($PIL_1$, $PIL_2$, $PIL_3$ and $PIL_3$) as maternal parents and three commercial cultivars (Celia, Acala and 4S) as pollinators for three consecutive growing seasons. At the last year, the offspring of the crosses formed 12 families that were evaluated with the three commercial cultivars and a mixture of seeds of the crosses from the previous generation in a honeycomb design R-16. The experiment was established at the Farm of the Aristotle University of Thessaloniki in Greece. All cotton families displayed increased morphological uniformity and higher germination ability in comparison with the PIL, an indication that the stability of PIL could be increased through crossing with commercial cultivars. Moreover, self plants that combined high yield with superior quality properties (fiber strength and length) were selected for further improvement.

# RELATION OF COMPONENT CONTENT OF GLIADIN WITH BAKING QUALITY OF WHEAT GRAIN

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One of the major difficulties of bread wheat breeding is the creation of varieties that could realize the potential productivity in the same growing conditions, thus forming stable grain quality indicators at the high level of standard requirements. Therefore, genetic aspect of breeding needs not only more effective methods of assessment of wheat quality, but also genetic markers for these traits to use in the selection of pairs for crossing, as well as for the selection of genotypes from hybrid population. The material for the study included 27 varieties of bread wheat created by Azerbaijan Farming Institute. As a result of studying the role of allelic variants of gliadin coding loci in grain quality formation it was found that the presence of block components of gliadin coding loci Gld 1A5 in genotypes leads to increased gluten content, sedimentation indicator, bread volume compared to genotypes containing block component Gld 1A4. No differences were found among genotypes for protein content. Based on a comparative analysis of genotypes with the presence of block components Gld 1A5 and Gld 1A6 it was shown that Gld 1A5 produced more qualitative wheat grain. The study found that the varieties with allelic blocks of gliadin components Gld 1A4 and Gld 1A5 formed a high baking quality of grain compared to varieties whose genotype content block components Gld 1A6. Also, the study of block components Gld 1B3 showed that this locus leads to poor quality of wheat grain, but the level of protein and gluten content higher than the genotypes with block components Gld 1B1. We found out that the presence of Gld 6A4 resulted in better baking quality compared with the genotypes with block components Gld 6A1.

# EARLY SELECTION FOR HIGH SPIKE FERTILITY IN BREAD WHEAT

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Early selection for high spike fertility (SF), combined with rapid development of advanced lines with high SF, may contribute to increase the efficiency of the breeding process and, ultimately, grain yield.  In order to ascertain the effectiveness of selection for high SF in the $F_2$ generation followed by generation advance without selection through the single seed descent (SSD) method, SF was determined under field conditions in 143 $F_2$ plants from a cross between varieties with contrasting SF (Baguette 10 / Klein Chajá) and in the derived $F_5$ and $F_6$ generations. At physiological maturity, all spikes from each $F_2$ plant or 15 spikes per plot in $F_5$ and $F_6$ lines were cut at the lowest spikelet level, air-dried and weighed. After threshing, grains were counted and weighed. Spike fertility was calculated as the quotient between grain number and spike chaff dry weight. Broad sense heritability estimated by the parent–offspring regression was 0.34 and 0.26 respectively for $F_2$-$F_5$ and $F_2$-$F_6$. Realized heritability, using a 15% selection intensity, was 0.39 in the $F_5$ generation and 0.28 in the $F_6$ generation. These results indicate that (1) SF is a moderately inherited trait, and (2) early selection for high SF without further selection yields advanced lines with increased SF respective to the population mean.

# DETERMINATION OF YIELD PERFORMANCES AND STABILITY ANALYSIS OF SOME RICE CULTIVARS GROWN UNDER THE OSMANCIK CONDITIONS

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This study was conducted in Çorum (Osmancık County) during two years, in 2009 and 2010 with three replications, to determine yield performance, stability analysis and quality values of 12 rice cultivars released in Turkey (Osmancık 97, Neğiş, Aromatik-1, Beşer, 7721, Halilbey, Gönen, Karadeniz, Kızılırmak, Koral, Durağan ve Şumnu) under the conditions of Osmancık County. Cultivar Osmancık 97 had the highest yield with 805 kg/da, followed by Beşer with 788.5 kg/da. The lowest yield was obtained from cultivar Neğiş with 614.8 kg/da. Quality and yield components such as yield, plant height, and panicle length, grain number per panicle, 1000 grain weight, lodging and head rice yield were examined individually during study. Varieties stability parameters have been identified.

**Keywords:** rice, yield, quality, stability

# MICROARRAY ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES UNDER WATER DEFICIT STRESS IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.)

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Cotton is the most important textile plant in the world and is one of the most important crops for the production of oilseed. *Gossypium hirsutum* L., known as upland cotton, is the most widely planted species of cotton, worldwide. Because of the anticipated increase of agricultural water demand, crops should be developed that use less water or use water more efficiently. Recently, microarray-based gene expression analysis has commonly used to decipher genes and genetic networks controlling the traits of interest. In this study, identification of differentially expressed genes in response to water deficit stress in cotton were investigated. Fourteen cultivars of *Gossypium hirsutum* L., were subjected to drought stress; two cultivars, BA525 and TamcotSP23, were selected as being the most tolerant and most sensitive to drought stress, respectively. Affymetrix microarray and Cotton Genome Array GeneChips were used. Total RNAs were extracted from cotton leaves, and hybridizations were done. Analysis was done based on GeneChip Expression Analysis Technical Manual of Affymetrix. Statistical analysis was performed on GeneSpringGX program. Totally, 221 and differentially expressed transcripts were determined. The analysis of physiological measurements was supported gene expression profiling studies. A subset of differentially expressed transcripts was verified using reverse transcription-polymerase chain reaction (RT-PCR). This study demonstrates complex mechanisms of polyploid cotton's transcriptome response to water deficit stress. The identified genes will provide candidate targets to study drought characteristics of cotton at the molecular level.

**Keywords:** Cotton, drought, microarray, gene ontology.

**Acknowledgement:** This study was supported by TÜBİTAK-TEYDEB/7090874 Project.

# DETERMINATION OF GRAIN YIELD POTENIAL OF SINGLE, THREE-WAY AND DOUBLE CROSSES CORN

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This research was conducted to determine comparative grain yields of single, three way and double crosses of maize in Çukurova Agricultural Research Institute. In the study, 6 single, 12 three way and 6 double crosses corn derived from four dent homozygous inbred lines developed by Çukurova Agricultural Research Institute were used as trial material. Combined analysis of variance indicated that there were significant differences among the single, three way and double crosses types. The yield levels of all hybrids varied from 944 to 1362 kg da$^{-}$1 and average grain yield was 1171 kg da$^{-}$1. The highest grain yield was proved from three way cross (3*4)*1 and the lowest grain yield was proved from three way cross (2*3)*4. According to results of research, generally higher grain yield were obtained from cross of parent which is numbered 1 but lower grain yield were obtained from cross of parent which is numbered 4. Generally three way crosses gave grain yield higher from double crosses and single crosses. But some single crosses and double crosses were in the same group as statistical with three way crosses in term of grain yield.

**Key Words:** Hybrid Corn, Single Cross, Three Way Cross, Double Cross and Grain Yield

# DETERMINATION OF CORRELATIONS BETWEEN GRAIN YIELD AND YIELD COMPONENTS OF SINGLE, THREE WAY AND DOUBLE CROSSES CORN

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This research was conducted to determine between grain yields and yield components of single, three way and double crosses corns. In the study, 6 single, 12 three way and 6 double crosses corn derived from four dent homozygous inbred lines developed by Çukurova Agricultural Research Institute were used as trial material. In the study, it was not found statistical difference between yield and yield components for coefficient of correlation in terms of characters studied such as time emergence of ear tassel, plant height, first ear height, stem diameter, number of kernels per ear and kernels weight per ear. It was found statistical difference for coefficient of correlation between yield and ear length, 1000 kernel weight and cob diameter. The highest (0.70) and the lowest (0.06) correlations were observed in the parental and their single crosses progeny in terms of ear diameter and grain yield respectively. Our results showed that inbred lines having high grain yield does not necessarily lead to high yielding single crosses. Only plant and ear traits of inbreed lines were not good indicators for their single cross hybrids in determination of their performance.

**Key Words:** Hybrid Corn, Cross Typees and Correlations

# VARIATION IN MORPHINE OF SIX TURKISH OPIUM POPPY (*Papaver somniferum* L.) LINES

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Opium poppy (*Papaver somniferum* L.) has two major products: alkaloids in the capsules and the seeds. It is known that opium poppy today contains alkaloid in great quantities. Opiate alkaloids and their synthetic derivatives are widely used in medicine which are produced in hundreds of tons for the medicine industry [1, 2]. The study aimed to screen the capsules of six Turkish opium poppy lines to evaluate their morphine percentage. The trial was carried out at the Experimental Fields of the Agronomy Department, Faculty of Agriculture of Ankara University, Turkey during 2010-2012. The materials were collected from opium poppy collections in the department. All seeds were sown during first week of October and harvested during second week of July during three years of experimentation to investigate the variation of morphine content. During first year hairless stem and strong capsule types were selected and sown followed by. Alkaloid analysis was performed at the laboratory of the alkaloid factory at Bolvadin province of Turkey in three years. Morphine ratio of six different lines were determined. The results showed that the avrage of morphine contents of lines ranged 0.731-0.851%, 0,813-1,147% and 0.815-1.142% during 2010, 2011 and 2012 respectively. In conclusion, these opium poppy lines could serve as major source of morphine in future.

# DETERMINATION OF HETEROSIS AND HETEROBELTIOSIS VALUES FOR YIELD AND YIELD COMPONENTS OF HOMOZYGOUS MAIZE INBRED LINES

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This research was conducted to determine heterosis and heterobeltiosis values for yield and some yield components on four homozygous maize inbredlines in Çukurova Agricultural Research Institute. In the study, 6 single crosses corn derived from four dent homozygous inbred lines developed by Çukurova Agricultural Research Institute were used as trial material. Heterosis and heterobeltiosis values were investigated. Research data indicated that the highest heterosis ratio, estimated based on mid-parent was % 167,07 for grain yield, while the lowest heterosis ratio estimated based on mid-parent was % -4,23 for time emergence of ear tassel. The highest heterobeltiosis ratio, estimated based on higher parent was % 96,67 for grain yield, while the lowest heterobeltiosis ratio estimated based on higher parent was % -5,88 for time emergence of ear tassel. In this study materials were found hopeful in term of source material for breeding studies because of hybrids showed that high heterosis and high grain yield.

**Key Words:** Hybrid Corn, Heterosis, Heterobeltiosis and Grain Yield

# DETERMINATION OF RESISTANCE OF SOME ADVANCE BREAD WHEAT LINES GENOTYPES TO COMMON BUNT (*TILLETIA* SPP.) DISEASES

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Bunt diseases (*Tilletia* spp.) cause yield losses in wheat. In Central Anatolian Plateau of Turkey wheat is affected by bunt diseases. The aim of the study was to determine reactions to bunt diseases using artificial inoculation in Central Anatolian conditions. Twenty five bread wheat genotypes developed by Central Research Institute for Field Crops (CRIFC) in irrigate advance yield trial were evaluated for bunt in İkizce/Ankara Turkey under artificial epidemic condition. Genotypes were sown by hand in 1 m long row, with 3 replications on 2011–2012 growing season and cv. Yakar was planted as susceptible check in İkizce - Ankara, Turkey. The evaluation was done percentage of infected spikes in the total spike. As a result, two (8%) of the genotypes were determined resistant (1-10 %), one (4%) of the genotypes were determined moderate resistant (11-25 %), while twenty two (88 %) genotype were determined as susceptible (%41-100) infected heads. The results indicate that there are resistance genotypes of bunt diseases. The resistant genotypes can be used as genetic resources among the germplasm.

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# DETERMINATION OF RESISTANCE OF SOME TURKISH BREAD WHEAT GENOTYPES TO YELLOW RUST AND STEM RUST

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Yellow rust (*P. striiformis* f. sp. *tritici)* and stem rust *(P. graminis* f.sp. *tritici)* cause yield losses in wheat. In Central Anatolian Plateau of Turkey wheat is affected by all the Yellow rust (*P. striiformis* f. sp. *tritici)* and stem rust *(P. graminis* f.sp. *tritici* . The present study was planned to screen that twenty five bread wheat genotypes developed by Central Research Institute for Field Crops (CRIFC) in irrigate advance yield trial were evaluated for adult plant resistance to local yellow and stem rust races in Turkey under artificial epidemic conditions. Genotypes were sown by hand in 1 m long row, with 2 replications on October 24, 2011 and cv. Little Club was planted as susceptible check in İkizce - Ankara, Turkey. The diseases were scored on June 20 and on July 5, 2012. Reaction types and rust levels based on the modified Cobb scale were recorded at both locations. Coefficients of infection (CI) were calculated and values below 20 were considered resistant. Seventeen (68 %) genotypes were resistant to the local *Pst* race (virulent on seedlings of Lee, Heines Kolben, Heines Peko, Kalyansona, Sonalika, Federation*4/Kavkaz and Avocet S), eleven (44 %) genotypes were resistant to the local *Pgt* population (avirulent on seedlings with Sr24, Sr26, Sr27 and Sr31) in İkizce - Ankara, Turkey.

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# EFFECT OF GROWTH REGULATORS ON TISSUE CULTURE PARAMETERS IN RICE (*Oryza sativa* L.)

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The aim of this study which was conducted in Ankara University, Faculty of Agriculture, Department of Field crops, Biotechnology Laboratory, was to determine the effects of growth regulators on tissue parameters in rice. In this study, mature embryos of three rice cultivars (Aromatik, Baldo ve Karadeniz) were used as plant material, in different growth regulators such as 2,4-Dichlorophenoxyacetic acid (2,4-D) and Picloram. For callus induction, mature embryos were placed with scutellum upwards on three different medium (MS mediums which involves; as control hormon-free MS-0, MS + 2 mg/l 2,4-D, MS + 2.5 mg/l Picloram) in sterile Petri dishes for two weeks at 26±1$^0$C and continuous darkness. Following their incubation; the calli were transferred to hormon-free MS-0 medium for regeneration. According to obtained results, the effect of growth regulators and genotypes on callus induction and plant regeneration in rice were found to be statistically significant

# EFFECT OF HIGH SALT CONCENTRATIONS ON $H^+$-PUMPS IN ROOT SYSTEM AND NADP-MALATE DEHYDROGENASE ACTIVITY IN LEAVES OF DIFFERENT WHEAT GENOTYPES

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NADP-malate dehydrogenase (NADP-MDH) catalyses oxaloacetate conversion into malate in the presence of NADPH. Physiological function of the enzyme is regulated by light and its activity is found to be higher in young leaves than in old ones. The dynamics of change in the enzyme of $CO_2$ metabolism, NADP-MDH in leaves and in the function of root system $H^+$-pumps have been comparatively studied for some wheat genotypes (Garagilchig-2 drought-sensitive, high productive; Azemetli-95 drought-tolerant, high productive; Girmizi bugda drought-tolerant, low-productive) differing in their salt and drought tolerance. In high-productive Azemetli-95 increase of NaCl concentration to 200 mM caused the proportional increase in $H^+$-pump activity ($\Delta H^+$), leaf growth rate ($\Delta V_L$), NAD-MDH activity, soluble protein and chlorophyll (Chl) amount, wheras NADP-MDH activity remained constant. At 200-300 mM concentrations of NaCl $\Delta H^+$ and $\Delta V_L$ were unchanged, NADP-MDH activity decreased. The more pronounced increase in $\Delta H^+$, $\Delta V_L$, NAD-MDH, Chl (a+b) and protein amount at 200 mM NaCl were observed for Girmizi bugda contrary to Qaragilchig-2. Since at 200-300 mM concentrations of NaCl the decrease in $\Delta H^+$ and $\Delta V_y$ and increase in NAD-MDH activity caused the intensification of synthesis of $C_4$ acids (malate, aspartate) in leaf mesophyll cells, even the closure of bundle sheath cells under drought and high salinity conditions did not lead to disturbances of Calvin cycle reactions. As malate and aspartate provide Calvin cycle with $CO_2$ when its intake from atmosphere terminated and gas-exchange weakened. It was found that activities of enzymes involved in $CO_2$ metabolism and the function of $H^+$ -pumps in the root system did not depend on the plant tolerance degree under high salt concentrations. The enzyme isoforms were revealed to follow Michaelis-Menten kinetics. Oxaloacetate and malate being substrates of direct and reverse reactions competitively inhibited each other. Thus, during the direct reaction malate acted as an inhibitor.

# YIELD PERFORMANCE EVALUATION OF DIFFERENT DURUM WHEAT VARIETIES IN MENEMEN CONDITIONS

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This research was conducted under Menemen-İzmir conditions in 2011-2012. 18 spring durum wheat varieties registered in Turkey Costal Zone between 1975-2008 were used to determine yield and other characteristics. Experiment was established in a randomized complete block design with four replicates. In this research, yield (kg/da), spike number in $m^2$, number of tiler, kernel number of spike were investigated. There were significant statistical differences between these characteristics. The yield of varieties changed between 574-762 kg/da. GAP variety was had top scores at yield, in terms of spike number in $m^2$ was Sham 1, number of tiler was Ceyhan 99 and kernel number of spike was Gediz 75 had top scores.

**Key Words:** Durum Wheat, Yield, Spike number in $m^2$, Number of tiler, Kernel number of spike

# INDUCTION OF HAPLOID EMBRYOS AND PLANTS THROUGH IRRADIATED POLLEN TECHNIQUE IN COTTON (*Gossypium hirsutum* L.)

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There hasn't been any effective method for shortening to obtain the pure lines in cotton breeding programs yet. Our studies were carried out to investigate the possibility of inducing haploid embryos and plants through irradiated pollen technique to produce doubled haploids in cotton breeding programs since 2005. In the light of the results of these studies, present study was carried out to determine the most suitable gamma ray dose in 2008. Çukurova 1518 cotton variety was used as the plant material. Flowers were pollinated with pollens irradiated with four different gamma ray doses (40, 50, 60 and 75 Gray) in two different dates. 18 and 21 days old bolls were harvested and 4272 immature seeds were investigated under binocular. The embryos observed at different stages (globular, arrow tips, heart, torpedo, amorphous) were cultured *in vitro*. Depending on the gamma ray doses embryo induction rates were found 19.3%, 13.1%, 5.4%, 3.9% respectively. In the study 441 immature embryos were cultured on modified MS medium (with vitamins of B5 medium and 2mgl$^{-1}$Glutamine). Unfortunately very few of those were converted into plantlets and rooted. From the results of the study, it was concluded that it is needed advanced studies to optimize an efficient regeneration protocol to improve the effectiveness of the method.

***Keywords:*** *Gossypium hirsutum* L., irradiated pollen, haploid

# DETERMINING YIELD AND SOME FIBER TECHNOLOGICAL PROPERTIES OF $F_6$ GENERATION LINES OBTAINED BY HYBRYDIZATION OF COTTON (*Gossypium hirsutum* L.) VARIETIES

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This study was carried out to determine yield and some fiber technological properties of $F_6$ generation cotton lines obtained by hybrydization of different varieties in Cukurova Region. 13 $F_6$ generation cotton lines obtained from 5 different hybrid combinations (DES 119/Flora, DES 119/Carmen, Carmen/DP 388//DP 50, C.Queen/153-F, BA 119/DP 50) and 2 regional standart cotton varieties were used as materials. Those lines evaluated in 2012 as $F_6$ generation were obtained from the hybrydization studies carried out 2006 then selected and maintained according to pedigree selection method. The study was conducted in the East Mediterranean Agricultural Research Institute's experimantal area in the randomized complete block design with four replications in 2012. Seed cotton yield, ginning percentage, fiber lenght, fiber fineness, fiber strenght and fiber maturity were investigated in the study. As a result some of the lines investigated had superior values for yield, fiber lenght, fiber fineness and fiber strenght comparing the control varieties.

**Key Words:** Cotton, Hybridization, Yield, Fiber Quality

# STUDY AND USE OF WHEAT INTRODUCED FROM INTERNATIONAL NURSERIES IN AZERBAIJAN

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The key position on food security maintenance of Azerbaijan belongs to grain production. In this respect leading status has winter wheat which sown areas annually constitute more than 650 thousand hectares. In successful development of effective breeding strategy for a concrete agroecological region of Azerbaijan, along with local collections, the great role have played introduced materials received from International Breeding Centers, such as CIMMYT and ICARDA. The main goal of collaboration with International Centers is realization and improvement of wheat resistant to biotic and abiotic factors of environment for various soil-climatic zones. Since 1995 the Azerbaijan Research Institute of Crop Husbandry, on purpose of ecological testing and selection of advance lines for further breeding works, have introduced 34182 wheat samples. According to the results of the complex estimation more than 2000 advance lines were selected, with distinctive high productivity (8.0 tons/hectare) and drought resistance. These samples were biologically winter and facultative type on seasonality, with high wintering, were resistant and moderate resistant to rust diseases, had short and medium height with medium and late heading periods (110-125 days on 1st January). Samples basically belonged to nurseries FAWWON-IR, FAWWON-SA, IWWYT-IR, IWWYT-SA, RBWYT, WDYT etc. During collaboration 7 wheat varieties were transferred to the State Commission for Testing and Protection of Selection Achievements for realizing. 4 varieties of bread wheat – Azamatli-95, Nurlu-99, Gobustan and Tale-38 were realized, which sown areas constitute more than 300 thousand hectares in the country. The international nurseries received from centers of CGIAR have huge scientific and economic value on realization of new valuable, advance wheat varieties.

**Key words**: winter wheat, International Breeding Centers, productivity

# IMPORTANCE OF PHOTOSYNTHETIC SIGNS FOR THE BREEDING OF HIGH-YIELDING WHEAT VARIETIES

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Improvement of leaf photosynthesis is an important strategy for greater crop productivity. During 60 years of comprehensive investigations on photosynthesis and productivity of various wheat genotypes in natural conditions of cultivation, characteristics and parameters of photosynthetic activity of these genotypes most closely correlating with plant productivity have been established. The overall activity of researches cover physiological, biophysical, biochemical and molecular-genetic bases of plant productivity and also the study of production processes from molecular to the whole plant and sowing levels. The rich Gene Pool, comprising several thousand wheat genotypes, selected from both the ancient, aboriginal varieties of national selection and introduced from *CIMMYT, ICARDA* and other international centers with contrasting photosynthetic traits, productivity and tolerance to water stress, was created. By analysis of parameters and attributes of photosynthetic activity, morphophysiological and agronomic peculiarities, factors of external environment and using the results of study of real and potential possibilities of wheat genotypes the principles that determine an efficient and high yield of the 'ideal' wheat type were developed. The optimum plant height and favorable spatial arrangement of leaves in compact sowings contribute to the effective absorption of solar radiation and development of vegetative and economically valuable organs and activate those key links of productivity, which ultimately determine the high grain yield of wheat variety of the 'ideal' type. High rates of photosynthesis and photorespiration, high activity of primary photochemical processes in conjunction with favorable phenotypic traits, the optimum leaf area index and architectonics are also crucial for the breeding of high grain-yielding wheat genotypes. As a result of realization of fundamental researches a large number of durum and bread wheat varieties with high grain yield and excellent grain quality were developed.

**Key words:** photosynthesis, grain yield, Gene Pool, wheat genotypes, field

# MICROPROPAGATION OF *ASTRAGALUS VULNERARIAE* DC – A POTENTIAL PLANT FOR USE IN ARID LAND SCAPING

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TThe genus *Astragalus* (Leguminosae) is represented by approximately 380 species in Flora of Turkey and all of them are of economic importance. Perennial endemic legume *Astragalus vulnerariae* DC.(Vulneraria-milkwetch*)* has attractive yellows flowers and is endemic to the arid lands of Marmara and Central Anatolian region in Turkey. Vulneraria-milkwetch has very high horticultural potential. The seeds that germinate face difficulties in competing with weeds during the initial years of growth. Plant biotechnology can be used as an alternative to solve this problem. Regeneration of *A. vulneraria,* is not reported in any of the previous reports. This study aimed to induce shoot regeneration and rooting of in vitro micropropagated *A. vulneraria.* which may offer a potential for improvement of the plant that carries importance as an alternative for dry lands urban land scaping in areas receiving limited rainfall. The leaves and hypocotyl segements were used as explant. These explants were cultured on MS medium containing 0.5, 1, 1.5 and 2 mg/l Kinetin and 0.5 mg/l NAA Maximum shoot regeneration frequency and number of shoots per explant was obtained on cotyledon leaf using MS medium containing 2 mg/l Kinetin and 0.5 mg/l NAA. The results showed that the plants could be regenerated and established to external environmental conditions following above mentioned protocol without any difficulty.

**Key words:** Micropropagation, *Astragalus vulnerariae*, acclimatisation, drought

# EVALUATION OF WINTER WHEAT VARIETIES FOR RESISTANCE TO YELLOW RUST IN AZERBAIJAN

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Yellow (stripe) rust of wheat caused by fungus *Puccinia striiformis* f.sp*. tritici* is an important disease and one of the important factors limiting grain yield and quality loss in wheat worldwide. In Azerbaijan, wheat is an economically important crop and yellow rust resistance in wheat has been a major goal of numerous breeding programmes. Genetic resistance is the most economical and environmentally safe control measure, so use of genetic resistance and development of resistant cultivars are very important to control the disease. Identification and selection of novel sources of yellow rust resistance is a preliminary step that forms the basis of developing genetically diverse cultivars. To date 53 stripe rust resistance genes (**Yr1**–**Yr53**) and numerous temporarily designated genes have been reported in wheat. The main objective of our work was to identify effective yellow rust-resistant genes for wheat improvement. Using molecular markers associated with yellow rust resistance *Yr18* и *Yr9* genes, evoluation of 61 bread wheat (*Triticum aestivum* L.) samples was conducted. All plants are taken from Research Institute of Crop Husbandry (Baku, Azerbaijan). PCR amplification of the SSR marker located in the chromosome 7D Xgwm295 (3’GTGAAGCAGACCCACAACAC; 5’/3’GACGGCTGCGACGTAGAG5’) linked to the Yr18 gene showed a fragment of 250 bp only in 40 genotypes. The primer pair of the SSR marker XGWM582 (3’AAGCACTACGAAAATATGAC; 5’/3’TCTTAAGGGGTGTTATCATA 5’) in the chromosome 1B, associated with gene Yr9 amplified a band of 150 bp in almost all genotypes. Unfortunately, these markers did not amplify specific bands in 4 studied genotypes.

**Key words**: yellow rust, Triticum aestivum L., Yr genes

# GENOTYPIC VARIATION FOR DROUGHT TOLERANCE IN WHEAT ACCESSIONS

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Drought is a world-spread problem seriously influencing on crop production and quality. A wide range of strategies, which have been used to enhance the tolerance to drought depend on the genetically determined plant capacity and sensitivity, as well as on the intensity and duration of the stress. Understanding the physiological, biochemical and molecular mechanisms providing drought tolerance is very important in terms of developing selection and breeding strategies. Among crop plants, wheat is often grown in water-limited conditions. Numerous winter durum and bread wheat genotypes were the main targets of this study. Plants were grown in the field conditions in a wide area at the Absheron Experimental Station of the Research Institute of Crop Husbandry under normal irrigation and dryland conditions. Upon dehydration, a decline in total chlorophyll and relative water content was evident in all cultivars, especially in later periods of ontogenesis. Generation sites of superoxide and hydrogen peroxide radicals were studied in drought subjected wheat plants. A certain changes were observed in the composition and content of thylakoid membrane proteins. RAPD-PCR spectra were analyzed in 220 bread and 46 durum wheat genotypes. Using primer P6 (5′ TCGGCGGTTC 3′), the 920 bp fragment was revealed in 234 genotypes. Primer P7 (5′ TCGGCGGTTC 3′) produced a 750 bp band only in 203 genotypes. Results obtained with the use of both P6 and P7 primers match in 74% of analyzed genotypes. In 13 genotypes none of the primers amplified specific fragments. So, these data might be used for future selection stress-resistant varieties.

**Key words:** drought, ROS, chlorophyll, protein, RAPD, PCR, ontogenesis, wheat

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# DROUGHT-INDUCED CHANGES IN ISOZYME PROFILES OF ANTIOXIDANT ENZYMES IN WHEAT CULTIVARS

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Drought stress is a serious problem adversely affecting physiological and metabolic processes, finally diminishing crop productivity. Wheat is essential nourishment for more than 1/3 of the world population and crop yield will be considerably influenced in the perspective of global climate change and limitation of water resources in the environment. The aim of this study was to analyze the effect of soil drought on activities of antioxidant enzymes. Experiments were conducted with 6 contrasting bread (*Triticum aestivum* L.) and durum (*Triticum durum* Desf.) wheat cultivars grown under field conditions at the Absheron Experimental Station of the Research Institute of Crop Husbandry. Native polyacrylamide gel electrophoresis (PAGE) revealed the presence of 1 isoform of catalase, 9 isoforms of superoxide dismutase, 7 isoforms of ascorbate peroxidase and 7 isoforms of glutathione reductase in wheat leaves during drought. The electrophoretic separation showed that the amount of antioxidant isoforms varied in leaves depending on the wheat varieties, duration of drought and stages of leaf development. The least amount of APX was observed at the beginning of the flowering phase (4 isoforms), the most-at the end of the wax ripening phase (7 isoforms). Mn-, Fe-, Cu/Zn containing isoforms of one of the key antioxidant enzymes - superoxide dismutase-were shown to function in wheat plants. It was concluded that drought caused increases in APO, SOD, CAT and GR activities in wheat leaves compared with their initial levels. Increases in APO and GR activities were more pronounced, indicating an intense work of the ascorbate-glutathione cycle, which breaks down $H_2O_2$.

**Key words:** drought, antioxidant enzymes, wheat

**Acknowledgement**

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# EFFECT OF WATER STRESS ON ACTIVITIES OF SUCROSE-METABOLIZING ENZYMES IN GRAINS OF WHEAT (*TRITICUM AESTIVUM* L.) DURING GRAIN FILLING

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Wheat (*Triticum aestivum* L.) occupies an important place among cereals and it serves as a staple food for about 35% of the world population. Drought, being the most important environmental stresses, severely impairs plant growth and development, limits plant production and the performance of crop plants, more than any other environmental stresses. Starch in the endosperm of wheat is the major form of carbon reserves and comprises 65% to 75% of the final dry weight of the grain. The enzymatic activities are necessary for starch synthesis and amylopectin structure, which include sucrose synthase (SuSase), ADP-glucose pyrophosphorylase (AGPase), soluble starch synthase (SSS), granule bound starch synthase and starch-branching enzyme (SBE). The four genotypes *i.e.* two tolerant (WH 1021 and WH 1080) and two susceptible (WH 711 and HD 2687) were raised in late sown conditions under irrigated and drought stress conditions. Water stress was created by withholding the irrigation at anthesis stage. Analysis of data reavealed that during grain development, starch metabolising enzymes *i.e.* sucrose synthase, ADP-glucose pyrophosphorylase, soluble starch synthase, starch branching and starch debranching enzyme increased in all genotypes and reached their peaks but their maximum peak values and time at which they reached were different in different genotypes. Increase in sugar content was found under drought stress conditions in comparison to irrigated conditions at different days after anthesis. Water stress caused a marked reduction in starch content of grains. In all genotypes level of ADP-glucose and UDP-glucose increased up to 21st DAA and then declined. Physiological parameters like relative water content, osmotic potential, chlorophyll content, chlorophyll fluorescence, cell membrane thermostability and canopy temperature depression declined under drought stress conditions over irrigated conditions. Quality parameters like moisture content and crude fibre decreased whereas, sedimentation value, gluten, protein content and grain hardness increased under drought stress condition over irrigated conditions. Yield parameters like grain number per spike, grain weight, number of productive tillers, biomass per plot and grain yield decreased under drought stress. The reduction in physiological, biochemical, yield and grain quality traits was found to more pronounced in the susceptible genotypes in comparison to the tolerant ones. WH 1021 was adjudged to be most tolerant genotype.

**Key words:** Late sown wheat, developing grains, starch, proteins, enzymes, quality, yield.

# EVALUATION SPAD METER READING AT DURUM WHEAT POPULATIONS UNDER DIFFERENT NITROGEN CONDITIONS

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This study was conducted to evaluate the effectiveness of SPAD-502 chlorophyll meter reading as indirect selection criteria for yield under different nitrogen (N) conditions in durum wheat populations. Six durum wheat parents and their 6x6 half-sib $F_2$ diallel cross populations were grown under zero, normal and high N conditions at 2010-2011 growing season. SPAD readings at anthesis of $F_2$ populations were affected by nitrogen applications. Genotypic variance of SPAD readings increased from zero N to high N dose. Significant genotypic variations and general combining ability (GCA) effect were observed for plant grain yield at normal N conditions. Significant GCA and specific combining ability (SCA) effect for SPAD readings were found at high N conditions. The results indicate that a high nitrogen condition is the most effective way to detect genotypic differences for SPAD reading among durum wheat genotypes in $F_{2}$. progenies.

**Key words:** *durum wheat, diallel, nitrogen, SPAD reading,*

# GENOMIC SELECTION IN WHEAT BREEDING USING DIVERSITY ARRAYS TECHNOLOGY (DART)

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Grain cereals -mainly wheat, rice and maize- represent a major renewable resource and wheat (*Triticum aestivum* L.) is the most widely grown crop worldwide. Major efforts are underway to improve wheat production by increasing genetic diversity in breeding materials. But the very large size and polyploid complexity of the bread wheat genome have been substantial barriers to genome analysis. DNA-based molecular markers have several advantages over the traditional phenotype trait selection and also new breeding methods relying on high throughput genotyping methods, such as Genomic Selection (GS), assessed in several crops and promise improved efficiency and accelerated genetic gain. GS uses genome-wide molecular markers to predict complex, quantitative traits in plant breeding. In this study, genomic selection of wheat were investigated using Diversity Array Technology (DArT). DArT-Seq markers are Single Nucleotide Polymorphism (SNP) markers which are commonly used for genomic selection. The extracted DNAs were analyzed for genotyping resulting in 1488 genotyped lines with about 10000 high-quality codominant SNP marker allowing to estimate the rate of heterozygosity as well as about 10000 dominant marker for binary evaluation. Using the additional quality scores provided by DArT, the best 7230 co-dominant markers where chosen for forming the initial training population for the genomic selection models. Phenotypic data have been processed using linear mixed models. A unique linear mixed model, accounting for environmental factors and trial designs was used to for each environment. For broad adaption, best linear unbiased predictions (BLUP) for yield and protein content comprising of all environments were calculated. GS models incorporating BLUPs for yield, protein yield, Fusarium and rust resistance have been used to select new wheat cultivars.

**Keywords:** wheat, genotyping, SNP, yield, resistance, BLUP.

**Acknowledgement:** This study was supported by TÜBİTAK-TEYDEB/9110049 Project.

# RESISTANCE TO BARLEY YELLOW DWARF VIRUS IN COMMERCIAL WHEAT VARIETIES OF PAKISTAN

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Viral diseases are considered to be the major limiting factor in crop production globally. Barley yellow dwarf Virus (BYDV) is one of the important disease having a linear relationship in disease incidence and yield loss in wheat. Ninety eight commercial wheat varieties of Pakistan were evaluated to confirm the presence of *Bdv1* gene and *Bdv2* resistant genes in these cultivars. Results revealed that out of 98 varieties, a product 250 bp was amplified in 86 varieties (88%) confirming the presence of *Bdv1* gene which confers field resistance by only inducing slow yellowing, while no product was amplified in 12 varieties (12%) indicating the absence of gene. Same varieties were tested for the presence of *Bdv2* gene which gives the true resistance by restricting cell to cell movement of virus. None of the varieties has expected size of amplified product indicating the absence of this gene. As the *Bdv1* gene induces slow yellowing but does not provide any resistance to varieties so it is essential to incorporate *Bdv2* gene into commercial wheat varieties to provide true resistance against BYDV.

# SAFFLOWER BREEDING RESEARCH and the VARIETIES DEVELOPED by TRANSITIONAL ZONE AGRICULTURAL RESEARCH INSTITUTE

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Safflower is a drought-resistant annual crop having different ways of use. In our country, research on this crop was initiated at Eskisehir Sazova Plant Breeding Station in 1930. As a result of these studies, Yenice and Dincer varieties were registered while the line no. 5-154 has been given seed production permit. Despite long years' research on breeding and agronomy of safflower, breeding program was ended in 1988 due to its failure to create the expected demand in Turkish agriculture. The Institute continued its efforts with genetic stock renewal and multiplication of breeder seed. Breeding research was re-started in 2000, considering the national demands, and line 5-154, which previously had seed production permit, was registered with the name Remzi Bey-05. Thanks to the ongoing breeding program of the Institute, Balci, which is superior to existing varieties in terms of oil content, was registered in 2011. The main objective of the safflower breeding research at Transitional Zone Agricultural Research Institute is to develop varieties meeting demands by producers, consumers and industrial end-users. Selection, crossing and mutation methods are being used in these breeding efforts.

**Key words:** safflower, breeding methods, variety

# POTATO BREEDING IN EASTERN ANATOLIA REGION

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Potato breeding in Turkey has traditionally involved making crosses between pairs of parents which produced as a commercial public variety and introduced material with complementary phenotypic and quality features and this is still the main route to evaluate new cultivars. The aim is to generate genetic variation on which to practice phenotypic selection across a number of vegetative generations for clones with as many desirable characteristics as possible for release as new cultivars.

As well as genotypic variaton potato yielding varies with environmental factors and locations. Eastern Anatolia Region (average altitude is 2,200 m) potato breeding program uses traditional plant breeding techniques and aims to produce superior clones for Eastern Anatolia ecological conditions. It starts with crossings among different pairs of parents to obtain true seeds and then early generation selection (3th-5th year), clonal generations (6th-7th year), regional yield trials (8th year) with 5-10 clones ( min. 2 locations), rapid propagation by tissue culture (9th year), On-farm trials and entry into seed certification system (11-12th year), licensing and seed multiplication (13th year) and distribution to industry (14th year). This article reviews potato variety and clone improvement from 1988 to the present at EAARI, in terms of the needs potato industry and consumer choice.

**Key words**: Breeding, clonal selection, potato industry,

# INFLUENCE OF EPICUTICULAR WAX ON HEAT AND DROUGHT TOLERANCE IN WINTER WHEAT

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High temperature and drought are major constraints to wheat production. Collectively or individually heat and drought are the primary constraints to yield in wheat on a global basis. However, there are certain genotypes that tolerate high heat and drought through various adaptations such as high leaf wax content, leaf rolling and efficient root structure. We hypothesize that high leaf wax content is directly correlated to heat and drought tolerance in wheat in terms of yield, disease resistance and quality stability. For this study, a RIL population derived from TAM 111 and TAM 112 were grown in controlled greenhouse and multiple field locations. In the greenhouse at 10 days after pollination (DAP) plants were subjected to a three-day 38°C/18°C day/night heat stress treatment. Both in greenhouse and field flag leaf and glumes were sampled at 10 DAP for wax analysis. The heritability of wax was low (14%) in combined analysis. As an adaptive trait it varies with environmental conditions. Eberhart and Ecovalence were used to calculate stability analysis. The data collected were being analyzed for co-association between quantitative trait loci (QTL) regulating these traits using SNP markers. This will help to determine the influence of leaf wax on the maintenance of yield performance during heat and drought stress in wheat.

# PLEIOTROPIC EFFECTS OF DWARFING GENES ON GENOTYPES OF WINTER BREAD WHEAT ANALOGUE-LINES

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Dwarfing (*Rht*) genes, especially *Rht8*, *Rht-B1* and *Rht-D1*, have played an important role in "Green revolution" of XX century. Now days about 70 % of worldwide wheat varieties contain the dwarfing alleles of some of these genes. In Ukraine proportions of varieties with the dwarfing genes in spring (30 %) and winter (95 %) wheat are different. Four analogue-lines created on genetic background of well-known Ukrainian varieties with the identified by molecular markers alleles of dwarfing genes were investigated in wide rows and plots during several years. Comparison of the plants grown in the plots and the wide rows has shown the significant differences by all the investigated traits except the weight of one kernel. According to the data of two factor variance analysis the effects of the dwarfing genes on plant height, length of the main ear, number of spikelets in the spike, number of kernels from the main ear, ear density were detected in plots. Lines yield depended on the factor "Year" and the interaction of the factors "Year" and "Genotype". According to the laboratory experiments the dwarfing genes does not lead to decrease of the plant frost resistance, on some genetic backgrounds the plants with two dwarfing genes were more frost resistant than the plants without the dwarfing genes. Winter hardiness data obtained in the field experiments does not significantly differ between the lines with the dwarfing alleles and without them. We have not detected any negative influence of the dwarfing genes on the frost resistance and the winter hardiness.

# USING POLYMORPHISM OF GRAIN STORAGE PROTEINS FOR IDENTIFICATION OF MALTING BARLEY VARIETIES

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This study attempts to identify distributed malting barley varieties and construct their hordein formulae through the polymorphism of storage proteins in grains. The available biotypes and the frequency of their expression were identified in the investigated varieties. The electrophoretic mobility and the molecular weight of the hordein components were determined. The obtained results are the basis for further investigations on the use of biochemical markers in the breeding and seed production of malting barley.

**Key words:** malting barley, hordeins, identification, electrophoresis

# WINTER BARLEY AND OAT BREEDING PROGRESS IN BULGARIA

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The Institute of Agriculture – Karnobat is the main barley and oat breeding center in Bulgaria. The present investigation represents barley and oat breeding activities in the Institute for the period 1961-2012. The survey of the utilized in the breeding program approaches, methods and techniques for: creation of genetic variation, optimization of the breeding process and evaluation of the breeding materials on biotic- and abiotic stress resistance and grain quality, is done. The progress in barley breeding was the creation of lines combining high cold and drought tolerance in one genotype. Other achievement in barley breeding was combination in one genotype of resistance to one or more diseases with good biological and agronomic characteristics. Major oat breeding successes include the development of high-yielding, logging tolerant oat genotypes, which has improved winter hardness. More recently registered Bulgarian varieties of winter feed and malt barley and winter oat are reported. They could be characterized as high yielding with good winter hardness and grain quality, wide adaptation and drought tolerance.

**Key words:** barley, oat, breeding, progress

# EFFECT OF GENOTYPES AND PLANT GROWTH HORMONES ON SOMATIC EMBRYOGENESIS IN PEANUT USING EPICOTYL EXPLANTS

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Epicotyl explants of four peanut varieties were inoculated on callus induction medium (CIM) consisting of MS salts and B5 Vitamins supplemented with 2, 4, 6, 8 and 10 mg/l picloram. Maximum (98.3%) number of explants responded to embryogenic callus induction on 8mg/l picloram. After three weeks the callus was transferred to embryo conversion medium (ECM) consisting of MS salts and B5 Vitamins supplemented different concentrations of 2,4-D (0.1, 0.5, 1.0, 1.5, 2.0 mg/l). Maximum 19.33 embryos/explant were observed in Golden variety on ECM containing 1.5 mg/l 2,4-D. The embryos thus developed were shifted to embryo germination medium (EGM) consisting of MS salts and B5 Vitamins augmented with different concentrations of BAP (0.1, 0.5, 1.0, 1.5, 2.0 mg/l). Maximum (74.72%) embryo germination was observed at 0.1mg/l BAP in Golden variety.

# DETERMINATION OF HETEROTIC EFFECTS OF SEED COTTON WEIGHT PER BOLL IN $F_1$ HYBRIDS DOUBLE CROSS IN COTTON

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Double-crosses, compared to the single-mulattos, a larger wealth of genetic terms (diversity) have, where they are ecologically wider spans, more adaptable to environmental conditions, in other words the general adaptation to the environment (adaptation) are the ability to cause a high particularly in the textile industry overcome many problems that may occur with a mixture of varieties increases the likelihood of success. This study was carried out in order to determine the heterotic effects of investigated properties in the population which created from 45 double cross $F_1$ generation, using the double cross breeding method, in Diyarbakır ecological conditions in 2010. The trials are conducted as complete block design (RCBD) with three replications. In the study boll number was studied. Eighty hybrid cotton combinations had positive and high values heterosis and heterobelitosis in terms of seed cotton weight per boll was determined as promising and future studies that need to be taken into consideration in this hybrid combinations.

**Keywords:** Cotton, double cross, heterosis, heterobeltiosis.

# OCCURRENCE OF *SEPTORIA* LEAF BLOTCH IN ALGERIA AND ASSESSMENT OF WHEAT RESISTANCE

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Septoria tritici (*Mycosphaerella graminicala) and* Septoria nodorum (*Leptosphaeria nadorum)* causal agents of *Septoria* leaf blotch of wheat occur throughout the major wheat growing regions in Algeria. The Septoria diseases are the source of major damage on susceptible varieties on bread and durum wheat. Surveys have been performed during the last decade covered wheat growing areas of eastern and central regions (Annaba, Skikda,Tizi Ouzou, Boumerdes, Algiers) and sub- littoral (Guelma, Souk Ahras, Constantine, Sétif, Mila, Bouira). The disease development was always observed except during 2000-2001 and 2001-2002 (excessive drought conditions). The surveys showed that *Septoria* diseases are more prevalent in coastal areas and sub-littoral where risk is very high. The surveys also revealed the presence of both septoria species (M. tritici and *L. nodorum*), but septoria tritici was more prevalent. Algerian National Wheat improvement Program conducted in collaboration with ICARDA conducts routine screening for resistance to septoria since 2005. A collection of 150 durum wheat and 100 genotypes of bread wheat were tested under natural conditions at two septoria hot spots representing high and low rainfall areas, where the foliar diseases are normally expressed each year under field conditions. Wheat lines that carry resistance to *Septoria* leaf blotch were identified. Resistant lines were tested under controlled condition. Introduced and local germplasm with resistance to septoria were identified.

**Key words**: *septoria leaf blotch, wheat, resistance, survey, Eastern Algeria*.

# VARIATION IN FATTY ACID COMPOSITION OF THREE TURKISH SLIT FLOWER OPIUM POPPY (*Papaver somniferum* L.) LINES

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The opium poppy (*Papaver somniferum* L.) a member of *Papaveracae* family is a multipurpose medicinal or ornamental plant and a source for seed oil [1]. Quality and nutritive value of poppy seeds is based on oil content and mainly polyunsaturated fatty acids [2]. The United Nations recognize Turkey and India as traditional poppy producing countries. The aim of this study was to evaluate the seeds of three different Turkish slit flower opium poppy lines for their fatty acids percentage. The trial was carried out at the Experimental Fields of the Agronomy Department, Faculty of Agriculture of Ankara University, Turkey during 2010-2011. The material was collected from opium poppy collections in the department. All seeds were sown on 8 October 2010 and harvested during second week of July 2011. The oil of two samples of each line was extracted with hexane by foss soxtec 2055 apparatus. Fatty acids were analyzed by gas chromatography. Seed fatty acid percentage of three different slit flower lines was determined. The major fatty acid in seed oils was linoleic acid (72.17– 74.66%); whereas, oleic and palmitic acid contents of seed oils ranged 13.21 -15,55% and 8.25 – 8.85%, respectively. It is concluded that these poppy lines could be used as high linoleic acid, oleic acid and palmitic acid containing lines.

# WHEAT CROP IMPROVEMENT AND BREEDING GOALS IN SUDAN

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Sudan is characterized by different climatic zones which extends from the desert in the north where the rainfall is almost zero to rich savannah in the south where the rainfall is more than 1000 mm. Wheat production in Sudan faces a biotic stresses (mainly heat and drought), biotic stresses (diseases, insect pests, weeds), and socioeconomic constraints (smallholder, resource-poor farmers, high-cost inputs and machinery, unavailable or difficult access to credit, and unfavorable marketing). Historically wheat is produced in the northern part of the country during the winter season in which the temperature is low. During the last century wheat cultivation was introduced in Gezira scheme in the central part of the country and well as in White Nile region and new halfa scheme. It is noticed that productivity of wheat per feddan in the northern region, where the winter season long and cool, is higher compared to the central part of the country. The percapita consumption as well as the total consumption is increasing due to urbanization. The current total consumption is about 2.4 million ton per year. The production in the best years does not exceed 25% of the total requirement or demand. To increase wheat production in Sudan we will need more research genetic engineering and genomics in wheat crop.

# APPLICATION OF RNA SILENCING: A CHANGING PARADIGM IN CROP IMPROVEMENT

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Significant yield losses due to the attack of pathogen occur in most of the agricultural and horticultural crop species. More than 70% of all major crop diseases are caused by fungi. Plant diseases are usually handled with applications of chemicals which also kill beneficial organisms along with pathogens and also produce undesirable effects on health, safety and cause environmental risks. Traditional plant breeding methods have been used to develop cultivars resistant to various diseases. RNA-mediated functions has been greatly increased with the discovery of small non-coding RNAs which play a central part in a process named RNA silencing. RNA silencing is a novel gene regulatory mechanism that limits the transcript level by either suppressing transcription (TGS) or by activating a sequence- Specific RNA degradation process. The discovery of these species of small RNAs opens the door to understand advanced usage of genome and the number of genes present.  It also has complicated the situation in terms of biochemical attributes and functional genesis of these molecules and provides new avenues for developing eco-friendly molecular tools for crop improvement by suppressing the specific genes which are responsible for various stresses and improving novel traits in plants including disease resistance. It has emerged as a method of choice for gene targeting in microorganisms and plants. It can silence a gene throughout an organism or in specific tissues, offer the versatility to partially silence or completely turn off genes, work in both cultured cells and whole organisms and can selectively silence genes at particular stages of the organism's life cycle. Because of unique features of RNAi, our review is focused on the current knowledge of RNAi concept and its applications in plants.

**Key words:** RNAi, Functional Genetics, Gene Silencing, crop improvement.

# EFFECT OF DIFFERENT NACL CONCENTRATION ON *IN VITRO* REGENERATION IN *ONOBRYCHIS VICIIFOLIA* AND *ONOBRYCHIS OXYDONTA VAR. ARMENA* SPECIES

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This research was carried out to determine the response of NaCl salinity on *in vitro* regeneration of *Onobrychis viciifolia* and *Onobrychis oxydonta var. armena* species. For this purpose, explants of stem and leaf were transferred regeneration media with doses of (0, 5, 10, 20 and 30 dS/m) of NaCl and 4 mg/l BAP plus 0,5 mg/l NAA. After eight (8) weeks, calli induction, calli fresh and dry weights, numbers of shoot per explants, number of explants which creating shoot were measured. With increasing of NaCl doses, decreasing was determined at all parametres which were measured. In term of plant regeneration, high callusing creating rate was induced on stem explants at all NaCl. In consideration of all parameters, high values were obtained from *Onobrychis viciifolia* species.

# EVALUATION OF SELECTION CRITERIA FOR ASSESSING DROUGHT STRESS TOLERANCE OF THIRTY MAIZE INBRED LINES

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Drought is a major cause of yield loss worldwide. Therefore, the development and dissemination of drought tolerant varieties that will yield well under a broad range of environmental conditions is an important breeding goal. Several stress indices have been developed, aiming to assist identification and selection of stable, high-yielding, drought tolerant genotypes. A novel equation (B value) that predicts crop yield potential of a genotype at normal farming densities has been also suggested. The estimation of B value relies on plant yield potential at ultra-low densities and on the coefficient of variation (CV) of individual plants. Thirty inbred lines were evaluated during the 2012 growing season in the absence of competition (0.74 plants/m$^2$) and across two locations of the northern Greece at normal and water-stressed conditions (see also Gekas at al., this congress). For each genotype, B value and nine other stress indices based on their yield under normal and water stress conditions were calculated, including stress susceptibility index (SSI), mean relative performance (MRP), stress tolerance (TOL), mean productivity (MP), relative efficiency index (REI), stress tolerant index (STI), geometric mean of productivity (GMP), yield index (YI) and harmonic mean (HM). It was found a strong and positive correlation ($P<0.001$) of B values with all indices, except SSI, for both experimental locations. These results suggest that B value matches the ability of the other stress indices to identify drought sensitive and tolerant genotypes and is an effective selection criterion for high yielding genotypes with stable performance under variable environmental conditions.

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# IMPLICATIONS OF COMMON BEAN CENTROMERE STRUCTURE ON BREEDING EFFORTS

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Centromeres in higher eukaryotes are composed of long arrays of tandemly organized satellite repeats. Despite the functional importance, our knowledge of centromere structures is limited to several model species. This is also the case for the centromere structure of common bean, Phaseolus vulgaris, an important legume species. Given the recent availability of whole genome draft sequence in common bean, a comprehensive analysis of centromeric satellite DNA sequences is crucial and would possibly broaden our understanding of genome structure and evolution. A unique organization of two unrelated centromeric satellite DNA sequences suggests a chromosome specific homogenization mechanism in the functional centromeres of common bean. We will discuss our recent findings in relation with the possible implications of centromere satellites on the common bean breading efforts.

# IMPROVEMENT OF SALINITY TOLERANCE IN BARLEY: CONTRIBUTION OF *IN VITRO* TECHNIQUES

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Barley is a strategic culture in North Africa and is a fundamental component of food security in these regions. However, this culture is dependent on unpredictable and erratic climatic conditions and displays production levels vary widely. To cope with climate change facing the barley crop, we had to resort to the creation of new productive and salinity-tolerant varieties. In addition to the classical field selection different biotechnological routes are designed to increase the potential of salt stress tolerance following a rediversification fundamental biological and genetic bases may appear after in vitro regeneration following selective pressure. In this work, a saline test (0.5 and 10 g / l) was performed in situ on new andro-and gynogenetic progenies of barley, including regenerating were obtained with or without NaCl in the culture medium in vitro. It reveals a variability of expression for the number of tillers, plant height, grain mass and weight of 100 grains. The results suggest that the gynogenetic produce more tillers than androgenetic and the witness. Treatment without salt, regenerating gynogenetic obtained in vitro without NaCl, 9.20% mass produced grain more than the control. In salt stress conditions, the mass gain in grain compared to the control remains very high in gynogenetic and lower in androgenetic.

**Keywords**: Barley, Gynogenetic, Androgenetic, Salinity, Tolerance

# MONITORING OF CEREAL PESTS AND DISEASES AND IDENTIFICATION OF RESISTANT VARIETIES IN TAJIKISTAN

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Cereals pest and diseases can be a reason for significant losses of yield in Tajikistan. As cereal crops, especially wheat plays a crucial role on achieving food security, thorough investigations of all constraints are important. Thus, with technical support of FAO-SEC we are conducting surveillance of pests and diseases in main wheat growing areas of Tajikistan starting from 2012. During the 2012 surveillance main foliar diseases, yellow rust (caused by *Puccinia striiformis,* f.sp. *tritici*), leaf rust (*P. recondita,* f.sp. *tritici*) and stem rust (*P. graminis,* f.sp.*tritici*) were seen very rarely, with very low incidence only in few fields. Compare to previous year in 2013 local epidemics of yellow rust was observed mainly in Hisor valley. Other parts of the country were not highly affected by the diseases, although major wheat varieties were affected by disease. Common bunt (*Tilletia laevis*) and loose smut (*Ustilago spp.*) found to be serious mostly in rain fed areas. During 2012 insect damage was found to be more serious and significant than 2013, insect pests, such as cereal leaf beetle (*Oulema melanopus*), sunn pest (*Eurygaster integriceps*), aphids (*Schizaphis graminum*, *Diuraphis noxia*) and sawfly (*Cephus cinctus*) are causing most insect damages. Weeds are spread throughout all the cereals fields, this problems need a serious attention, especially in the seed crops. Most spread weed plants of cereal crops are *Convolvulus arvensis, Avena fatua, Gallium apparene, Sinapis arvensis, Chenopodium album* etc. Within the project 38 seed samples of released and widely grown wheat varieties were submitted for testing to resistance to main diseases in hot spots/or under artificial conditions to Turkey, Kenya, USA and Mexico (CIMMYT).

# OPIUM POPPY (*Papaver somniferum* L.) PRODUCTION AND BREEDING GOALS IN TURKEY

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Opium poppy (*Papaver somniferum* L.) has been grown as an annual field crop since 3000 BC in Anatolia. As a gene center, there are many Papaver species and subspecies exist in Turkey. Turkey, India, Australia, France, Spain and Hungary are legal producers of opium poppy. At the same time Turkey and India are known as traditional producers. Turkey has 54% of opium poppy cultivation area of the world with 22% of morphine production of the world. Although, opium poppy capsule contains many different alkaloids, it has mainly morphine, thebaine, noscapine, papaverine, and codeine. There are plenty of registered opium poppy varieties and land races with different seed color exist in Turkey. However, the economically important types have yellow, white and blue seed colors which are preferred by industry. The opium poppy breeding goals are to develop the varieties with high morphine rate, cold resistance, disease and insect resistance and also high seed and capsule yield.

# WHEAT LANDRACES INVENTORY IN TAJIKISTAN

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Presence of high diversity of small grain cereals, especially wheat in the current territories of Tajikistan were described in many historic and geographic books. Nikolai Vavilov, well-known by his theory of Centres of Origin and Diversity of Plants and his expeditions around the Globe has visited Tajikistan two times and collected huge amount and valuable genetic materials. Vavilov in Tajik Pamirs found genetic materials of wheat, barley, rye and aegilops totally differing from other parts of the world and described influence and specificity of the region for formation of new adopted forms. Before Second World War in Tajikistan people were mainly growing their own wheat varieties known as Safedak, Surkhak, Lailaki bahori, Sabzak, Irodi etc. During the 1960th number of locally bred varieties were released in Soviet Tajikistan, which was initial point of official variety testing in the country, some of these varieties were either selected or improved from local landraces or local materials were used as a parent. Through years by developing agricultural sector new foreign varieties were introduced to the country and released and this process nowadays is continuing. Using valuable genetic materials of local origin for improving wheat is essential for current breeding projects. Currently landraces are only grown in limited areas in the mountainous regions in rainfed lands, mainly in small scale farms. With the purpose of identifying areas were wheat landraces are still grown and their inventory FAO-SEC provided technical assistance. Besides identifying areas, farmers who still keep these landraces were interviewed for revealing socio-economic issues of growing landraces. Survey was carried out in 10 mountainous districts of Tajikistan during July and August of 2013. During the survey following landraces and old Tajik wheat varieties were found and samples were collected for further characterisation and use: Safedak, Surkhak, Irodi, Dandoni Ushtur, Uruqlii bahori, Surkhsuk, Shukhak, Boboi, Bobilo, Kilaki Bartang and Safedaki Ishkoshimi.

# THE DETERMINING OF THE EFFECTS OF SOME GROWTH REGULATOR PRODUCTS ON MALE STERILITY IN SUNFLOWER (*Helianthus annuus* L.) HYBRID SEED PRODUCTION

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Male sterility is key issue both in hybrid breeding programs to cross inbred lines obtaining hybrids easily and in hybrid seed production in sunflower. This study was conducted to determine the effects of some growth regulators on male sterility in sunflower (*Helianthus annuus* L.) hybrid seed production in Trakya Agricultural Research Institute fields in Edirne, Turkey and institute lab in 2008 and 2009. In the first year of the research; gibberellic acid, salicylic acid and ethrel growth regulators were applied to flower buds of sunflower in 0.5 cm or less and 6 - 8 leaf stages ($T_1$ period) and in 0.5 - 2 cm and 10 - 12 leaf stages ($T_2$ period) at 0.1%, 0.2% and 0.3% doses respectively. In the second year; gibberellic acid, salicylic acid and ethrel were applied to the bigger flower buds of sunflower than 2 cm and 12 – 16 leaf stages ($T_3$ period) at 0.1%, 0.2% and 0.3% doses respectively. Total flower number, fertile flower number, the rate of male sterility, selfing rate and germination rate were evaluated in the research. The highest rates on male sterility were obtained from gibberellic acid and these rates were observed as 99.5 – 100 % in 2008 and 99.6 - 100% in 2009. In salicylic acid applications; male sterility rates was calculated as between 9.34 % and 34.94 % in 2008 and between 19.96 % and 36.0 % in 2009. However, these values were determined as between 24.52 % and 42.5 % in ethrel applications. As results, it was concluded that gibberellic acid could be used effectively especially 0.1% and 0.2% doses at in $T_3$ period to obtain male sterility in sunflower hybrid seed production.

**Key Words:** Gibberellic Acid, Salicylic Acid, Ethrel, Male Sterility, Selfing Rate

# DEVELOPING CONFECTIONERY SUNFLOWER HYBRIDS AND DETERMINATION OF THEIR YIELD PERFORMANCES IN DIFFERENT ENVIRONMENTAL CONDITIONS

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Although sunflower grows mainly for producing vegetable oils in the world, sunflower is one of the most consumed confectionery snack both in Turkey, in Eastern Europe, US, Canada and also in some Asian countries such China, Pakistan, Iran, Middle East countries, etc.. They generally are white color with grey stripes (however black ones are also popular in Slavic countries), and larger than the oil-type, with a lower oil percentage. In the confectionary sunflower sectors; highest quality seeds including the largest and cleanest seeds are used for snack, hulled sunflowers are seeds that are still food-grade quality, but they do not possess the characteristics to be in the food-grade category and smaller, lower quality seeds are used for birdseed. Confectionery type sunflower grows generally in Eastern and Middle Anatolia in Turkey but there is no certified seed in the production due to mostly planted village populations which have white color with grey stripe. The study is covered the confectionery sunflower hybrids developed in Confectionery Sunflower Breeding Project conducted by Trakya Agricultural Research Institute, Edirne, Turkey. The candidate confectionery hybrids were tested and evaluated in the regional yield trials in Trakya Region in 2009-2010 with 4 rows 4 replications as randomized completely block design. Seed yield, 1000 seed weight, flowering and physiological maturity period, plant height, head diameter, oil content were measured. Based on trial results; some experimental hybrids exhibited higher performance than controls for both for seed yield and seed weight and promising candidate hybrids were selected to send registration trials. From these promising hybrids, 09 TRÇ 003 were sent in 2011 and 09 TRÇ 003 confectionery hybrid were sent registration trials in 2012 production permission were obtained for them. After evaluation of candidate hybrids in these years, having higher general combining inbred lines were also sent to National Registration Office for registration too. In 2010; 08-9322-29-A-ÇRZ female line and, 08-9640-1-R-ÇRZ, 08-9717-4-R-ÇRZ, 08-9775-23-R-ÇRZ restorer (male) lines were sent to registration. In 2011; 96171-A ÇRZ female line and 9892-R ÇRZ male line and, 9707-A female and 9881-R male lines sent for DUS tests and then registration in 2012.

**Key words:** Sunflower, Confectionery Hybrid, Seed Yield, Seed Quality

# DETERMINATION OF YIELD PERFORMANCES OF OLEIC TYPE SUNFLOWER (HELIANTHUS ANNUUS L.) HYBRIDS RESISTANT TO BROOMRAPE AND DOWNY MILDEW

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Sunflower is the most important oil crop in Turkey. Downy mildew (*Plasmopara halstedii* (Farl.) Berl. et de Toni) and broomrape (*Orobanche cumana* Wallr) are the most important limiting factors for yield production in sunflower areas both in Turkey and also Eastern Europe and Black Sea countries which have more than 60% of world sunflower production. On the other hand, high oleic type sunflower have recently started to gain importance year by year in the world because of that high oleic acid sunflower oil frying is more appropriate so it is more beneficial to health. Therefore, higher oleic varieties will be demanded frequently in the future both in Turkey and also in the world. The study is covered the oleic type sunflower hybrids developed in Hybrid Sunflower Breeding Project conducted by Trakya Agricultural Research Institute. The measured values were evaluated in oleic type hybrids in conducted regional yield trials in dry conditions at Edirne and Luleburgaz in the project in 2011-2012. Oleic type hybrids resistant to broomrape and downy mildew were tested in yield trials with 4 rows 4 replications as RCBD. Seed yield, 1000 seed weight, flowering and physiological maturity period, plant height, head diameter, oil content were measured. Some experimental hybrids exhibited higher performance than controls in some locations both for seed yield and seed weight and promising candidate hybrids were selected to send registration trials. Based on yield trials in 2011, 11TR072, 10TR048, 11TR068, 11TR076 and 11TR066 oleic type candidate hybrids exhibited higher performance in terms of grain yield than other varieties. These varieties were also resistant to broomrape and downy mildew and their oleic acid contents were measured as 84.42%, 58.70%, 72.53%, 68.16% and 83.21% respectively. 12TR013, 12TR001, 12TR008 and 12TR012, 12TR003 were observed as promising candidate hybrids resistant to broomrape and downy mildew in seed yield in 2012 yield trials. Their oleic acid contents are as well as 85.72%, 61.66%, 83.66%, 59.96% and 83.36% respectively. Among these high oleic varieties, 11TR072, and 11TR066 varieties were high oleic acid type, 11TR068, 10TR048 and 11TR076 varieties were mid oleic acid type in 2011. Additionally, 12TR013, TR12, TR003, and 12TR 012 sunflower hybrids were high oleic acid, 12 TR 001 and 12TR008 candidate hybrids were categorized as mid-oleic acid content in 2012.

**Key words:** Sunflower, Fatty Acids, Oleic Acid, Hybrid, Yield, Broomrape, Downy Mildew, Resistance

# YIELD AND QUALITY CHARACTERISTICS OF SOME IZMIR TYPE TOBACCO GENOTYPES

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This study was carried out using 11 İzmir type tobacco (*Nicotiana tabacum*) varieties registered for Aegean Region of Turkey and 8 advanced lines developed from İzmir type tobacco populations in order to determine their yield and quality performances in two locations (Menemen and Buca) of İzmir province during the growth season of 2011. Trials were designed in Randomized Blocks with 3 replications. In the study, important characters for tobacco breeding such as plant height, number of leaves per plant, days to flowering, dry leave yield, quality and expertise were evaluated. Findings and results showed that genotypes were statistically different by the characters analyzed in the study. Means for some characters in the trial were determined as follows: dry leave yield: 63-114 kg/da, plant height: 73-92 cm, number of leaves per plant: 19-43. Four of the genotypes developed by selection breeding were considered as promising advanced lines and used in registration trials in the year 2012.

**Key Words:** İzmir tobacco type, tobacco dry leave yield, tobacco crop quality

# AROMATIC BASMATI AND NON-BASMATI RICE VARIETIES GROWN IN HARYANA, INDIA FOR EXPORT

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Basmati, the unique aromatic quality rice is a nature's gift to Indian sub-continent. Epicureans acclaimed its delightful fragrance, taste and texture which makes it the best among the aromatic rices of the world. The plant of Basmati rice is very tall and weak and hence prone to lodging. Basmati rice is photo-period sensitive and susceptible to most of the insect pests and diseases. Basmati rice is grown in traditional areas comprising the foot hills of the Himalayas in the northwestern parts of Indian sub-continent comprising the states of Haryana, Punjab, Uttaranchal, Western Uttar Pradesh, Jammu & Kashmir due to an interaction of genotype, soil and environmental factors. In India major states producing Basmati rice are Punjab (27.23 lac ton), Haryana (24.26 lac tons) and Uttar Pradesh (17.53 lac tons). India's total basmati production for the 2011/12 crop year that ended June was 5 million tones. The major rice quantity (1544641 lac tons per year) is exported to western countries and Middle East. In the export markets still the traditional tall basmati variety Taroari Basmati followed by Basmati 370 and Type 3 (Dehradun) has supremacy over other varieties. Immense aromatic rice diversity does exist and not all aromatic types are recognized as Basmati. Pusa basmati 1121 due to its extra long slender grains along with Pusa Basmati 1 have carved a special niche in the international market. Sugandha and Shabnum are other such varieties. The non-basmati variety being preferred for export have an aroma ( 2-acetyl-1 Pyroline) and the grains are are 6.6 to 6.8 mm long..

# INNOVATIVE TRANSGENIC APPROACH TO IMPROVE DROUGHT TOLERANCE OF MAIZE IN SYRIA

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Drought is a major agricultural threat reducing crop productivity and limiting the use of land throughout the world and this is particularly acute in the Middle East region. Maize fits well in the existing cropping systems in a wide range of production areas of Syria but successful cropping will depend on using varieties that are adapted to the dry environmental conditions prevailing in these areas.  Maize breeding with improved drought-tolerance is of huge importance. *Agrobacterium*-mediated transformation system is the most widely applied methods for genetic transformation of many plants such as  maize. An updated and efficient protocol for year-round production of fertile transgenic Syrian maize plants with improved drought tolerance using *Agrobacterium tumefaciens* strain EHA105 harboring a standard binary vector is reported here. Resistant callus derived from transformed immature zygotic embryos (IEs) of Syrian maize genotypes was selected and regenerated on kanamycien containing medium. Results showed that the response of “varieties” to produce transformation events using IEs was higher than for “hybrids”. This study reported that efficient transformation of maize requires the correct choice of starting materials (IEs size1.5-2.0 mm) and inoculation conditions such as bacterial concentration to efficiently ensure gene transfer. PpCBF gene expression was monitored in the R0 generation via PCR using gene-specific primers confirming the integration and inheritance of the CBF in the transgenic plants. To our knowledge, this is the first report for a reproducible method for Syrian maize germplasm transformation using *A. tumefaciens* standard binary vector system with an average transformation efficiency of 7.2 %.

# MEIOSIS OF FERTILE AND STERILE SUNFLOWER AT THE CYTOLOGICAL AND MOLECULAR LEVEL

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The life cycles of all sexually reproducing eukaryotes are dependent on the process of meiosis. A detailed cytological description of meiosis has been built up over many years, based on studies in a wide range of plants. Meiotic process includes a number of important events as crossing over, synaptonemal complex and recombination nodules formation which is under the strict control of highly specialized genes. Molecular analysis of these genes leads to obtain new various information relating to the genetic mechanism, which is included in the functional activity of the meiotic process in plants, therefore the molecular study of meiosis gene represents fundamental and actual problem. The present study reports the meiotic behavior in fertile and sterile sunflower lines investigated at cytological level using light microscopy and at molecular level – through estimation of meiotic gene expression via quantitative PCR technique. Cytological researches have highlighted shape, size and degradation level of meiocytes in five stages of microsporocyte development. Expression level was estimated for some genes involved in meiotic control such as cyclins, histones, proliferating cell nuclear antigen and male sterility1. It was established correlation between male sterility, meiocytes degradation and specific gene expression. Obtained results extend knowledge about meiosis process of sunflower and offers useful information for breeders which could facilitate creation of $F_1$ hybrids.

# APPLICATION OF FOOD BIOTECHNOLOGY IN AGRICULTURE: BENEFITS AND RISKS

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Innovation in plant breeding is necessary to meet the challenges of global changes like population growth and climate change. Agriculture has been able to cope with these challenges. However, further efforts are needed and therefore plant breeders search for new techniques like Food Biotechnology to strengthen the results of breeding techniques like increased productivity, improved quality particularly. In the developing world where the population is continuing to increase and Farmers must consistently produce an extra 30% more cereal in order to maintain current nutrition levels and food security, this task does not become any easier with diminishing land and water resources, Biotechnology offers a challenging role to reduce the gap of yield improvement. Plant biotechnology and, in future, nanobiotechnology, can bolster plant-breeding efforts to meet these new challenges in a sustainable way. Breeding a new variety of crop takes around 12 to 15 years of intensive effort while biotechnology could develop the desired varieties in short span of time and this could be a boon for plant breeders. The application of modern / Food biotechnology to plant breeding is considered to be more efficient and quicker than conventional breeding techniques in the development of new and more resistant, genetically modified (GM), firm structural as well as industry specific characteristics crop varieties.

**Key Words:** Food Biotechnology, GM, nutritional level, global changes.

# USING SUNFLOWER GENETIC RESOURCES, TO IMPROVE RESISTANCE TO THE MAIN DISEASES AS WELL AS TO THE BROOMRAPE PARASITE (*Orobanche cumana* Wallr.)

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Genetic resources in sunflower, which could to be used as base of creating new inbred lines or as donor sources for genes controlling different characteristics, in the inbred lines breeding, are made up of old or new varieties, hybrids and inbred lines, induced mutations, synthetic populations, as well as sunflower wild species. For improving sunflower resistance to the main diseases as well as to the broomrape parasite, it can be used all these genetic resources. In our sunflower breeding program, at NARDI Fundulea, we have used specially, varieties, hybrids, inbred lines and sunflower wild species. The varieties and inbred lines have been used for creating synthetic populations which formed the base of obtaining new inbred lines resistant to *Plasmopara halstedii* (genes for resistance to different races of this pathogen) as well as lines resistant to *Orobanche cumana* parasite. By doing selfpollination in different commercial hybrids we have obtained inbred lines with high resistance to the pathogen *Phomopsis helianthi* as well as to *Sclerotinia sclerotiorum*. Sunflower wild species have been used for crossing with cultivated sunflower, being obtained interspecific hybrids which permitted creating of different donor sources of genes for resistance to broomrape parasite. The same, we have obtained some populations which are still in the breeding process for creating inbred lines with high resistance to *Phoma macdonaldii* and *Phomopsis helianthi* pathogens. The new inbred lines obtained by using different genetic resources have been studied as general and specific combining ability for the seed yield and oil content. Most of them have been positive significantly as the general combining ability, for the seed yield or for oil content, or for both of them.

**Key words**: sunflower, genetic resources, diseases, broomrape, combining ability.

# SCENTED VERITIES OF RICE CULTIVATED IN UTTAR PRADESH, INDIA FOR EXPORT

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Uttar Pradesh is the fourth largest state in country & is divided in two physiographic regions viz. Gangetic plains and southern plateau. From cultivation view point gangetic plains cover major portion of the state. Agriculture is the most important in the state because about 80% of its population resides in rural areas and 75% of the total workers are involved directly or indirectly in cultivation/farming which accounts for 27% of state's GDP. The important crops of Uttar Pradesh are rice, wheat, maize, sugarcane, chick pea, pigeon pea, mustard, lentil, urd and moong. Majority of the agriculture land is used to grow major cereal crops: rice & wheat. Rice is the major crop in Uttar Pradesh and is grown in about 5.90 mha which 13.5% of total rice produced in India is secured 3rd position in India. Uttar Pradesh has favourable & suitable climate, vast areas of fertile soils, sunshine and adequate water resources. Rice farming in the state is most vulnerable and risk prone due to complex ecological situations marked by frequent flood or drought or both. Uttar Pradesh is the rich source of scented rice like Kalanamak, Basmati-1, Kalanamak, Adamchini, Bindli, Badshahbhog, Batanphul, Benibhog, Dhania, Dulhania, Hansraj, Jeerabati, Kamaljira, Lalmati, Ramjawain, Shakarchini, Phoochameli, Laungchoor, Sonachur, Tilakchandan, Tulsimanjri, Vishnuparag and Shushk Samrat. As a report of Directorate of Rice Development, Patna; Uttar Pradesh is the second largest producer of scented rice state in India and have great potential of export.

**Key Words:** Scented rice, Gangetic plains, GDP, Rice farming

# CHARACTERIZATION OF CONFECTIONARY SUNFLOWER (*Helianthus annuus* L.) LAND RACES OF TURKEY

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Sunflower (*Helianthus annuus* L.) is one of the important oilseed crops and landraces of oil and confectionary types have significant diversity in Turkey. Sunflower landraces were collected and conserved *ex situ* at the National Gene Bank within the framework of National Industrial Plant Genetic Resources Project. Characterization of local variety and land race collections is necessary for the sustainable utilization and help to optimize the germplasm management in plant breeding program. In this study agro-morphological characterization of confectionary sunflower land races maintained at National Gene Bank are conducted for assessing sustainable utilization in the breeding program. Ecological differences affect morphology of sunflower; thus, quantitative aspects of variation were evaluated using plants grown under same conditions. Thirty two characters were evaluated and Multivariate analysis (PCA) was performed for diversity determination and for evaluation assessment of confectionary sunflower accessions at national collection. The morphological variation on the observed characters was found highly variable for most of the characters. All accessions have released the fertile pollen, and alternate leaf arrangements, hairy stem, absent branching, short hairy leaves, triangular leaf shape, confectionary type of kernel, dark yellow head flower. No anthocyanin coloration on the disk flower was observed. Plants were mostly vigor. Almost all leaf characters showed variation. Leaf blistering was mainly strong and medium; leaf serration coarse and medium; leaf shape of cross section flat and weakly convex; leaf auricules medium and large; leaf wings none or very weakly expressed and weakly expressed; leaf angle of lowest lateral veins acute and right angle or nearly right angle; leaf height of the tip of the blade compared to insertion of petiole low and medium. Seed shape presented mainly as elongated, narrow ovoid and broad ovoid. Seed main color was white and whitish grey; seed stripes was observed with all types as none or very weakly expressed, weakly expressed and strongly expressed. Head attitude was variable at maturity; mainly half-turned down with straight stem and turned down with slightly curved stem were observed. Head shapes were presented as concave, flat, convex. In case of days to physiological maturity, they exhibited high range and some of the accessions had shorter physiological maturity period. The results indicated that continuous variation model of confectionary sunflower land races. The informal seed exchange mechanism among the farmers effect the some degree of similarity of the some accessions collected from different localities.

**Keywords:** Sunflower, *Helianthus annuus* L.*,* diversity, agro-morphological variation, Principle Component Analysis (PCA).

# INBREEDING IN THE BREEDING OF WINTER RAPESEED IN UKRAINE

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Winter rapeseed in Ukraine has more than one million hectares last five years. It makes up certain requirements to varieties and hybrids, especially for quality of oil and yield stability. Using inbreeding during 2006-2013 years, was found that the highest manifestation of yield decline were at 4th and 8th years, they are particularly evident in mass of 1000 seeds, plant height and habit, size and shape of a flower. The 00-type winter rape variet BE-0127 had mass of 1000 seeds 5.4 g in 2006, four years inbreeding weight was 2.2 g , and in 2013 ( 8 year inbreeding ) only 1.8 g. Variet BE-0127 was divided into 5 homogeneous similar lines were grown separately. In 2010 was a performance comparison between source material BE-0127 and united lines to determine the effect of heterosis. Yield initial sample was in 2010 5.4 t / ha, in 2011 - 5.3 t / ha, in 2012 - 5.4 t / ha, accordingly, yield of united lines was 2.7 , 5, 5 and 7.2 t / ha. Weight of 1000 seeds in the initial sample 5.4 g , and united lines respectively 2.2 g , 5.0 g and 5.5 g. In lines derived by inbreeding over 4 years, with their following uniting heterosis effect described by quantitative characteristics begins to consistently exceed original sample after 3 year. Samples had identical marker signs.

# CRYOPRESERVATION TECHNIQUES OF CEREAL GENETIC RESOURCES

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Since the beginning of agriculture conservation of cereal grains is popular practice among growers. Plants belonging to different genetic resources and seed conservation have become more important in recent times. Losses occurring due to the development of natural disasters (earthquakes, floods, forest fires) and infrastructure (dams, highways, etc.) has caused considerable damage to plants (genetic erosion) that emphasise need of conservation of plant genetic resources. Static shielding  of plant genetic resources (ex situ conservation) like the seeds stored in gene banks is the cheapest and most convenient method of storage . Vegetatively propagated potatoes, cassava and sweet potatoes, or wild and cultivated forms of the species with recalcitrant seeds, plant tissue cultures stored in tubes, vegetative propagation cocoa, live gene banks of plants such as coconut or maintained field gardens are the most important method of preservation. Since 1970's, Long-term storage of plant material is done using ultra- cold liquefied gases including of liquid nitrogen is noteworthy. Long-term storage of of genetic material is performed by storage in liquid nitrogen ( $LN_2$ ) storage system at ultra-low temperatures (-196 °C) in programmable freezers and other liquefied gas with liquid nitrogen tank combinations that are based on the latest technological developments. Several cold storage methods have been developed to date. Seed genetic resources of approximately 90 species including cereals have been preserved using cultured material and the meristems collections on long-term bases. A cryopreservation study for maize vitrification method has been used. It was observed that the maize embryos did not lost vitality when they were cryopreserved in liquid nitrogen (-196 ° C) by directly immersing. At the same time, 5 different maize vitrification solutions at different concentrations (PVS2) were tested using five different maize genotypes. The results showed that their vitality rates varied from 47.5 to 75 % at ultra-cold temperatures, with provision of (50-100%) vitality using PVS2 high concentrations. In another study that focused on storage of of barley and triticale in liquid nitrogen, germination percentage of barley and triticale were recorded after 5 minutes, 1 hour, 1 day, 1 week and 1 month no variation was noted in the $LN_2$ storage results. Caryopsis germinated with Isoperoxide treatment for 24 hours at ultra cold temperatures did not show variations in enzyme contents.

# EFFECTS OF INBREEDING DEPRESSION IN VEGETATIVE AND REPRODUCTIVE PARAMETERS OF *ANAGYRIS FOETIDA* (LEGUMINOSAE, PAPILIONOIDEAE) IN TWO POPULATIONS FROM SW SPAIN

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*Anagyris foetida* L. is a Mediterranean shrub with medicinal properties. It is the first native European species where pollination by birds was demonstrated and these results were mainly obtained in two populations from SW Spain. Because of its mixed mating system, the existence of some male-sterile individuals and the frequent observation of anomalous flowers and inflorescences could indicate a strong inbreeding depression. To determine the effect of inbreeding depression in these populations, hand pollinations were performed to obtain selfed and outcrossed seeds. From these seeds two progeny were obtained in different years. First progeny was only studied along its first year of life because of it was destroy by human activities close to the natural populations. This progeny showed no differences in vegetative parameters (germination, seedling emergence, height, biomass, survival) between the two populations, so that no differentiation was made between populations in the second progeny. Second progeny was studied during 4 years, and reproductive parameters were determined during the first two flowering seasons. Our results showed inbreeding depression to be manifest in the studied populations throughout the life cycle, adversely affecting the reproductive parameters more than the vegetative parameters, with the male capacity being strongly affected. The findings may have important implications for the long-term conservation management of the populations and show the need to study the entire life cycle of a species to understand how it is affected by inbreeding depression, and to analyze more than one flowering period in long-lived species.

# WHEAT LANDRACES POTENTIAL OF TURKEY: A SWOT ANALYSES

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Turkey is one of the Centers of Origin of wheat and wheat has been grown around 8.5 million ha with production of around 20 million tons annually. Though modern varieties have been widely grown in most areas, some Land Races (LR) have still been planted in some niches, especially in remote and mountainous areas mainly for home consumptions with small marketing. This is reality that landraces are no longer preferred by the producers because of higher yield potential of modern what varieties. Cultivation areas and production of landraces decreased dramatically. This might lead to the loss or even extinction of landraces. Therefore, in *situ* and *ex situ* conservation strategies should be supported to conserve them for future generation. For this aim, Ministry of Food Agriculture and Livestock researchers with ICARDA and CIMMYT scientists started a project to determine the last statements of wheat landraces at national level in 2009. With FAO contribution in 2012 and 2013, the project was accomplished and In total, 1795 questionnaire forms were fulfilled with 1556 wheat landrace producers via face to face in 61 provinces of Turkey. As results of the survey and collection activities, 1304 spikes and 182 seed samples were collected and then sent to the Gene Banks (İzmir and Ankara) for *ex situ* conservation. Now, they have been being used in different parts of breeding studies and researches (drought, heat, cold tolerance, disease resistance etc.). One of the important result of the project was that the potential of wheat landraces were determined. It is second largest study on wheat landraces in side of Botanical Variety (BV) description after Mirza GÖKGÖL's study "TurkiyeBuğdayları" and it is the first largest study on determination of socio-economic situation of wheat landrace producers. In this study, according to the project results, the general potential of wheat landraces was evaluated by SWOT analyze for Turkey.

**Keywords:** Wheat Landraces, Policy, Genetic Resources, SWOT Analyze, Turkey

# THE MODEL OF THE STUDY: DETERMINATION OF DROUGHT TOLERANCE IN LOCAL DURUM WHEAT CULTIVARS USING CONVENTIONAL METHODS AND MODERN BIOTECHNOLOGICAL TECHNIQUES

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Drought, the most important abiotic stress limiting durum wheat production, is one of the very few of stress-tolerant genotypes reported in the literature. Cultivation of summer durum wheat varieties in our country is held mostly in southeastern and eastern Anatolia where hot and dry period coincides with the period of plant growth and therefore the yield decreases. On the other hand, the most important reasons which limit the increase in yield of durum wheat cultivars (*Triticum durum* L.) are inadequate irrigation activities in rainless arable field and the low amount of organic matter in the soil. The studies about the quality improvement for competition with market conditions and the development of drought tolerant cultivars become more of an issue considering our country is the second largest pasta manufacturer in the world after Italy. The model of the study, which is announced first time here, is aimed to develop drought-resistant wheat germplasm according to differences in wheat spike morphology collected from local pasta wheat varieties present in Turkey Seed Gene Bank stock. Ex-situ conservation of materials will be performed from selected a single spike on the basis of some morphological observations and also subjected to selection for use in plant breeding. So, both drought resistant and request of quality properties to meet quality durum varieties by consumers and pasta industry will contribute to the development of pasta wheat cultivars. On the other hand, the molecular characterization of the previously as drought-sensitive and-resistant varieties of durum wheat and standard durum varieties will be carried out by microarray analysis. In addition, the results are very high potential for use throughout the country. In this regard, the study has the ability to cater to all research institutions related with wheat breeding in Turkey.

**Keywords:** *Triticum durum*, drought tolerance, local varieties, pasta quality, gene expression profile, microarray

# DEVELOPMENT OF SYNTHETIC CULTIVAR OF ALFALFA (*MEDICAGO SATIVA* L.) ON THE BASIS OF POLYCROSS PROGENY PERFORMANCE IN THE SOUTHERN ANATOLIA

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This research was carried out to develop synthetic cultivar of alfalfa with high forage yield and high quality under Mediterranean environment of Turkey in seven consecutive years 2002-2009. To ensure a broad range of genetic variability, different alfalfa entries including cultivars, introductions and bulked populations, collected from different sources, were used to establish source nursery. From the original source nursery 380 superior plants (genotypes) out of 7680 individuals were selected and cloned. Thirty-two selected plants from the clonal line nursery were cloned and transplanted to an isolated polycross seed production nursery and were allowed to intermate randomly. Seed harvested from all prologues within a clone, then composited and sown in replicated progeny test plots. In the progeny plots 32 lines and two standard check cultivars (Mesa-Sirsa and Artal) were evaluated for dry matter yield (DMY), crude protein (CP) content, crude protein yield (CPY), acid detergent fiber (ADF), neutral detergent fiber (NDF) and estimated digestible dry matter yield (EDDMY) during the 2008 - 2009 growing seasons. According to average of two years progeny test results, there were significant differences among alfalfa lines and cultivars in terms of above all mentioned components. Mean DMY, CP content, CPY, ADF, NDF concentrations, and EDDMY were determined as 18.184 kg ha$^{-1}$, 18.1 %, 3271 kg ha$^{-1}$, 40.7%, 46.7 % and 10.290 kg ha$^{-1}$ respectively. The results indicated that selection for most vigorous tall-growing plants during the selection phases generally increased DMY, CPY and EDDMY but slightly decreased digestibility and intake potentials. It is concluded that lines 31,15, 2, 20,16, 24,17, 25, 23, 13, 30, 28, 32, 5,10 and 18 showed good adaptation and performed well under Cukurova ecological conditions by producing more EDDMY and CPY. These genotypes chosen as components for establishment of a high-yielding nondormant synthetic variety.

***Key words***: Alfalfa; synthetic cultivar; dry matter yield; herbage quality

# COMPARISON OF NEAR-ISOGENIC LEAFED AND SEMI LEAFLESS PEA GENOTYPES IN SEED YIELD COMPONENTS

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The normal-leafed plants (AFAF STST) of pea (*Pisum sativum* L.) exhibited higher yield potential, but also the largest yield reduction due to natural lodging. Yield potential of the ‘semi leafless’ plant type (afaf STST) was less than that of the leafed  type but, due to its better standing ability, the yield of the semi-leafless pea was less reduced by lodging than was the yield of the leafed type. However, yield differences between leaf types closely associated with the location and management. The main aim of this research to find differences of several morphological characteristics and seed yield between leafed and semi leafless Jof genotypes in this 3-year irrigated study under three seeding densities (50, 100 and 150 seeds $m^{-2}$). Princess (semi leafless pea variety) was crossed to Jof (leafed pea variety). In the $F_2$ generation of each backcross, semi leafless genotypes were crossed to the recurrent Jof parent. This resulted in a near isogenic semi leafless Jof genotype in which the genotype of the recurrent parent 98.6%. No significant differences were found between leafed and semi leafless Jof genotypes in measured morphological characteristics, dry matter and seed yield, 1000 seeds weight. However, semi leafless genotype showed better standing ability, even at seed maturing stage. The lowest dry matter and seed yield were obtained in 50 seeds $m^{-2}$, and the highest in 150 seeds $m^{-2}$ densities in both genotypes.

# NON-HOST RESISTANCE TO WHEAT STRIPE RUST IN BARLEY

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Stripe rust caused by *Puccinia striformis* f.sp. *tritici* (*Pst*) is one of the most important diseases of wheat worldwide. Non-host resistance is a form of durable resistance which is effective against pathogens of other species. Based on earlier research, some barley accessions can be infected by *Pst* with some accessions e.g. Fong Tien being susceptible to most isolates of *Pst*. In our study we used three Australian barley lines which were resistant and two which were susceptible to two races of *Pst* at seedling stage. The resistant lines had different levels of resistance when examined macroscopically and microscopically. We crossed resistant lines with susceptible barley lines to generate BC1 populations. 58 BC1F2 families were phenotyped and several families appear to segregate for a single gene. In one family the resistance gene was mapped to chromosome 1H. F2 families require progeny testing before additional genes can be mapped. In parallel to the linkage analysis, we have treated resistant lines with chemical mutagen (sodium azide) and are screening M2 families for susceptible mutants. Barley genes effective against *Pst* may provide new sources of durable stripe rust resistance in wheat.

# A NEW SEMIDWARF CULTIVAR URUQ WAS DEVELOPED BY IRRADIATED STORAGE SEEDS OF INIA-66 CULTIVAR

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Cultivar Uruq has many quantitative and qualitative characters which are surpassed its parent (Inia-66), first of all, by reduction of height by 25 cm, which leads to lodging resistant character, and, the locally desirable amber seeds color instead of red seeds color which characterize the seeds of parent plant (Inia-66). Uruq cultivar is also surpassed its origin in yield components at different environmental conditions, resistant to brown leaf rust, and suitable for bread making according to their physical and chemical characters and baking test.

# researching RESULTS OF ECOLOGICALLY CLEAN SOYBEAN CULTIVARS OF DOMESTIC AND FOREIGN BREEDING

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The increase in soybean production is one of the most important ways to address the shortage of feed and food protein. Kazakh Research Institute of agriculture and plant growing is the only originator of 20 soybean cultivars, 10 of which are registered. By vegetation period of cultivars created and dominated by medium and medium late cvs (I and II groups of ripeness). National breeding of soybean cultivars compared with Canada, Ukraine, Serbia, Russia, Switzerland, China cvs in the South-East Kazakhstan in demonstration nursery. (In 2010 - 57 cvs, in 2011 - 62 cvs, and in 2012 - 68 cvs). Cultivars vary in ripeness groups from 00 groups with a period of vegetation in conditions of Almaty region 90 - 95 days - Lada (Russia), Tanais (Ukraine) to group III vegetation period 135 -140 days – Nadezhda, Lastochka (Kazakhstan), Vesta (Russia). The average yield on varieties in 2010 was 3.67 t/ha with the minimum and maximum values of this index 2.13 - 5.83 t/ha, in 2011, the average yield totaled 3.56 t/ha (1.87 - 6.25 t/ha), and in 2012 – 3.68 t/ha (1.95-5.31 t/ha). The amount of protein in the seeds on average was in 2011 - from 32.2 (Lada-Russia) to 38, 7% (Sulamit - Kazakhstan), and in a dry and hot in 2012 - from 37,3 (Buster - Canada) to 44.0% (Horol - Ukraine). The amount of fat in the seeds of cultivars researched in 2012 was also more and averaged 22.5% compared to the fat content in seeds in 2011 - 20.6%. The most productive cultivar of national breeding - Zhansaya, with yields over the test period 3.83-4.58 t/ha has been authorized for use in 2012. Cultivars Zara stood out as a high-protein, 37,7-43,3%) is located in the state variety testing in 2011. The block of early ripening (75-87 days) soybean genotypes and promising for cultivation in the North of the Republic was isolated and formed.

# THE CONTENT AND QUALITY OF FAT IN THE RAPESEED, SOYBEAN AND SAFFLOWER BREEDING

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Varietal resources of oilseeds in Kazakhstan by 40 varieties and hybrids of sunflower, safflower 6 varieties, 23 varieties of canola, 20 soy, and 7 flax from 1 to 4 varieties of corn, castor bean, mushroom and mustard. For rapeseed on the fat content selected varieties Rusich, Gladiator, NPC 0607, Likolli, Jerry, DC 71-20, Zolotonivsky, Caviar, Yubileynaya with an average oil content of the tests, not lower than the average of all cvs, are not less than 46.5%. Analysis of the integral evaluation of the oil (Dolgih L.A. Abugalieva A.I., 2010) defined the priorities for the composition and quality of rapeseed oil for the following varieties according to the content and quality of the oil: Maibulak, Lipetsk, Safia, DC 71-2 Miley, Jubileinniy, Gladiator. Rape distinguished by higher oleic acid content from 58.0% (for cvs Maibulak, Lipetsk) to 65.8% (Gladiator), and a high ratio of unsaturated / saturated fatty acids from 6.70 (cvs Lipetsk) to 7.80 (cvs Jubilee ). Negative for food use erucic acid is in the range of 0.17% (cvs Jubilee) to 1.83% (mail). Safflower oil contains linoleic acid, 76-82%, the highest rate among the country produced in vegetable oils. Oil content of the seeds of dry matter is 36% - 52.7% kernel. Linoleic acid content in varieties Kazakhstan ranges from 67.5% (Akmai) to 73.9% (Nurlan), the ratio of unsaturated / saturated varies from 5.79 (Akkyzyl and Akmai) to 7.69 (cultivars Nurlan). The content of erucic varieties minimal for Akmai (0.04%), for a maximum Ak Kyzyl variety (0.27%). The fat content in seed soybean cvs ranged from 18.0% to 26.9% system, depending on the condition and year of reproduction. Almaty cvs is characterized by the high content of oleic acid (35%), and cultivars Zhalpaksay - high in linoleic acid (47.5%) and Vitamin F to 58.4%.

## HORTICULTURAL CROPS PAPER LIST

1----BATEM’DE GELIŞTIRILEN YENI LIMON ÇEŞITLERI; BATEM SARISI VE BATEM PINARI

2---COMPARATIVE ASSESSMENT OF SSR AND SRAP MARKERS FOR CHARACTERIZATION OF SEVEN ACCESSIONS OF CITRUS

3----EVALUATION OF OKRA (ABELMOSCHUS ESCULENTU) GENOTYPES FOR OKRA YELLOW VEIN MOSAIC VIRUS IN NEPAL

4----IDENTIFICATION OF TUNISIAN APRICOT GENOTYPES FOR FUTURE BREEDING PROGRAM

5----IMPROVEMENT IN TRANSCRIPTOMES ANALYSIS OF HORTICULTURAL CROPS USING NEXT GENERATION SEQUENCING

6----İNCE KABUKLU YENI SATSUMA ÇEŞITLERI; BATEM İNCISI VE BATEM YILDIZI

7----MARKERS ASSISTED ASSAY OF THE TEA CULTIVARS GROWN IN PAKISTAN

8----QTL ANALYSIS TO IDENTIFY METABOLITES POTENTIALLY RELATED TO THRIPS RESISTANCE IN PEPPER (CAPSICUM)

9----RESPONCE OF SHALLOT CULTIVAR ILOKOS SOMATIC EMBRYO TO POLYETHILENE GLICOL 6000 IN IN VITRO CULTURE

10----YERLI TURUNÇ EMBRIYO KÜLTÜRÜ

11---DETERMINATION OF HIGH TEMPERATURE TOLERANCE OF SOME PEPPER GENOTYPES

12---BATEM GÖRAL; YENI MANDARIN ÇEŞIDI

13---BAZI LIMON ÇEŞITLERININ ÇIÇEK TOZU CANLILIK ORANLARININ BELIRLENMESI

14---CHARACTERIZATION OF THE GALAPAGOS ENHANCED TRICOMES (GET) LOCUS THE FIRST STEP IN THE RESISTANCE AGAINST INSECTS.

15---GENETIC ARCHITECTURE OF RESISTANCE TO MAJOR BIOTIC STRESSES IN OKRA

16---COMBININGABILITYTHROUGHDIALLELANALYSISINOKRA (ABELMOSCHUSESCULENTUS(L.) MOENCH)

17---DNA BASED DETECTION OF MYCOTOXIN PRODUCING PHYTOPATHOGENIC FUNGI

18---GENETIC ANALYSIS OF ASSOCIATION STUDIES IN SEGREGATING POPULATION OF OKRA [ABELMOSCHUS ESCULENTUS (L.) MOENCH]

19---HIGH-FREQUENCY DEVELOPMENT OF LEAF-DERIVED CALLUS IN HAZEL (CORYLUS AVELLANA)

20---PHENOTYPIC AND NUCLEAR DNA VARIATION IN TUNISIAN CULTIVARS OF DATE PALM

21---POMOLOGICAL AND ORGANOLEPTIC EVALUATION OF ORANGES VARIANTS OF

22---SELECTION OF CLEMENTINE VARIETIES USING AS FEMALE PARENT

23---THE RESULTS OF BREEDING SEA-BUCKTHORN (HIPPOPHAE RHAMNOIDES L.) IN AZERBAIJAN

24---VARIABILITY IN THE POD AND SEED PARAMETERS AND NUCLEAR DNA CONTENT OF TUNISIAN POPULATIO_

25---ZEYTIN (OLEA EUROPAEA L.) GENOTIPLERININ DNA MARKÖRLERI YARDIMI İLE KARAKTERIZASYONU

26---COMBINING ABILITY AND GENE ACTION FOR FRUIT CHARACTER IN CHERRY TOMATO

27---HYBRID PURITY TESTING OF CHILLI HYBRID (PUSA JWALA×ARKA LOHIT) THROUGH RAPD AND ISSR MOLECULAR MARKERS

28----HETEROSIS AND INBREEDING DEPRESSION IN TWO CHILI PEPPER

29----IMPROVING NEW TRAITS BY MUTATION BREEDING IN SWEET CHERRY

30----IN VITRO SHOOT REGENERATION STUDIES IN BIRD OF PARADISE

31----STUDY OF NATURAL CROSS-POLLINATION IN CHILI PEPPER

32----YIELD AND QUALITY TRAITS OF DEVELOPED TOMATO LINES BY MUTATION BREEDING

33---DEVELOPMENT OF RESIST VARIET TO TOMATO SPOTTED WILD VIRUS ROOT KNOT NEMATODES IN PEPPER BY USI MOLEC MARKERS

34---EVALUATION OF CHRYSANTHEMUM VARIETIES FOR OPEN FIELD PRODUCTION

35---FROM FIELD TO THE GENES APPROACH FOR BREEDING OF POPULUS NIGRA

36---HETEROSIS AND COMBINING ABILITY STUDIES FOR HIGH TEMPERATURE TOLERANCE AND YIELD TRAITS IN TOMATO

37---MOLECULAR DETECTION AND BREEDING OF TOMATO YELLOW LEAF CURL VIRUS

38---MORPHOLOGICAL CHARACTERIZATION OF BOTTLE GOURD (LAGENARIA SICERARIA GENOTYPES COLLECTED FROM DIFFEREN

39---TOWARDS IDENTIFICATION OF RAPD MARKER LINKED TO THE VIGOR IN OLIVE TREE (OLEA EUROPEA )

40----A FIRST LOOK INTO PERCEPTION, SIGNALING AND GENE REGULATION OF FLAVONOID SYNTHESIS IN RESPONSE TO UV-B RADIATION IN GRAPEVINE

41---DETERMINATION OF TOLERANCE OF DEFICED IRRIGATION APPLICATION OF SOME PEPPER GENOTYPES

42----THE ESTIMATION OF COMBINING ABILITY AND HETEROSIS EFFECT FOR YIELD AND YIELD COMPONENTS IN TOMATO AT LOWLAND

43---CHARACTERIZATION OF S-ALLELES IN SWEET AND SOUR CHERRY BY ALLELE SPECIFIC PCR AMPLIFICATION IN CZECH REPUBLIC

44---DAMAGES OF GENERATIVE ORGANS BY MONILIA LAXA (ADERH.ET RUHL.) IN EARLY AND LATE FLOWERING APRICOT HYBRIDS

45---DETERMINATION OF PROPER GAMMA RADIATION (60CO) DOSE IN MUTATION BREEDING IN EGGPLANT (SOLANUM MELONGENA L.)

46--- DEVELOPMENT OF POLYMORPHIC MICROSATELLITE PRIMERS IN WALNUT (JUGLANS REGIA) DESIGNED FROM JUGLANS NIGRA GENOMIC GA ENRICHED LIBRARY SEQUENCES

47---DEVELOPMENT OF THE NEW CULTIVARS OF HAZELNUT BY SELECTION FROM TOMBUL HAZELNUT POPULATIONS IN GIRESUN AND TRABZON PROVINCES

48---EVALUATION OF GARLIC CULTIVARS FOR RESISTANCE TO ASPERGILLUS NIGER AND DISEASE MANAGEMENT OF NEW GARLIC DISEASE IN EGYPT

49---HAZELNUT BREEDING IN TURKEY

50---PRELIMINARY STUDY ON ANTHER CULTURE OF CABBAGE AND BROCCOLI

51---IDENTIFICATION AND PATHOGENICITY OF FUNGAL PATHOGENS CAUSING ROOT ROT AND WILT DISEASES IN WINTER SQUASH

52----MOLECULAR MAPPING OF ZYMV-1, A NEW DOMINANT GENE FOR ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV) RESISTANCE IN SQUASH (CUCURBITA PEPO)

53----BREEDING VALUE OF PARENTS AND PROGENIES OF SOME COCOA GENOTYPES FOR COCOA POD AND BEAN TRAITS

54----DEVELOPMENT OF POLYMORPHIC SSR PRIMERS IN PISTACHIO FROM ENRICHED GA REPEAT LIBRARY IN SIIRT CULTIVAR

55---PHYTOSANITARY STATUS OF FICUS CARICA COLLECTION IN CRIMEA AND FEATURES OF FIGS IN VITRO MICROPROPAGATION

56---GENETIC VARIATION AND MULTIVARIATE ANALYSIS OF FRUIT TRAITS FOR IMPROVEMENT OF POMEGRANATE (PUNICA GRANATUM L.) CULTIVARS

57---IMPROVED VEGETABLE VARIETIES FOR CENTRAL ASIA AND THE CAUCASUS DEVELOPED FROM

58----INHERITANCE AND STABILITY OF SOME AGRONOMIC TRAITS OF AFRICAN YAM BEAN (SPHENOSTYLIS STENOCARPA (HOCHST EX. A. RICH) HARMS)

59----INVESTIGATIONS ON THE RESISTANCE OF SOME PROCESSING WHITE HEAD CABBAGE

60----STRENGTHS AND WEAKNESSES TRAITS FOR BRASSICA VEGETABLE CROPS PRODUCTION OF TURKEY

61----THE DETERMINATION OF SALINITY TOLERANCE LEVELS AND THE EFFECT THE PLANT GROWTH AS USING ROOTSTOCKS OF TURKISH WINTER SQUASH GENOTYPES

62----USING DIFFERENT MOLECULAR MARKERS FOR BREEDING OF SOME HORTICULTURAL PLANTS

63----BREEDING OF PEAR CULTIVARS RESISTANT TO FIRE BLIGHT DISEASE MOLECULAR CHARACTERIZATION OR

64----GENETIC CONTROL RESISTANCE TO YELLOW VIRUS IN MELON (CUCUMIS MELO L.)

65----IMPROVEMENT OF F1 HYBRID VEGETABLE VARIETIES AND QUALIFIED LINES PROJECT IN TURKEY

66----LONG TERM ONION BREEDING PROGRAM IN TURKEY

67----PREPARING RNAI CONSTRUCT FOR FAD2 GENE FRAGMENT OF BRASSICA NAPPUS AS A STEP TOWARDS GENE SILENCING

68----SELECTION BREEDING OF WILD PRUNUS CERASUS L. CLONAL ROOTSTOCKS FOR SWEET AND SOUR CHERRIES

69----THE ROOTSTOCK BREEDING AND SELECTION STUDIES FOR CUCURBITACEAE VEGETABLES IN TURKEY

70-AUTHENTICITY OF TURKISH OLIVE CULTIVARS USING SNP MARKERS

71-CARROT BREEDING STUDIES AND CHARACTERISTICS IN TURKEY

72-CHARACTERIZATION, SOME AGRONOMIC TRAITS AND Β-CAROTENE CONTENTS OF ORANGE FLESHED ALTINBAŞ MELON DIHAPLOID LINES

73-DETERMINATION OF F1 HYBRID ABILITY OF SOME SQUASH LINES

74-DETERMINATION OF GENETIC DIVERSITY ON GENOTYPES OF TOMATOES BY SSR

75-DETERMINATION OF ROOTSTOCK POTENTIAL FOR ROOT-KNOT NEMATODE RESISTANCE OF CUCURBITA SPP. GENOTYPES

76-DETERMINATION ON MORPHOLOGICAL AND BIOACTIVE CHARACTERISTICS OF SOME WATERMELON LINES

77-DETERMINE THE MORPHOLOGICAL CHARACTERIZATION SELECTION BREEDING OF LOCAL TOKAT PEPPER POPULATION

78-DEVELOPMENT OF DOWNY MILDEW RESISTANT MARKERS FOR CUCUMBER BREEDING PROGRAM

79-DEVELOPMENT OF PEPPER LINES RESISTANT TO POTATO VIRUS Y (PVY)

80-DEVELOPMENT OF QUALİFİED MELON LİNES ACCORDİNG TO POWDERY MİLDEW

81-EFFECTS OF GRAFTING WATERMELON GENOTYPES FOR PLANT GROWTH, YIELD AND FRUIT QUALITY

82-FINE MAPPING OF SALT TOLERANCE TRAITS IN SOLANUM PENNELLII INTROGRESSION LINES

83-HYBRID SPINACH BREEDING-I

84-IDENTIFICATION AND ANALYSIS OF MDSEF1 GENE FROM APPLE (MALUS DOMESTICA)

85-IMPROVEMENT TO RESISTANT LINES FOR FUSARIUM OXYSPORUM

86-MEIOSIS OF FERTILE AND STERILE SUNFLOWER

87-MICROSATELLITE ASSESSMENT OF GENETIC DIVERSITY AMONG JORDANIAN TOMATO (SOLANUM LYCOPERSICUM L.) LANDRACE

88-NEW LIMONIUM SELECTIONS FOR CUT FLOWER SUMMER PRODUCTION

89-PERFORMANCE OF SOME EGGPLANT GENOTYPES UNDER COLD STRESS

90-PRELIMINARY RESULTS OF GENETIC LINKAGE MAP IN EDIBLE FIG (FICUS CARICA L.)

91-STUDIES ON IMPROVING CUCUMBER (CUCUMIS SATIVUS L.) LINES FOR CHILLING TOLERANCE VEYA

92---STUDIES ON VARIETAL SELECTION IN WALNUT (JUGLANS REGIA L.) POPULATIONS OF ÇANKIRI PROVINCE

93-STUDY OF THE INTERACTION OF PHYSCOMITRELLA PATENS AND PHYTOPATHOGENIC BACTERIA

94-THE DEVELOPMENT OF XANTHOMONAS AND TUMV RESISTANT DOUBLED HAPLOID LINES OF BRASSICA

95-USING DETERMINATION OF MORPHOLOGICAL CHARACTERISTICS DEVELOPED F1 HYBRID VARIETIES OF WHITE HEAD CABBAGE

96- ---HIGH RESOLUTION MAP OF EGGPLANT (SOLANUM MELONGENA)

97---GENOME POLYMORPHISM OF XANTHOMONAS ARBORICOLA

98---A NEW PROMISING FRUIT CHERRY LAUREL (PRUNUS LAUROCERASUS L.) AND STEPS ON BREEDING

99---AEGEAN AGRICULTURAL RESEARCH INSTITUTE TOMATO BREEDING STUDIES

100----CLEMENTINE × BLOOD ORANGE CROSSES

101----IN VITRO POLLEN VIABILITY AND POLLEN GERMINATION IN PRUNUS LAUROCERASUS L. (CHERRY LAUREL)

102----STUDY OF OVULE FERTILITY IN THE MANDARIN GROUP UNDER MANUAL AND OPEN POLLINATION CONDITIONS

103---DEVELOPMENT OF BAC-END BASED SIMPLE SEQUENCE REPEAT (SSR) MARKERS IN APPLE

104----AN EXAMPLE TO THE USE OF GENETIC RESOURCES FOR IMPROVEMENT THE RESISTANCE THE DEVELOPMENT OF NEW POWDERY MILDEW TOLERANT GRAPE VARIETIES

105---ANTHER CULTURES IN DIFFERENT ORNAMENTAL PEPPER GENOTYPES

106---BIOTECHNOLOGICAL STEPS IN STRAWBERRY TREE (ARBUTUS UNEDO L.) BREEDING

107---BREEDING OF SCAB RESISTANT APPLE VARIETIES

108----COLLECTION AND EVALUATION OF FRAGARIA GENOTYPES FROM TURKEY

109----CLONAL SELECTION OF CHERRY ROOTSTOCK CANDIDATES IN THE CENTRAL AND EASTERN

BLACK SEA REGION IN TURKEY

110---COMPARATIVE STUDY OF CALLOGENESIS OF TWO DATE PALM CULTIVARS

111---TRANSCRIPTIONAL CHANGES OF TOMATO PLANTS INFECTED WITH CLAVIBACTER MICHIGANENSIS SUBSP. MICHIGANENSIS

112---VVSTK1 ENCODES A PUTATIVE PROTEIN KINASE EXPRESSED DURING GRAPE BERRY DEVELOPMENT

113---INTRODUCTION TO PROTOPLAST CULTURE OF ALLIUM URSINUM AND A. SATIVUM

114---SCREENING OF TEN CITRUS ROOTSTOCKS TO DROUGHT STRESS

115---RED FLESH APPLES AND BREEDING STUDIES

116----MOLECULAR MARKER ANALYSES OF ALMOND AND PLUM F1 PLANTS FOR RESISTANCE TO ROOT KNOT NEMATODES

117---FRESH APRICOT BREEDING AT ALATA HORTICULTURE RESARCH STATION

118---THE NEW TABLE GRAPE CULTIVARS AND CANDIDATES

119---STATUS AND PROSPECTS OF PISTACHIO, PRODUCTION, BREEDING AND ITS GOALS IN KYRGYZSTAN

120---DEVELOPING CONFECTIONERY PUMKIN LINES AND HYBRIDS AND DETERMINATION OF THEIR YIELD PERFORMANCES

121---STUDIES ON CORRELATION AND PATH ANALYSIS OF TOMATO

122---IMPACT OF THE CITRUS CULTIVARS AND PEEL FIRMNESS ON FRUIT INFESTATION BY CERATITIS CAPITATA

123---NATURAL FORMATION OF VOLATILE CHLORINATED HYDROCARBONS

124---DETERMINATION OF CHROMOSOMAL GARNISH WITH SOME TABLE GRAPE VARIETIES AND THEIR HYBRIDS GROWN IN R. MACEDONIA

125---WINTERHARDY VEGETABLE PEA BREEDING FOR WYOMING, USA

126---INFLUENCE OF GROWTH REGULATORS ON CALLUS INDUCTION FROM EMBRYOS OF FIVE CITRUS ROOTSTOCKS

127--- BATEM SEKERI A NEW ORANGE SELECTION FROM CV. WASHINGTON NAVEL

128---INVESTIGATE OF SOME TOMATO GENOTYPES IN BREEDING OF TOMATO ROOTSTOCKS

129---TOMATO VARIETIES WITH HIGH INDICES OF PRODUCTIVITY AND RESISTANCE TO ENVIRONMENTAL FACTORS

130---EFFECT OF PLANT DENSITY ON THE STRUCTURE OF THE MONOBULB GARLIC HARVEST

131----COLLECTING, IDENTIFYING AND CULTIVATION OF NATIVE TULIPA ARMENA IN THE FLORA OF TURKEY

# DEVELOPED NEW LEMON VARIETIES AT BATEM; BATEM SARISI AND BATEM PINARI

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Between 1979-1983, carried out in all the Mediterranean and Aegean regions citrus “Citrus Budwood Selection-Certification and Variety Development” project 1 section, with different citrus ecological regions top selection of qualified individuals are selected from the Interdonato lemons. 4 promising types were determined and 2 of them has been registered as new lemon cultivars in 2011. BATEM Sarısı and BATEM Pınarı have been compared with Interdonato lemon in distinctness, uniformity and stability tests (DUS). In study results showed that BATEM Pınarı has larger fruit diameter and higher cumulative yield than Interdonato lemon. BATEM Sarısı has weaker prominence of nipple, thinner fruit peel thickness and higher average yield. The fruit maturation time was first week of October for both of them and Interdonato lemon.

**Key words:** Lemon, variety, register, selection

# COMPARATIVE ASSESSMENT OF SSR AND SRAP MARKERS FOR CHARACTERIZATION OF SEVEN ACCESSIONS OF CITRUS

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Molecular marker techniques allow the analysis and detection of genetic variation at the genomic level. The aim of the study is to compare different molecular markers (SSR and SRAP) and their application in seven citrus characterization. The study would also evaluate the genetic similarity obtained with both markers and compare their effectiveness in estimating genetic similarity among the Citrus accessions. Young leaves of Citrus plant collected from National Center of Citrus Breeding (NCCB), Huazhong Agricultural University (HZAU) Wuhan, China were used for genomic DNA extraction. Simple sequence Repeat (SSR) and Sequence related amplified polymorphism (SRAP) markers were used to identify, characterize and detect variation among the seven Citrus accessions. Significant molecular marker polymorphisms were detected among seven Citrus.  SSR proved to be the most efficient marker because of their capacity to reveal several bands in single amplification. The genetic relationship between the Citrus varieties was determined using Numerical Taxonomy System (NTSYS) statistical software.

# EVALUATION OF OKRA (*ABELMOSCHUS ESCULENTU)* GENOTYPES FOR OKRA YELLOW VEIN MOSAIC VIRUS IN NEPAL

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Okra is an important vegetable crop in the tropical and subtropical region of the world. Okra Yellow Vein Mosaic Virus (OYVMV) is one of the most important limiting factor for it's successful production in Nepal especially in rainy season. Yield loss 20-30% is common and it may increase up to 80-90% in case of a severe infestation. Use of resistance genotypes despite of manipulation of the sowing dates and vector controls are the main way of controlling OYVMV in Nepal. Therefore, a field screening of 48 okra genotypes collected from National Gene bank, Khumaltar against the disease was undertaken at Regional Agricultural Research Station (RARS) Khajura, Banke, Nepal in two main okra growing season (Summer and rainy seasons) of 2012-13. Disease were scored in 0-6 scale at seven days interval beyond 30 days after sowing, final disease severity (FRS), area under the disease progress curve (AUDPC) were calculated to assess the lines for resistance. The okra lines showed diversity in their responses ranging from highly resistant to highly susceptibility. Among the tested 46 lines, 14 lines were found highly resistant, 12 moderately resistant, 5 susceptible and 15 highly susceptible. The genotypes Arkaanamika, Parwani Kranit, ACCN#8418, ACCN#8419, ACCN#8427, ACCN#8113, ACCN#8409, ACCN8413, ACCN8415, ACCN#8416, ACCN#8418, ACCCN#8110, ACCN#8447 and ACCN#8438 were found highly resistant in natural infection condition of Khaura. The results obtained in this initial study reveal the future research thrust, potentiality and directions for the deployment of resistance source in development of OYVMV resistant okra varieties in Nepal.

# IDENTIFICATION OF TUNISIAN APRICOT GENOTYPES FOR FUTURE BREEDING PROGRAM: SELF-COMPATIBLE WITH FLOWER AND GOOD FRUIT QUALITIES

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Based on fruit characteristics (TSS, acidity, size, firmness, *etc*.), floral biology parameters (flower bud density, flower bud drop, flower necrosis, *etc*.) and self-compatibility trait, twelve local early ripening cultivars were studied, in order to select self-compatible ones and with good flower and fruit qualities as genotypes for new breeding program. Three cultivars Sayeb, Asli and Raki were identified as self-compatible ($S_7Sc$, $ScSc$, $ScSc$, respectively) with high flower bud density, lower flower bud drop and good fruit quality (juiciest, sweetened and the highest fruit weight, respectively). These cultivars are recommended for commercial plantations. Four cultivars Ouardi ($S_2S_7$), Oud Rhayem ($S_7S_{12}$), Oud Hmida ($S_2S_{12}$) and Oueld El Oud ($S_7S_8$) were described as self-incompatible. Ouardi had high flower bud density and the lowest flower bud drop, unlike the others three native cultivars. These cultivars had good fruit quality (the highest weight, juicy, the firmer and the sweetened, respectively) and were selected as genitors for new apricot breeding program.

***Key words:*** apricot, self-(in)compatible, flower quality, fruit quality, breeding, Tunisia.

# IMPROVEMENT IN TRANSCRIPTOMES ANALYSIS OF HORTICULTURAL CROPS USING NEXT GENERATION SEQUENCING

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In the last few years there has been rapid progress in the area of plant structural and functional genomics. Annotated genome sequences, transcriptomic data and genetic maps of plant species are potentially useful resources for improving crop breeding programs. Next generation DNA sequencing technologies which permit whole genome and transcriptome sequencing are relatively inexpensive and accessible for many research groups. In addition, these techniques will impact many of the current uses of molecular tools in plant evolution, phylogenetics, fingerprinting, linkage mapping and marker-assisted selection. As utilization of genomics knowledge and tools in different areas of plant breeding is still limited and challenging, so there is a strong need to push the development of plant genomics for the benefit plant breeding. Horticultural crops are playing significantly important roles in supplying nutritional, medicinal and economical demands of the world's population. According to importance of horticultural crops, use of the next-generation sequencing technologies has begun in these valuable crops. This paper highlights the evaluation of the next generation sequencing for transcriptome of horticultural crops for purposes of genome annotation, gene discovery and high throughput fingerprinting.

**Key words**: next generation sequencing, horticultural crops

# NEW SATSUMA MANDARIN VARIETIES WITH THIN PEEL; BATEM INCISI AND BATEM YILDIZI

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Mandarin production is 874.832 tons in Turkey and 61,33 % of total mandarin production is Satsuma mandarin in 2012. Between 1979-1983, Different citrus ecological regions top selection of qualified individuals at “Citrus Budwood Selection-Certification and Variety Development Project” are selected 23 promising types from the Satsuma mandarin types and 2 of them has been registered as mandarin cultivars in 2011. BATEM İncisi and BATEM Yıldızı have been compared with Satsuma Owari mandarin in distinctness, uniformity and stability tests (DUS). In study results showed that BATEM Yıldızı and BATEM İncisi have thinner fruit peel thickness than Satsuma Owari mandarin. Growth habit of BATEM İncisi trees have more drooping than Satsuma Owari and BATEM Yıldızı trees.

**Key words:** Mandarin, Satsuma, variety, register, selection

# MARKERS ASSISTED ASSAY OF THE TEA CULTIVARS GROWN IN PAKISTAN

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Tea crop is recently introduced in Pakistan. A large number of tea cultivars have been tested here, some of which have successfully gone to commercial cultivation. Most of these cultivars are unknown with respect to their botanical origin or have been mixed up during cultivation or nursery raising, hence their differentiation was imperative, which was carried out through the classical phenotypic and advanced DNA markers. Here we are presenting the analyses of 13 recognized cultivars and 130 tea accessions grown in Pakistan. The analyses is based upon for 18 quantitative, 7 qualitative traits, and two types of DNA markers viz. SSR and RAPD. The RAPD and SSR markers detected 87 and 75 alleles in 115 and 103 accessions, with an average 4.0 and 6.25 bands per accession per primer, respectively. Cluster analyses of the data discriminated all the accessions into two groups viz. broad and narrow leaved, corresponding to the species *Camellia sinensis* and *C. assamica*, respectively. The markers assisted assays confirmed that the origin of 11/ 13 cultivars was to *C. sinensis* and only two cultivars (CL-01-05 and IN-01-07) differentiated into *C. assamica*. On the basis of cluster analyses the origin of 117 unknown cultivars were also recognized. It was concluded that the tea crop grown in Pakistan is mostly of *C. sinensis* type.

**Key words:** Markers; RAPD; SSR, *Camellia,* Pakistan

# QTL ANALYSIS TO IDENTIFY METABOLITES POTENTIALLY RELATED TO THRIPS RESISTANCE IN PEPPER (*CAPSICUM*)

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In earlier studies we have shown that resistance to trips is expressed in leaves of certain *Capsicum* accessions. The current study was aimed at the identification of metabolites in pepper leaves that might be responsible for the thrips resistance, for which we used GC-MS and LC-MS analysis in combination with mQTL (metabolite quantitative trait loci) mapping. We could detect 55 metabolites by GC-MS and 674 by LC-MS. Of these, 242 could be mapped on the *Capsicum* genome and were shown to be unequally distributed, resulting in 'hotspots' and 'coldspots' of mQTLs. Of the metabolites, eighteen were significantly correlated with larval survival of thrips. Unfortunately, for only two of the correlated compounds the chemical identity could be determined from available libraries.The QTL mapping showed that mQTLs for two metabolites overlap with those for resistance parameters, which may indicate a relation between these metabolites and resistance against thrips.

**Keywords:** *untargeted analysis, larval mortality, GC-MS, LC-MS, metabolomics*

# RESPONCE OF SHALLOT CULTIVAR ILOKOS SOMATIC EMBRYO TO POLYETHILENE GLICOL 6000 IN IN VITRO CULTURE

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The aims of the experiment was studied the responce somatic embryo to polyethilene glicol 6000 (PEG-6000) as in vitro drought selection agent in *Allium ascalonicum* L. cultivar Ilokos. The experiment held at tissue culture laboratory, Agronomy and Horticulture Department, Faculty of Agriculture, Bogor Agricultural University, from August to December 2012. Experiment used Completely Randomized Design, single factor of PEG-6000. The factor was concentration of PEG-6000 consisted of 0%, 5%, 10%, and 20%, each treatment repeated 13 times. The results showed that 100% initial explant were induced become embriogenic callus in 2.4-D 2 mg $l^{-1}$ medium in third weeks after aplication. Good effect was obtained to complete somatic embryo growth from BAP 10 mg $l^{-1}$ with total number of somatic embrio formed was 454 embryos, but it could not encouraged plant regenaration. Generally, somatic embryos was supposed still survive for two weeks in 5%-20% PEG-6000 selection mediums.

**Keywords:** drought selection, 2.4-D, PEG-6000, shallot, somatic embryogenesis.

# DETERMINATION OF SUITABLE GA$_3$ CONCENTRATION AND EMBRYO GROWING STAGES FOR CULTURE OF EMBRYOS OBTAINED WITH HYBRIDIZATION OF COMMON SOUR ORANGE X CARRIZO CITRANGE, COMMON SOUR ORANGE X ALANYA DILIMLI ORANGE AND COMMON SOUR ORANGE X FLYING DRAGON

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Citrus rootstock breeding is quite important to improve their resistance against diseases, pests and adverse environmental conditions. Majority of citrus seeds have nuceller embryony. In this study; Sour orange x Carrizo citrange, Sour orange x Alanya Dilimli Orange and Sour orange x Flying Dragon were crossed. The seeds were gathered from the crossed plants 105, 115 and 125 days after pollinations. The immature embryos were removed from the seeds and these embryos were transferred to 0; 1 and 2 mg/l GA$_3$ containing Murashige&Tucker basal medium to germination. The highest germination rate was observed from 2 mg/l GA$_3$ containing M&T media which were harvested 125 days after pollination. Research results were showed be GA$_3$ in the medium for the immature embryo culture is necessary that 2 mg / l GA$_3$. Moreover, 125 days after pollination has been the best time for immature embriyo culture.

**Key words :** *Citrus*, pollination, embryo culture, GA$_3$, germination

# DETERMINATION OF HIGH TEMPERATURE TOLERANCE OF SOME PEPPER GENOTYPES

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Heat tolerance is generally defined as the ability of the plant to grow and produce economic yield under high temperatures. Heat stress due to high ambient temperatures to a serious threat to crop production worldwide. Especially, came out problems with production affect to producer directly. This study conducted to aim determine of high temperature of some pepper genotypes which suitable for grown open field and under greenhouses at growth room and two different locations. Fort his aim, screened 23 pepper genotypes (5 of them are sensitive and 18 of them are tolerant) at growth room were screened to Alata and conditions. It was determined fruit number (number/plant) and total fruit weight (g/plant). As obtained results, 32, 36, 414, 407, 441, 425, 100, 213, 414, 1747, and 475A number genotypes which screened and determined as tolerant at growth room were determined tolerant at two locations (Alata and Şanlurfa) had high performance. This results show that it can be develop high temperature tolerant genotypes which grown open field and under greenhouses.

**Key words:** Pepper, high temperature, tolerance

# BATEM GÖRAL; NEW MANDARIN CULTIVAR

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Citrus is the most widely produced fruit group in the world. Approximately 3 million tons of citrus fruit are produced in Turkey. With total export of one million tons, our country is ranking as the 4th Citrus exporter in the world and ranking as the 2nd among in the Mediterranean countries. Mandarin production is 874.832 tons in Turkey and 8,72 % of total mandarin production is Clementine mandarin in 2012. Different citrus ecological regions top selection of qualified individuals at “Citrus Budwood Selection-Certification and Variety Development Project” are selected 13 promising types from the Clementine mandarin types and BATEM Göral has been registered as new mandarin cultivar in 2011. BATEM Göral have been compared with Clementine mandarin in distinctness, uniformity and stability tests (DUS). In study results showed that BATEM Göral has larger fruit diameter.

**Key words:** Mandarin, Clementine, variety, register, selection

# DETERMINATION OF POLLEN VIABILITY PERCENTAGE AT SOME LEMON VARIETIES

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In this study, the viability and germination of pollen from some lemon varieties (*Citrus limon* (L.) Burm f.) (BATEM Sarısı, BATEM Pınarı, İnterdonato, Kütdiken, İtalyan Memeli, Meyer ve Lamas) were investigated. The viability test with TTC and in vitro germination test with agar–plate were used to estimate pollen viability and germination in these varieties. Experiment results showed that pollen of Meyer lemon had the highest viability with of 86.74%. Pollen viability of Kütdiken lemon with 54,57% followed Meyer lemon. It obtained that pollen of Lamas and Meyer lemon varieties had the highest *in vitro* germination with 39,77% and 39,04% respectively. This study results showed that 20% and 25% sucrose concentrations in the agar plates had the highest germination with 36,16% and 32,12% respectively.

**Key words:** Lemon, pollen, viability, germination, sucrose

# CHARACTERIZATION OF THE "*GALAPAGOS ENHANCED TRICOMES* (*GET*)" LOCUS: THE FIRST STEP IN THE RESISTANCE AGAINST INSECTS

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Trichomes are specialized epidermic structures mostly responsible for plant herbivory protection. The *Solanum* genus has been used as a model to study trichome differentiation. The genus contains a large range of different types of trichomes, including the glandular ones. Glandular trichomes are been called "biological chemical factories", since they produce and accumulate specialized metabolites. Cultivated tomato (*S. lycopersicum*) does not have type IV glandular trichomes, which are present in some wild species (e.g. *S. galapagense*) and are the main sources of the natural insecticide acyl sugar. The present work is an attempt to characterize a novel natural genetic variation from *S. galapagense* introgressed into *S. lycopersicum* cv. Micro-Tom (MT) that produces type IV trichomes. The locus was denominated *Galapagos enhanced tricomes* (*Get*). The most evident feature in the near isogenic line (NIL) harboring the *S. galapagense* allele is the presence of glandular trichomes type I and IV in both sides of the leaves. Since no enhanced AS production and neither insect resistance (*Bemisia tabaci*) were found in the NIL MT-*Get* we propose that the resistance should be the result of three requirements: i) the capacity to develop special glandular trichomes; ii) the correct localization of the trichomes in the leaves and iii) the capacity of the trichomes to produce specialized metabolites. The cloning of *Get* will give some insights about the development of glandular trichomes, besides to be a useful tool for breeding new resistant varieties with reduced use of pesticides.

# GENETIC ARCHITECTURE OF RESISTANCE TO MAJOR BIOTIC STRESSES IN OKRA (*Abelmoschus esculentus* (L.) Moench)

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Generation mean analysis of four crosses of okra (*Abelmoschus esculentus* (L.) Moench) *viz*., NBPGR/TCR-1498 x NBPGR/TCR-2060, NBPGR/TCR-2019 x Parbhani Kranti, MDU-1 x Varsha Uphar, NBPGR/TCR-985 x Parbhani Kranti was conducted for resistance to two major diseases viz., yellow vein mosaic (YVM) and leaf spot and to two major pests *viz*., fruit and shoot (F & S) borer and leaf roller. Six generations of each of the four crosses were grown in Randomized block design with three replications at a spacing of 60 x 45 cm during Summer season under field conditions at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram – 695 522, India. Data on five randomly selected plants from each plot in parents and $F_1$ and fifteen plants per plot in $F_{2,}$ $BC_1$ and $BC_2$ were recorded for the incidence of diseases and pests under study. In all the crosses evaluated, high significance could be noticed for *m* effect. Duplicate gene action was observed for resistance to all the biotic stresses under study, which indicated hindrance to improvement by simple selection. Hence reciprocal recurrent selection would be useful for the effective utilisation of both types of additive and non-additive gene effects simultaneously.

# COMBINING ABILITY THROUGH DIALLEL ANALYSIS IN OKRA (*ABELMOSCHUS ESCULENTUS* (L.) MOENCH)

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Combining ability analysis was carried out for fruit yield and its components in okra in a 6 x 6 diallel cross (excluding reciprocals). Both general combining ability (GCA) and specific combining ability (SCA) variances were highly significant for all the characters except days to first flowering and fruit diameter indicating the importance of both additive and non-additive gene actions. However, preponderance of additive gene action was recorded for the traits viz., number primary branches per plant, ridges/fruit and fruit diameter, preponderance of non-additive gene action was recorded for plant height, days to 50% flowering, number of fruits per plant, fruit length, fruit weight and fruit yield per plant. The parents BH-5, BH-1 and BH-2 were found to be the best general combiners and close correspondence between *per se* performance of parents and their gca effects were observed. The cross combinations *viz* BH-2 x BH-6, BH-1 x BH-3, BH-2 x BH-3, BH-2 x BH-4 and BH-1 X BH-5 showed significant sca effects in desirable direction for fruit yield per plant and associated characters and were expected to produce transgressive segregants. Magnitude of heterosis over better parent, the best parent was highly significant for total yield per plant. Out of 15 crosses, three crosses over better parent, three crosses over the best parent exhibited positive and significant heterosis for total fruit yield per plant. The hybrid which exhibited maximum heterosis BH-1 x BH-3, BH-1 x BH-4 and BH-1 x BH-5 these hybrids can be commercially exploited after assessing its stability for yield.

K**ey words:** Combining ability, gene action, diallel, fruit yield, okra

# DNA BASED DETECTION OF MYCOTOXIN PRODUCING PHYTOPATHOGENIC FUNGI

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Aflatoxin producing fungi (*Aspergillus flavus* and *Aspergillus parasiticus*) contaminate crops and processed food products thereby, making a serious concern not only in India but also in many other countries of the world. Their detection is much more important as these toxins damage liver when ingested alongwith food and feeds thus causing liver cirrhosis, cancer, etc. The prior detection can provide a signal of contamination of food and its products. In this study consensus sequence of a gene involved in aflatoxin biosynthesis, was selected for designing a primer set to amplify the aflatoxin producing molds. The designed primers were highly specific, the non-aflatoxigenic strains of same species did not show any amplification.  The method developed was able to detect as little as 1 pg of the target DNA. The amplified product could also be used to discriminate between the species based on restriction digestion pattern.

# GENETIC ANALYSIS OF ASSOCIATION STUDIES IN SEGREGATING POPULATION OF OKRA [*Abelmoschus esculentus* (L.) Moench]

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**Abstract:**

An experiment was conducted at K. R. C. College of Horticulture, Arabhavi, Belagavi during *Kharif* 2012. Two populations of the okra *viz.*, single cross $F_2$, and double cross $F_2$ were developed using BH-1, BH-2, BH-3, BH-4, BH-5 and BH-6. The objective was to determine the genetic variability, nature of association among different yield attributes and their direct and indirect contribution towards yield. From the analysis of variance, it was observed that mean squares due to genotypes were significant for all the traits, indicating the presence of genetic variability in the experimental material. The values of PCV were higher than that of GCV values for all the twelve characters indicating influence of environmental effects in the expression of these characters and it was found more in DC $F_2$ compare to SC $F_2$ population for almost all the characters. The GCV, heritability and genetic advance were higher for plant height, fruit yield per plant, fruit weight and days to 50 per cent flowering which might be attributed to additive gene action of inheritance in DC $F_2$ population. Characters showing moderate to high genetic gain also showed high heritability, indicating that most genetic variations in these characters were due to additive gene effects. From the correlation and path coefficient analyses, it revealed that the top priority should be given to selection based on numbers of fruit per plant, fruit length, fruit diameter and fruit weight for yield improvement and could be considered while formulating selection indices in the improvement of okra. Path coefficient analysis revealed that fruit weight had maximum direct contribution (0.869) towards fruit yield followed by number of fruits per plant (0.323), fruit length (0.079) and plant spread in North-South direction (0.076). However, plant spread in East-West direction showed highest negative direct effect (-0.007) in DC $F_2$ population compare to SC $F_2$ population. This revealed that DC $F_2$ population showed more variability compare to SC $F_2$ because it involves diverse parents in its development compare to SC $F_2$ population.

**Keywords:** Okra, single cross $F_2$, Double cross $F_{2,}$ Genetic variability, Correlation and Path analysis

# HIGH-FREQUENCY DEVELOPMENT OF LEAF-DERIVED CALLUS IN HAZEL (*CORYLUS AVELLANA*)

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Common hazel (*Corylus avellana*) is extensively cultivated in North America, Northwest Asia and Europe; consumed both in raw and processed forms; as well as in pharmaceutical industries. The latter makes it a valuable species for *in vitro* propagation. Several studies have reported embryogenesis from different plant organs. This study is focused on producing embryos from petiole and leaf-derived callus cultures. Leaf (1×1cm$^2$ segments) and petiole (1cm) cuttings were surface sterilized and subcultured in MS medium containing gradient combinations of 2,4-D+BAP, cultures refreshed every four weeks. Each growth regulator combination was replicated three times, with five cutting in each container. The calli were then moved to MS media (both solid and liquid forms) supplemented with gradient levels of 2,4-D+BAP, IBA+BAP, and IBA+Kin for embryogenesis stage; maintained under standard growth chamber conditions. The highest frequency of pre-embryo structure was obtained under 0.1 mg.l$^{-1}$ 2,4-D+0.1 mg.l$^{-1}$ BAP and 0.1 mg.l$^{-1}$ IBA+0.1 mg.l$^{-1}$ Kin for petiole and leaf cultures, respectively. Leaf cutting expressed significantly higher frequency of pre-embryo structure compared to petioles, where all samples expressed formation of pre-embryos. Reducing the nitrate level to 1/4-strength increased the pre-embryo formation, however embryo development was not observed in low-nitrate treatments. Except for BAP-based media, all other embryo-development media resulted in re-appearance of necrotic and/or non-differentiated callus tissue structure. These results suggest that maintaining leaf cutting explants in BAP supplemented media is a promising method to obtain embryos from leaf-derived callus cultures. The feasibility of different approaches is discussed.

**Keywords:** *Corylus avellana*, embryogenesis, callus

# PHENOTYPIC AND NUCLEAR DNA VARIATION IN TUNISIAN CULTIVARS OF DATE PALM *(PHOENIX DACTYLIFERA* L.)

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Five Tunisian palm date cultivars were evaluated, based on morphological traits and nuclear DNA content. The analysis of variance revealed highly-significant differences among cultivars (Alig, Bsser, Deglet Nour, Kinticha and Hamra) for average palm length (LP) (m), perianth diameter (PD) (mm), pulp thickness (ThP) (cm), 30 fresh fruit weight (30 FrW) (gr), 30 fresh seed weight (30 SW) (gr), 30 SW/30 FrW ratio (%), fresh seed length (SL) (cm), fresh seed width (SWi) (cm), and water content (WaC) (%).The relationship among these characters was analyzed by principal component analysis (PCA), resulting in the separation of these cultivars into three groups. The first group included Alig and Deglet Nour, characterized by high values for perianth diameter, pulp thickness, 30 fresh fruit weight and water content. The cultivar Hamra (H) formed a separate group, characterized by high values for seed width, 30 seed weight and 30 seed weight /30fruit weight ratio. This research shows that certain Tunisian cultivars, apart from Deglet Nour (Alig and Hamra), are particularly recommended for future selection and breeding programs. The morphological variation was not due to differences in ploidy, since the tested cultivars had 2C nuclear DNA contents of 1.729–1.80 pg and were all diploids (2n = 2x = 36). The data suggest that the Tunisian cultivars have limited geographical distribution and that *P. dactylifera* is an ancestral species.

**Key words:** Date palm, Fruit, Genome size, Morphological traits, Seed.

# OPTIMIZATION OF THE SEEDLESS MANDARIN'S PRODUCTION BY IMMATURE RESCUE OF EMBRYOS TRIPLOIDS

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Morocco has nearly 81.500 ha of citrus, of witch 51% (41.730ha) are devoted to the growing of various orange cultivars. Clementine and mandarins are the most horticultural important. There is tendency to increase the number of citrus cultivars with the high quality because of domestic or export market in the future. The citrus varietals improvement program of Morocco was based on clonal selection from germplasm or after genetic variability induction. Triploidy has played an important role in development of new seedless mandarin cultivars for fresh fruit market. The present work was undertaken to select promising triploid hybrids. Seri of diploid x diploid crosses was assessed. At maturity, the fruits have been harvested, and small embryos were extracted from undeveloped seed and cultured on medium of Murashige and Skoog supplemented with 1mg/l acid gebberilic. Triploid seedlings selected by flow cytometry analysis were planted in the field. A clonale selection was realized on basis of results of five years (2005-2009) for quality traits. Three promising mandarins' clones were identified as the best and are recommended for larger trials to evaluate yield potential and commercial acceptance of fruit.

**Key words:** Citrus, mandarins, embryos rescue, triploidy, flow cytometry,

# SELECTION OF CLEMENTINE VARIETIES USING AS FEMALE PARENT ACCORDING TO TRIPLOID EMBRYOS SPONTANEOUS PRODUCTION

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A long term research program on citrus breeding in Morocco INRA in order to find triploids seedless varieties, especially among the mandarin group. The reason for using Clementine as the seed parent in the crossing were its earliness, self incompatibility and monoembryony. For that, the crosses were made in 2012 using 16 Clementine cultivars as mother's trees. At maturity, the fruits have been harvested, and small embryos were extracted from undeveloped seed and cultured on Murashig and Skoog medium supplemented with 1 mg/L gebberilic acid'. Triploid seedlings will be selected following flow cytometry analysis. The small and undeveloped seeds number is variable. The best result is obtained with varieties *Muska* (25%), *Nour* (22%), *Berkane* (19%), *Herrandina* (17%), *Nules* (14%) and *Sidi-Aissa* (13%). The low percentage (7%) is marked at varieties *Ain taoujdat, Oroval* and *Janvier2.*The best female parent will be another breeding program to optimize the spontaneous generation of hybrid triploids mandarin fruit seedless.

# THE RESULTS OF BREEDING SEA-BUCKTHORN (*HIPPOPHAE RHAMNOIDES* L.) IN AZERBAIJAN

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The results of sea-buckthorn breeding in Azerbaijan are discussed. Assessment of the main biomorphological and economical traits of local varieties of sea-buckthorn (*Hippophae rhamnoides* L.) is given. Testing of varieties of sea buckthorn from the Russian Federation in three climate zones (Apsheron, Karabakh, and Shaky) did not justify the expected results. The varieties were found to be less fertile with a short vegetation period and of low tolerance to diseases and pests. Taking into account the national economic importance of biodiversity, the Genetic Resources Institute of the Azerbaijan National Academy of Sciences (AGRI) has started to restore the gene pool collection of 1972 in order to create high-yield and qualitative varieties of sea-buckthorn from local forms and introduced Altai varieties. As a result of experiments the cultivars ‘Shafa’, ‘Zafarani’ (female varieties) and ‘Tozlayan’ (male variety), which are suitable to local soil and climatic conditions, have been created. These are high-yield varieties (18 - 25 t/ha), big-fruited (each fruit’s weight is 50 - 60 g), weak-thorned (Zafarani, Tozlayan) or thornless (Shafa). These new varieties of the sea-buckthorn are of universal character: they can be used as fresh fruits, to prepare jam, juice, oil, liqueur, stewed fruit and much more. Thanks to positive bio-economical peculiarities, the profitability level for the products is high.

**Keywords:** breeding, characteristics, sea-buckthorn, varieties, wild forms

# VARIABILITY IN THE POD AND SEED PARAMETERS AND NUCLEAR DNA CONTENT OF TUNISIAN POPULATIONS OF *CERATONIA SILIQUA* L.

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The carob tree (*Ceratonia siliqua* L.) is widely used in arid and semi-arid areas of Mediterranean countries. We wished to determine the variability of its morphological parameters in relation to its exploitation for commercial purposes. Thirteen cultivated and fifteen spontaneous populations of *C. siliqua* from various edapho-climatic zones of Tunisia were compared to determine the variation in pod and seed parameters, for trees growing in situ, and in 2C nuclear DNA content (determined by flow cytometry), for seedlings grown from seeds collected in situ. Analysis of variance showed significant differences ($P < 0.0001$) between sites for fresh weight, length, width, internal and external thickness of pods, the pod length/width ratio, percentage of viable seeds and seed fresh weight. The mean pod fresh weights (range 8.63 – 36.03 g) of cultivated *C. siliqua* were greater than those of spontaneous trees (7.70–19.39). Similarly, for other morphological characters (pod length, width and thickness and seed weight), the cultivated trees showed the highest mean values: 19.46 cm, 2.22 cm, 0.91 cm and 0.20 g, respectively. How this variability could be exploited for agronomic and commercial purposes is discussed. The variation of the examined morphological characters was not correlated with the quantity of DNA, since there were no significant differences in nuclear DNA content among the cultivated or spontaneous individuals. The mean 2C nuclear DNA content was 1.20 – 1.30 pg, indicating the trees to be diploid ($2n = 24$).

**Keywords** Carob tree _ Genome size _ Pod morphology _ Seed viability _ Seed weight

# CHARACTERIZATION OF OLIVE GENOTYPES (*Olea europaea* L.) BY MEANS OF DNA MARKERS

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In this study, 96 genotypes in the National Ex-situ Olive Germplasm Bank have been characterized by DNA-based marker techniques such as RAPD, AFLP and SSR. In the marker analyses, 215 polymorphic bands from 52 primers in RAPD, 919 polymorphic bands from 26 primers in AFLP and 62 polymorphic bands from 14 primers in SSR have been obtained. A dendrogram and a genetic distance matrix have been established with the data of each technique seperately. Besides, the dendrogram and the genetic distance matrix have also been constructed by evaluating totaly 1196 polymorphic bands as a result of combining the data of these techniques. In the studied 96 genotypes, it has been determined that the lowest genetic distance value was 0.05 and the highest genetic distance value was 0.84 in RAPD marker analysis. In AFLP marker analysis, the lowest value was 0.15 and the highest value was 0.71 within the population in the context of genetic distance. As for SSR, the lowest and highest genetic distance values have been determined as 0.00 and 0.87 respectively. Evaluating the data of RAPD, AFLP and SSR marker analyses together, it has been determined that the lowest genetic matrix value was 0.14 and the highest genetic matrix value was 0.70.

**Key words:** Olive, RAPD, AFLP, SSR

# COMBINING ABILITY AND GENE ACTION FOR FRUIT CHARACTER IN CHERRY TOMATO (*SOLANUM LYCOPERSICUM* L. VAR. *CERASIFORME* MILL)

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Genetic information on combining ability and the type of gene action that governs the inheritance of economically important quantitative characters can be an immense help to the breeder. Such information can assists the plant breeders in selection of suitable parents and the appropriate breeding procedure. A study was conducted on an 8 × 8, diallel mating design to determine combining ability and nature of gene action for nine fruit characters in cherry tomato. Significant differences among genotypes were obtained for all the traits. Among the eight parental lines, L 02846 , L 00427, Arka Vikas , L 00398, L 01696 and L 04780 were the best combiner for fruit firmness, pericarp thickness , *L** (lightness) and *b* *(yellowness) colour values, *a* *(redness), lycopene content, TSS, reducing sugar and ascorbic acid parameters respectively. Thus these parental lines could be used in cherry tomato hybridization programme. Crosses showing high specific combining ability (SCA) L 00427 x Arka Vikas, L 00427 x L 03686 and L 00427 x L 00196 for most of the characters. The dominance effects ($H_1$ and $H_2$) were higher than the additive effect (D), which showed preponderance of non-additive gene action plays a greater role in the inheritance for all the characters in this study. . Recurrent selection and reciprocal recurrent selection could be suitable breeding procedures for rapid improvement.

**Keywords:** Combining ability, gene action, quality, cherry tomato

# HYBRID PURITY TESTING OF CHILLI HYBRID (PUSA JWALA×ARKA LOHIT) THROUGH RAPD AND ISSR MOLECULAR MARKERS

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A fast and accurate genetic purity test of $F_I$ hybrid plants is essential for seed production and accelerating advanced breeding generations in breeding programmes. DNA technology has great potential for enhancing purity assessment of hybrids. Chilli $F_1$ hybrid (Pusa Jwala × Arka Lohit) and its parents Arka Lohit (male) and Pusa Jwala (female) was analyzed for the development of markers, identification of Hybrids and ascertaining genetic purity in *Capsicum annuum* L. through PCR based Random Amplified Polymorphic DNA (RAPD) and Inter Simple Sequence Repeats (ISSRs) DNA Markers. Twenty seven RAPD primers of Operon series and twenty ISSR primers were used for analysis. RAPD primer, OPA 15 and OPD 16 were found to be heteroallelic for parents. OPA 15 identified male specific amplicons of about 1200bp and OPD 16 produced male specific amplicon of about 1100bp in the hybrid (Pusa Jwala × Arka Lohit). The other repeats of different base pairs were homoallelic for both the parents. All twenty ISSR primers used were found to be homoallelic for both the parents. This was due to the RAPD marker system producing a greater number of markers than the ISSR system. OPD 16 identified a female-specific amplicon of about 800bp in the hybrid (Pusa Jwala × Arka Lohit). Comparison of the two RAPD banding pattern of the parents with respective hybrid clearly identified genuine hybrid. Thus RAPD markers individually have their own merits in the identification of parents and their hybrids. However, a combination of two PCR based markers can be used for testing the genetic purity of chilli seeds or seedlings, which will be more reliable substitute for GOT and a tool for seed certification. This study suggested that efficiency of RAPD assay was evaluated successfully for hybridity determination, which would be a valuable genomic tool for the chilli breeders.

**Key words:** Chilli, hybridity test, RAPD, ISSR and GOT

# HETEROSIS AND INBREEDING DEPRESSION IN TWO CHILI PEPPER (*CAPSICUM ANNUUM* L.) POPULATION THAT HAS DIFFERENT DEGREEL OF NATURAL CROSS POLLINATION

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The degree natural cross pollination of chili pepper which had not been consistently led to allegation of high heterosis and inbreeding depression in chili pepper. The objectives of this research were to study of heterosis and inbreeding depression in two chili peppers population that had different degree of natural cross pollination. The experiment was conducted from September 2012 to December 2012 at Bogor Agricultural University experimental field, Leuwikopo, Dramaga. The first population was IPB C2 x IPB C5 population (had high natural cross pollination) consist of seven set generations (F1, F2, F3, F4, F5, F6, and F7). The second population was IPB C120 x IPB C5 (had the lower natural cross pollination) consist of five set generations (F1, F3, F4, F5, and F6). All of those set generations planted at the same time. Beside those population, were planted too the parent genotypes (IPB C2, IPB C5, and IPB C120). Heterosis was estimated by comparing the means of F1 and the mid parents. Inbreeding depression was predicted by linier regression between level generation and the means of each character. The first population had positive heterosis in each character. But the second population just had positive heterosis in one character. Heterosis was varied from 3.8% - 41%. Inbreeding depression was clear in the first population, when the regression coefficient of each character was negative, but it was different with the second population which had positive regression coefficient in all of characters.

**Keywords:** Heterosis, inbreeding depression, chili pepper

# IMPROVING NEW TRAITS BY MUTATION BREEDING IN SWEET CHERRY

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In this study, mutaiton breeding aplications initiated in 2000 on 0900 Ziraat sweet chery variety and the achieved progres were presented. Buds were irradiated with eight differnt dose of gamma radiation. Effective mutation dose determined as 33.75 Gy and mutation frequency were calculated as 4.1%. Morphological, pomological and quality characteristics were investigated in the obtained population beginning from nursery to grown stage. Tree size, fruit weight, peduncle length, fruit size and % soluble solid content were used as selection criteria. Up to now, two mutant variety candidates on the way of registiration procedure.

**Keywords:** Sweet cherry (*Prunus avium* L.), mutation breeding, gamma ray

# IN VITRO SHOOT REGENERATION STUDIES IN BIRD OF PARADISE

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Bird of paradise is an important cut flower crop which is commercially propagated by suckers. The present investigation was undertaken to develop a viable protocol for micropropagation of bird of paradise to bypass the slow rate of multiplication of traditional methods. Shoot tip was used as explants after surface sterilization and tested for shoot multiplication and rooting. The best rate of shoot regeneration was obtained on MS medium supplemented with BAP 3.0 mgL$^{-1}$. The highest multiplication of shoots was observed on MS medium supplemented with BAP 3.0 mgL$^{-1}$ + NAA 0.3 mgL$^{-1}$. The early root initiation (35.9 days) with maximum per cent of rooting (84.44%) with was observed in half strength MS medium + 2.0 mgL$^{-1}$ IAA.

**Key Words:** Bird of paradise, Shoot regeneration, Shoot multiplication, Rooting

# STUDY OF NATURAL CROSS-POLLINATION IN CHILI PEPPER (*CAPSICUM ANNUUM* L.)

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The objectives of this research were to study the effects of genotypes and spacing radius on percentage of natural cross-pollination in chili pepper. The experiment was conducted from Oktober 2011 to March 2012 at IPB experimental field, Leuwikopo, Dramaga. The experimental design refers to Aries and Riesberg design. This experimental was used four genotypes (IPB C2, IPB C5, IPB C20, and IPB C120) and five spacing radius (0.5, 1, 1.5, 2.5, and 3.5 m). Determination of natural cross-pollination based on purple colour on pepper hypocotyl. The result showed that there were variation percentages of natural cross-pollination between chili pepper genotypes. Two genotypes had percentage natural cross pollination higher than 10%. The closest spacing radius wasn't show the highest percentage natural cross pollination.

**Key Words:** chili pepper, cross-pollination, genotype, hypocotil, purple

# YIELD AND QUALITY TRAITS OF DEVELOPED TOMATO LINES BY MUTATION BREEDING

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Some of the data obtained from the mutation breeding study of Ayaş originated field grown tomato which has an economic value for Central Anatolia Region have been presented in terms of the improvement of yield and quality traits. 150 Gy is used for seed irradiation as the effective irradiation dose ($ED_{50}$). Yield, fruit firmness, dry matter, brix and antioxidant (lycopene, beta carotene, lutein and vitamin C) content analysis have been started at $M_4$ generation and continued at each stage. In this study, results of the 16 selected mutant lines at $M_5$ stage and control material have been presented for yield, fruit firmness, dry matter, brix level. According to statistical results of brix and dry matter content, there is no significant difference between the mutants lines and control, whereas the statistical importance have been determined between mutants lines and control for both yield and fruit firmness. 9/31, 9/22, 8/127 and 8/50 coded mutant lines for fruit firmness and 9/22, 8/127, 8/135 and 8 /96 coded mutant lines for yield have shown better performance than control. The studies still continue in terms of registration process on selected mutant lines.

**Key words:** Tomato, mutation, mutation breeding, gamma irradiation

# DEVELOPMENT OF RESISTANT VARIETIES TO TOMATO SPOTTED WILD VIRUS AND ROOT KNOT NEMATODES IN PEPPER BY USING MOLECULAR MARKERS

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Pepper is one of the widely cultivated vegetables in the world. It also has a great significance in Turkey because of its product area, yield and import. The most important factor that restricts cultivation is management of the pathogens including viruses and root-knot nematodes. These pathogens have worldwide distribution and they are particularly devastating in regions where provides ideal conditions for disease development. Methods to control these pathogens such as cultural practices, the use of certified seed, weed control, solarization etc., and chemical control are inadequate. Negative effects of chemicals on human health and environment are also proven. These problems have led to the use of genetically controlled resistances as an alternative technique of disease control. Molecular markers have been used in plant breeding programs since they discovered. The major aim of this study is to develop pepper varieties which have several resistant genes (gene pyramiding) by using marker assisted breeding techniques. Pure and breeding lines that were obtained from Lider and AD-ROSSEN seed companies, domestic seed companies in Turkey, have been screened by molecular markers closely linked to genes confers resistance to tomato spotted wilt virus (Tsw) and nematodes (Me1, Me3, Me7 and N). As these lines have been scanned for the pathogen resistance, they have been appraised by their yield and quality performances as well. In total 773 individuals have been examined to identify their behaviors as an example of resistant or susceptible against the pathogens so far. After all screening and scanning process, 455 homozygous resistant and 117 heterozygous resistant individuals have been founded. Then various crossing and backcrossing programs have been carried out in cooperation with seed companies to improve their varieties. The expectation at the end of this study is having several F1 hybrid pepper varieties carrier of four or five resistant genes.

**Key words**: Molecular markers, resistant varieties, pepper, Tomato spotted wild virus, nematode

# EVALUATION OF CHRYSANTHEMUM VARIETIES FOR OPEN FIELD PRODUCTION

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This study was conducted to evaluate the outdoor production of chrysanthemum (*Dendranthema grandiflora*) cvs. Kodiak 'yellow', Ivyridgf 'white', Auburn 'red' and Lansing 'pink') by using the growth retardant Alar and slow-release fertilizer Osmocote applications. Significant differences were observed between varieties for all the morphological and floral characters studied. Alar at 0, 1500, 3000 and 4500 ppm as a foliar spray and Osmocote (14N-6.1P-11.6K) (14– 14–14) incorporated in potting substrate at 0, 70, 140 and 280 mg kg$^{-1}$soil. Among different treatments, 1500 ppm gave reduction in plant height, leaf area, node production or flowering and early flowering. However, the best performance was found for other characters like number branches, number of leaves per plant, maximum duration of flowering, time to marketability, flower weight, flower diameter, number of flowers per plant. The highest recorded data were obtained in plants treated with Alar 1500 ppm on chemical constituents, (chlorophylls relative content, reducing and non-reducing sugars and concentrations of N, P and total K).The remarkable increase in growth and flowering parameters were found with Osmocote treatment at 70 mg kg$^{-1}$soil. Therefore, single application of foliar Alar at 1500 ppm and Osmocote fertilizer at 70 mg kg$^{-1}$soil are the recommended treatments for raising productivity and improving quality of different cultivars chrysanthemum and may be exploited commercially in horticulture industry to fetch premium price for cut flowers.

**Keywords**: Slow release fertilizers, Alar, chrysanthemum plants, growth response.

# FROM FIELD TO THE GENES APPROACH FOR BREEDING OF *POPULUS NIGRA*

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Accomplishment of the whole genomic sequences of *Populus* provides an opportunity to interrogate the impact of environmental stress factors on the trees.  In Turkey, breeding program of Populus nigra accelerated with identification, selection and transferring of clones from almost all around the country in recent years. Therefore, it is time to go from field to the genes that are responsible in mechanisms of many stress factors. In the current study, the genetic nature of tree adaptation to drought stress was firstly examined in a field trial with 300 *Populus nigra* genotypes. After determination of contrasting tolerance to drought in the field, a greenhouse experiment was carried out with the most resistant (N.62/191) and susceptible (N.03.368.A) two *P.nigra* clones. During the experiment one year old trees were submitted to a moderate and severe water deficit by withholding irrigation and ended with re-watering of the drought treated trees. Microarray experiments conducted on the leaves collected at these different water deficit levels and compared with the control plants for both genotypes. Our analysis detected several candidate genes and processes that are differentially regulated in leaf for different drought level. Our analysis end up with identifiacation of bark storage proteins that are highy related with drought tolerance in populus. By using the genetic information obtained from microarray experiments we established a molecular breeding approach for *P.nigra*.

# HETEROSIS AND COMBINING ABILITY STUDIES FOR HIGH TEMPERATURE TOLERANCE AND YIELD TRAITS IN TOMATO *(SOLANUM L YCOPERSICUM* L.)

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Lack of tolerance to high temperature in most tomato cultivars presents a major limitation for growing them in regions where the temperature during part of the growing season, even for short duration, reaches 38°C or higher. In this view a study was conducted in tomato using a half diallel set (10 parents and their 45 hybrids) at vegetable Research farm, Institute of Agriculture Sciences, BHU, in randomized complete block design, with 3 replications. Each genotype was represented by 25 plants/replicate. Observations on pollen viability pollen germination, stigma exertion and yield under the high temperature conditions were recorded. The highest significant heterosis was recorded in crosses FLA-7171 x Selection-7 (57.57%) for pollen viability, NDTVR-60 x Selection-7 (25.54%) for pollen germination, Pusa Sadabahar x H-86 (-74.46%) for stgma exertion while FLA-7171 x Selection-7 (68.74%) manifested higher heterosis ability effect was recorded in Pusa Sadabhar for pollen viability, pollen germination stigma exertion while FLA-7171 and Selection-7 for yield per plant. The highest significant specific combining ability effect was observed in FLA-7171 x NDTVR-60 for pollen viability and pollen germination where as highest negative significant specific combining ability effect for stigma over better parent for yield/plant under heat stress. The highest general combining exertion was absorbed in crosses Kashi Amrit x Floradade. The crosses H-88-74-1 x Selection-7 exhibited the highest specific combining ability for yield per plant. Pusa Sadabahar, FLA-7171 and Selection-7 among lines and crosses FLA-7171 x Selection-7 and FLA-7171 x NDTVR-60 can be used for subsequent tomato breeding program for tolerance to temperature stress.

# MOLECULAR DETECTION AND BREEDING OF TOMATO YELLOW LEAF CURL VIRUS

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**Abstract:** Tomato yellow leaf curl virus (TYLCV) is currently considered as one of the most devastating viruses in cultivated tomatoes (*Solanum lycopersicum*) worldwide. We reported here the development of a PCR-based method to quickly detect TYLCV using the primer pairs (TYLCV-F: 5-ACG CAT GCC TCT AAT CCA GTG TA-3 and TYLCV-R: 5-CCA ATA AGG CGT AAG CGT GTA GAC-3), which was designed based on the genome sequence of TYLCV. A TYLCV-specific band of 543 bp was amplified from infected tomato plants. This protocol provides a rapid, reliable, and sensitive tool for molecular detection and identification of TYLCV in the industrial seedling and virus resistance breeding to facilitate safe and sustainable production of tomato.

**Key words**Tomato Yellow Leaf Curl Virus TYLCV, Specific Primer, Molecular Detection

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# MORPHOLOGICAL CHARACTERIZATION OF BOTTLE GOURD (*Lagenaria siceraria* (Malign) Stanley) GENOTYPES COLLECTED FROM DIFFERENT REGIONS OF TURKEY

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The bottle gourd [*Legenaria siceraria* (Malign) Stanley] was one of the first domesticated plant species for human utilization has been grown for different purposes in our country for many years. The collection works of the materials used in this study were conducted under frameworks two different projects supported by TUBITAK from 2003 to 2011. Genotypes collected from different regions of Turkey and introduced from different the international gene banks as well. Seed of the collected 402 genotypes were sown for seedling production under greenhouse conditions but 320 genotype emerged. The bottle gourd genotypes grown in open field were morphologically characterized for 25 quantitative and 30 qualitative traits in 2012. Results of qualitative traits were presented in this study. In morphological characterization, accessions were evaluated for 30 characteristics consist of 1 seedling, 3 plant, 8 leaf, 5 flower, 10 fruit and 3 seed characteristics. The genotypes showed variation at different rate in traits investigated in this study.

**Keywords:** Bottle gourd(*Lagenaria siceraria*), morphological characterization, Turkey.

# TOWARDS IDENTIFICATION OF RAPD MARKER LINKED TO THE VIGOR IN OLIVE TREE (Olea europea )

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## Abstract

Olive culture in Morocco occupies about 58 % of the total national arboricultural species. Despite the importance of this sector, the Moroccan olive does not yet meet the expectations for production and quality. Improving olive oil production can be achieved through genetic improvement, which involves the creation of genetic variability that will enable progress in performance and potential of our heritage Olive. Thus, a breeding program was set up by INRA since 1994. Crosses between selected clones from "Picholine Marocaine" ("Menara", "Haouzia", "M26") and foreign varieties ("Manzanilla", "Picholine de Languedoc" and "Arbequina") were performed. In this study, progeny from a cross between the variety "Menara" and "Arbequina" was characterized morphologically and by molecular markers RAPD (Random Amplified Polymorphism DNA). The technique Bulk Segregant analysis (BSA) was used to establish linkage between molecular markers and vigor tree. Thirty-seven decamer primers were used to compare the bulks of individuals having a high vigor and low vigor. six primers were selected for their ability to detect polymorphism between the two bulks. Subsequently, one of these primers was tested in parents and offspring separately. The analysis of individual RAPD profiles showed no linkage between RAPD band and the trait in the progeny. Further analysis is in progress to identify marker for vigor tree.

**Keywords:** *Olea europea,* morphological characterization, molecular marker, RAPD, BSA.

# A FIRST LOOK INTO PERCEPTION, SIGNALING AND GENE REGULATION OF FLAVONOID SYNTHESIS IN RESPONSE TO UV-B RADIATION IN GRAPEVINE

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Ultraviolet-B radiation (UV-B, 280-315 nm) is an intrinsic part of sunlight. Due to its high energy, this type of radiation causes significant biological effects in plants. To optimize their growth and survival, plants perceive and respond specifically to UV-B radiation. UV-B perception in the model plant *Arabidopsis* is carried on by the UV-B photoreceptor *UVR8*, which is linked to a specific molecular signaling pathway and leads to UV-B acclimation by mechanisms such as DNA damage repair, hypocotyl length reduction and flavonoids synthesis. Flavonoids encompass a diverse group of phenolic secondary metabolites with important roles in UV-B protection. Their biosynthesis is largely regulated by MYB-mediated control over the transcription of key genes of phenylpropanoid pathway. However, there are no information on perception, signaling and MYB-mediated transcriptional regulation of flavonoid synthesis in response to UV-B in *Vitis vinifera*. Therefore, understanding the effect of UV-B radiation on grapevines will help to determine the managements with higher impact on the accumulation of flavonoids in grapes. In this study, we characterize the grapevine UV-B photoreceptor homologue to *UVR8*, named by us *VvUVR1*; the bZIP transcription factor *VvHY5* and MYB transcription factors related to flavonoid synthesis in response to UV-B. Here, for the first time, we were able to correlated the expression of genes related to UV-B perception, signaling, transcriptional regulation and biosynthesis of flavonoids with the accumulation of these phenolic compounds in skin during grape berry development, when berries are exposed to UV-B radiation. The relevance of UV-B mediated gene expression controlling flavonoid biosynthesis for manipulation of wine quality is discussed.

**Acknowledgements:**

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# DETERMINATION OF TOLERANCE OF DEFICED IRRIGATION APPLICATION OF SOME PEPPER GENOTYPES

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Water deficit is one of the main limiting factors affecting plant distribution. Selection in water-limited environments can result in populations or species with suites of traits that improve their relative fitness in response to drought.  It occur decreases at yield and quality because of drought when it wouldn't managed to water resources in the world. It is important genotypes which will be tolerate to deficient irrigation application conditions in peppers. It is aimed that determine tolerance of deficient irrigation conditions of 69 pure pepper lines in this study. For this aim, experiment were conducted at growth room and two different field conditions (Alata and Sanlıurfa) as control (100%) and application(50%). Fruit weight, fruit length and fruit number were recorded. As obtained results, 1900, 896 A-W, 74, 760, 1560-W, 912 A-W, 405-A, 953-W, 226, 1105-W and 441 numbered pepper lines were determined as showing high performance pepper lines. Results of this study show that this pepper lines which used at this study can be used for develop cultivars which don't cause yield decrease at places which there is water deficit.

**Key words:** Pepper, water deficient, screening

# THE ESTIMATION OF COMBINING ABILITY AND HETEROSIS EFFECT FOR YIELD AND YIELD COMPONENTS IN TOMATO (*LYCOPERSICON ESCULENTUM* MILL.) AT LOWLAND

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A study was conducted on a 6 × 6 full diallel cross set of tomato including reciprocals to estimate of general combining ability (GCA), specific combining ability (SCA) and heterosis effect for yield per plant (g) and yield components, at the lowland area. Included as the yield components are number of fruits per plant, individual fruit weight (g), fruit length (cm), fruit diameter (cm), locule number, and fruit thickness (cm). The experiment was conducted from March to August 2013 at Bogor Agriculture University Experimental Field, Bogor-Indonesia. Randomized Complete Block Design was used with three replications. Data from Fl generation and parents were analyzed using the Griffing Method. Significant differences among genotypes were obtained for all of traits. The variances for GCA and SCA were highly significant indicating the presence of additive as well as non-additive gene effects except for the fruit thickness. The tomato genotype IPB T78 is the genotype with the best general combining ability for yield per plant, individual fruit weight, fruit length, and fruit thickness. The tomato genotype IPB T73 x IPB T3 proved to be the best general combiner for yield and number of fruits per plant. The tomato genotype IPB T3 x IPB T1 proved to be best heterosis for yield per plant and fruit thickness.

**Key Words:** Combining ability, diallel, GCA, heterosis, SCA

# CHARACTERIZATION OF S-ALLELES IN SWEET AND SOUR CHERRY BY ALLELE SPECIFIC PCR AMPLIFICATION IN CZECH REPUBLIC

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In sweet cherry self-incompatibility and cross incompatibility are governed by the S-locus. The exhibiting gametophytic self-incompatibility, individuals harbouring rare S alleles in cherry populations are likely to have a reproductive advantage over individuals having more common alleles. Thus, determination of the self-incompatibility haplotype of individuals is essential for genetic studies and development of informed management strategies. In this study the S-genotypes of 20 cultivars were characterized using previously published primers of sweet cherry ***S***-RNases conserved sequences and allele specific primers. Two S-alleles were amplified in all 20 cultivars. $S_3S_6$ was the most frequent cross incompatibility group observed in this study of sweet cherry cultivars. $S_1$ and $S_3$ are the most common in the cultivars evaluated, however $S_5$, $S_7$, $S_{10}$, $S_{12}$, $S_{14}$, $S_{16}$, $S_{18}$, $S_{19}$, $S_{21/25}$, $S_{34}$ and $S_{37}$ are rare alleles and not found among studied cultivars. Moreover, one rare cross incompatibility group was identified with $S_1S_{13}$ genotype comprising sour cherry cultivar 'Morella Feure'. Among two unknown cultivars expected 'Burlat' ($S_3S_9$) we determined $S_1S_2$ genotype, however individuality of variety could not be secured. The cultivar 'Janovka Msenska' was determined as $S_1S_2$ genotype while its expected replica has the $S_4S_6$ allelic constitution. We expected that it has been swapped during planting with Kastanka ($S_1S_2$) however yet to be determined with more supportive investigation. Allele-specific PCR amplification or using degenerated primers alone is not capable enough to identify all the S-alleles in the cultivars; however combination of methods provides a rapid and efficient approach for identifying the S-genotypes of sweet cherry cultivars.

**Keywords:** Sweet and sour cherry, gametophytic self-incompatibility, PCR

# DAMAGES OF GENERATIVE ORGANS BY *MONILIA LAXA* (ADERH.ET RUHL.) IN EARLY AND LATE FLOWERING APRICOT HYBRIDS

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The aim of the work was the determination of biological features for hybrid apricot plants and their original forms with different length of blossom period and intensity of damages by *Monilia laxa*. Investigations have been carried out during 2001-2010 years. The apricot cultivars Kostinsky, Olimp, Zapozdaly, Krasny Krym, Naslazhdenye, Pasynok, Forum and their hybrids have been studied. Signs “the date of blossom beginning”, “the date of mass blossom”, “the date of blossom end” and fruits productivity are connected to each other with close direct dependence. At the same time connection with the level of *Monilia laxa* damages is not substantial. Only during the evaluation of the selections included late flowering hybrids the direct reliable correlation between the length of blossom and the level of damages by *Monilia laxa* (r= 0.28; P= 0.95) has been shown. The great interest has the hybrid 89-547. During the nine years flowers and shoots of this hybrid haven’t damaged by this disease for more than 0.5-1.5 points. Only in 2008 they reached 2.0 points. The sign “the date of blossom end” is positively connected with plants’ productivity in all variants of the experiment and it testifies that breeding of late flowering forms is perspective. Breeding for apricot plants with late blossom period allows us to obtain hybrids damaged lightly by *Monilia laxa.*

# DETERMINATION OF PROPER GAMMA RADIATION ($^{60}$CO) DOSE IN MUTATION BREEDING IN EGGPLANT (*SOLANUM MELONGENA* L.)

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This study was counducted to determine the proper dose of gamma irradiation for the mutation breeding program of eggplant (*Solanum melongena* L.). To serve the purpose, seeds of BR-12 and Anamur eggplant genotypes were subjected to different doses of gamma rays (0, 80, 120, 160 and 180 Gy) with Cobalt 60 ($^{60}$Co) by irradiation and some characteristics of $M_1$ plants , emmergence rate (%), shoot length (cm), shoot fresh weight (mg/plant) and shoot dry weight (mg/plant) and leaf width / height index (cm), were studied. The experimental results revealed that doses of gama rays used to develop new generation and create variation were varied in accordance with genotypes and different doses lead to significant reductions in the inspected characters of two eggplant genotypes. Applicabe appropriate dose without any reduction, for BR-12 genotype was determined as 160gy, no sufficient reduction was observed for effective dose for Anamur cultivar.

**Key words:** Eggplant, mutation breeding, efficient dose, gamma ray

# DEVELOPMENT OF POLYMORPHIC MICROSATELLITE PRIMERS IN WALNUT (*JUGLANS REGIA*) DESIGNED FROM *JUGLANS NIGRA* GENOMIC GA ENRICHED LIBRARY SEQUENCES

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In this study, it was aimed to develop new polymorphic SSR primer pairs in walnut using sequences derived from *J. nigra* genomic enriched library with GA repeat. The designed 94 SSR primer pairs were subjected to gradient PCR in 12 walnut cultivars to determine their optimum annealing temperatures and to see whether they produce bands. Then, the primer pairs which had amplification in agarose gel were analyzed in capillary electrophoresis to determine their allel sizes. According to the gradient PCR and capillary electrophoresis reasults, 60.6 % of the SSR primer pairs did not amplified any bands in agarose gel. Rest of the 37 primer pairs produced bands and their annealing temperatures and allel sizes were determined. From the amplified primer pairs, 18 of them monomorphic, whereas 19 of them were polymorphic. As a result, 20.2 % polymorphism was obtained from 94 SSR primer pairs tested in this study which was low ratio when compared to literature.

**Key Words:** SSR, Walnut, Polymorphism, PCR

# DEVELOPMENT OF THE NEW CULTIVARS OF HAZELNUT BY SELECTION FROM TOMBUL HAZELNUT POPULATIONS IN GIRESUN AND TRABZON PROVINCES

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This research was conducted to selecting Tombul clones which carried out select on the highest character clones of Tombul hazelnut cultivar grown in Giresun and Trabzon Provinces between 2008 and 2012 years. In this research totally 380 Tombul hazelnut clones investigated. The results of the study were evaluated with the ‘Weight Ranked Method’. At the end of the evaluation hazelnut clones were selected and determined as yield 11.28-40.63g/cm², kernel percentage %50.08-54.07, nut weight 1.90-2.19g, kernel weight 0.99-1.19g, good kernels %77-92, shell thickness 0.89-1.10mm, number of nuts/cluster 2.43-3.67, full pellicle removal percentage %69.9-96.9, cracked nut percentage %0.33-7.67 and kernel cavity 1.78-2.88mm.

**Key Words:** Hazelnut, Tombul, Clonal Selection, Pomology

# EVALUATION OF GARLIC CULTIVARS FOR RESISTANCE TO *ASPERGILLUS NIGER* AND DISEASE MANAGEMENT OF NEW GARLIC DISEASE IN EGYPT

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Black mould of garlic (*Allium sativum* L.) caused *Aspergillus niger* Van Tieghem is the most important postharvest disease under hot and humid storage conditions. This study; investigated the disease incidence, cultivar reaction and chemical control of garlic black mold. According to our results, *A. niger* was identified as a causal organism of black rot of garlic. Infected garlic bulb with *A. niger* show streaks or spots of black colour appeared on or beneath the outer scales or the neck due to dark fungal growth. In contrast, small lesions and sporulation were observed when garlic scales were inoculated with 2.5 x $10^5$ spores/ml or incubated at temperature higher than 20°C. Garlic cultivars recently used in Egypt markets were evaluated under storage conditions for intensity of infestation by *A. niger*. Sods 41 garlic cv. (obtained from garlic breeding program in Department of Vegetable, Horticultural Research Institute, Agricultural Research Center, Dokky, Giza, Egypt) was the most resistance against black mold incidence. Whereas, Chinese commercial cv. was the least resistance. Amongst tested fungicides, Lunatranquality 50% SC and Ipromis 40% SC, brought about highest reduction followed by Switch 62.5%. The current study showed Sods 41 cv. the best garlic cvs. under Egyptian conditions was resistance to the black mold. Lunatranquality 50% SC and Ipromis 40% SC the effective fungicide for the disease control caused by *A. niger*. According to our knowledge this is the first report of garlic black mould disease caused by *A. niger* in Egypt.

***Keywords***: *Allium sativum*, black mould, cultivars, resistance,

# HAZELNUT BREEDING IN TURKEY

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Turkey's hazelnut plantations has a rich diversity. This diversity is very important in the hazelnut breeding. Our country *Corylusavellana* L. And *Coryluscolurna* L.'sis the natural distribution area. This speciesis the source of cultivars of hazelnut in the world. Turkey's oldest research institution engaged in research about the hazelnut Hazelnut Research Station. Station operating are carried hazelnut

breeding activities since 1969. There area number of universitiesengaged in researchabout the hazelnuts excepting to Hazelnut Research Station. The result of researches conducted at universities are written graduate theses and publications.

# PRELIMINARY STUDY ON ANTHER CULTURE OF CABBAGE AND BROCCOLI

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Two cabbage and one broccoli varieties, nine different flower bud stages and two different nutrient media were tested to develop an efficient anther culture protocole. Flower buds were stained with acetocarmene to find the most proper bud phase for anther culture. MS contained 4 mg $l^{-1}$ NAA, 1 mg $l^{-1}$ BAP, 30 g $l^{-1}$ sucrose, 0.25% activated charcoal, 15 mg $l^{-1}$ $AgNO_{3,}$ 8 g $l^{-1}$agar and B5 contained 4 mg $l^{-1}$ NAA, 1 mg $l^{-1}$ BAP, 30 g $l^{-1}$ sucrose, 0.25% activated charcoal, 15 mg $l^{-1}AgNO_{3,}$ 8 g $l^{-1}$ agar were used as nutrient media. Cultured anthers were incubated at 35°C for first two days in the dark. Then they were transferred to the growth chamber at 25°C and under 16 ours light and 8 ours dark photoperiod conditions. Broccoli flower buds were numbered from 1 to 9 according to their size. Seven flower bud stages selected from nine buds stained with acetocarmene were tested in broccoli. Embryo formation was observed in only number 2 flower buds. Therefore, these flower buds were used in cabbage. MS nutrient medium was found to be better than B5 in broccoli. Obtained embryos were transferred to hormone free MS nutrient medium. In cabbage, B5 nutrient medium was more successfull than MS.

**Key words:** Haploidization, anther culture, *Brassicaceae*, nutrient medium

# IDENTIFICATION AND PATHOGENICITY OF FUNGAL PATHOGENS CAUSING ROOT ROT AND WILT DISEASES IN WINTER SQUASH (*CUCURBITA MAXIMA* DUCH.) GROWING AREAS OF BLACK SEA REGION AND DETERMINATION OF REACTIONS OF SOME WINTER SQUASH GENOTYPES AGAINST THESE PATHOGENS

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This study was conducted with the aim of determining i) the fungal factors which cause root rot and wilt diseases in areas in which winter squash is grown, ii) the reactions of selected promising winter squash genotypes, which have potential to be used in fresh consuming, against these factors. The survey studies were conducted in 65 fields found in the provinces of Samsun, Amasya, Sinop and Ordu with the highest winter squash production level on July-June of 2011 year. Totally 258 fungal isolates were obtained from diseased plant samples. While 11 different species of *Fusarium* genus, which is an important soil pathogen, were obtained, the *F. oxysporum* was the species with the highest isolation ratio 11.6%. This species was followed by *F. solani* (7.3%) which causes root, crown and fruit rot in winter squash. The isolation ratio was 11.6% for *Rhizoctonia solani* AG 4. An other isolated species was *Pythium orthogonon*. Pathogenity tests were carried out with 78 isolates selected from *Fusarium* spp., *R. solani* and *P. orthogonon* isolates and on “Arıcan 97” winter squash variety. In the end of the experiment, 4 isolates [*F. solani* (F-42), *P. orthogonon* (Pyt-3), *R. solani* AG 4 (Rhi-3) and *F. solani* f.sp. *cucurbitae* race 1 (used for positive control)] were selected and the resistance reactions of 5 squash genotypes (G14, 55ÇA06, 57Sİ21, 55ÇA15, 55BA03) against to these isolates were determined under greenhouse conditions. The reactions of genotypes were determined different according to the durability test results. All of the genotypes used in this study were found moderately resistant (MR) against *F. solani* isolate. The same genotypes showed a low degree of durability against *R. solani* AG 4 and *P. orthogonon* isolates. Only 55ÇA06 genotype was found sensitive against *F. solani* f.sp. *cucurbitae* race 1.

**Key words:** Winter squash, soil borne fungal pathogens, *Fusarium* spp., *Rhizoctonia solani*, *Pythium* spp., pathogenicity, resistance, Turkey

# MOLECULAR MAPPING OF *ZYMV-1*, A NEW DOMINANT GENE FOR *ZUCCHINI YELLOW MOSAIC VIRUS* (ZYMV) RESISTANCE IN SQUASH (*CUCURBITA PEPO*)

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*Zucchini yellow mosaic virus* (ZYMV) is one of the most destructive viruses that badly reduce the production of squash (*Cucurbita pepo*) all over the world. Resistance is the best approach to control the disease. Squash inbred line ‘BS12’ showed a high-level of ZYMV resistance in our germplasm evaluations over several years. The genetic basis of the resistance in ‘BS12’ was elucidated through an inheritance study and molecular mapping. A total of 693 F2:3 lines from the crosses of BS3, a susceptible parent, with BS12 were tested with ZYMV-CH, a highly predominant ZYMV strain in China, under the controlled greenhouse conditions, and Bulked segregant analysis was carried out to identify SSR and EST-SSR markers linked to this resistance gene. Results indicated that resistance to this virus observed in ‘BS12’ was controlled by a single dominant gene, which was designated as *ZYMV-1*, and closely flanked by SSR markers *ZY-138* and *ZY-157* at a genetic distance of 0.4 and 2.6 cM, respectively. These markers were subsequently validated for detection of ZYMV resistance gene among 30 varieties, 10 squash genotypes were resistant for ZYMV, and 20 genotypes showed susceptible banding pattern. The MAB strategy with these two markers enabled the development of homozygous ($BC_4F_2$) ZYMV-resistance lines with the smallest introgressed region and 96.9% of the recurrent parental genome, which proved valuable for *ZYMV-1* gene transferring in future squash breeding.

**Keywords:** Squash **(***Cucurbita pepo*), *Zucchini yellow mosaic virus* (ZYMV), Resistance gene, Molecular markers, Marker-assisted selection (MAS)

# BREEDING VALUE OF PARENTS AND PROGENIES OF SOME COCOA GENOTYPES FOR COCOA POD AND BEAN TRAITS

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The evaluation of the parents and progenies from a hybridization programme provides information on the breeding value of the lines, testers and hybrids. Four cocoa genotypes (Testers) were crossed with two significantly distinct Lines (T65/7 and T86/2). The parents and the hybrids were established in a randomized complete block design of six replications at the Cocoa Research Institute of Nigeria, Ibadan, Nigeria. They were evaluated for six phenotypic traits: pod length (PL), weight (PW), number of beans per pod (NoB), bean length (BL), width (Bwi) and thickness (BT).The treatment, parent, crosses and line and tester were significant ($P \leq 0.05$) sources of variation in the analysis of variance. By proportion, the contribution to the total variance of PL, PW and Bwi was in the order of Tester > Line x Tester > Lines. The contribution of Line x Tester was higher for the other traits. The highest general combining ability (gca), 0.42 among the lines was in PW for T65/7. T9/15, a tester had the highest gca for NoB. The specific combining ability (sca) between T65/7 and T57/22 (L1xT4) was highest (4.33) for NoB, the same hybrid had the least sca for BT. Broadsense heritability for lines was highest (91.66% and 91.37%) in PW. Hybrids from the same maternal parent differed significantly ($P < 0.05$) for the six traits. Some of the progenies exhibited heterosis for most traits. The significance of the hybrids performance for most of the phenotypic traits assures of the evolvement of new cocoa variants and increase of the cocoa genetic resources in Nigeria.

***Key words***: parents, hybrids, progenies, line and tester, combining abilities

# DEVELOPMENT OF POLYMORPHIC SSR PRIMERS IN PISTACHIO FROM ENRICHED GA REPEAT LIBRARY IN SIIRT CULTIVAR

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In this study, it was aimed to develop new polymorphic SSR primer pairs in pistachio using sequences derived from cv Siirt genomic enriched library with GA repeat. The designed 83 SSR primer pairs were subjected to gradient PCR in 12 pistachio cultivars to determine their optimum annealing temperatures. Then, the primer pairs which had amplification in agarose gel were analyzed in capillary electrophoresis to determine their allel sizes and polymorphism. According to the gradient PCR and capillary electrophoresis reasults, 14.5% of the SSR primer pairs did not amplified any bands in agarose gel and 10.8% of them produced complex bands in capillary electrophoresis that were couldn’t scored. Rest of the 62 primer pairs produced bands and their annealing temperatures and allel sizes were determined. From the amplified primer pairs, 18 of them monomorphic, whereas 44 of them were polymorphic. As a result, 53% polymorphism was obtained from 83 SSR primer pairs tested in this study which was very good ratio when compared to the literature.

**Key Words:** SSR, Pistachio, Polymorphism, PCR

# PHYTOSANITARY STATUS OF FICUS CARICA COLLECTION IN CRIMEA AND FEATURES OF FIGS IN VITRO MICROPROPAGATION

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The Common Fig, *Ficus carica* L., is a deciduous tree or shrub in the family Moraceae grown for its edible fruits. It is also grown as an ornamental tree. The climate conditions of Crimea (Ukraine) give possibility to cultivate different subtropical horticulture plants, such as fig (*Ficus carica* L.). The phytosanitary status of fig collection in Nikitsky Botanical Garden (more than 100 cultivars and forms) have been investigated. The aim of study was improvement the plants, which are cultivated in collection plot. The vegetative buds of 19 fig cultivars (Cadota, Sabrucia Rozovaya, Smena, Finikoviy, Dalmatskiy, Beliy Ranniy, Moisoniere, Medoviy, Limonno-Zheltiy, Krimskiy 37, Verdino, Randino, Adriaticheskiy, Priyatniy, Krimskiy Cherniy, Kadota Zolotistaya, Violete, Fig Blanch, Yantarniy) have been cultivated on MS medium, supplemented by ribavirin (chemotherapy *in vitro*). Genotypic differences were observed in the regeneration ability of cultured explants. During of propagation as additional explants the leaf cuts have been used. From one explants 15-20 adventive microshoots have been direct regenerated. The method of fig *in vitro* micropropagation has been established. The obtained virus-free fig plants have been adapted to *in vivo* conditions and cultivated in greenhouse.

# GENETIC VARIATION AND MULTIVARIATE ANALYSIS OF FRUIT TRAITS FOR IMPROVEMENT OF POMEGRANATE (*PUNICA GRANATUM* L.) CULTIVARS

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A collection of twenty eight pomegranate cultivars was evaluated for three years based on fruit quality traits. On the basis of multivariate methods including cluster and principal components analysis, cultivars were separated into distinct groups. Phenotypic similarities and dissimilarities were revealed among cultivars. Some of these were individualized as presenting particular characters such as Jebali 3 (big fruit size and low juice acidity), Jebali 1 (red colored juice), Gabsi 4 (high juice yield and low skin thickness) and Zehri 4 (high aril yield and red colored skin). Significant cultivar, year and cultivar x year interactions found in all traits indicated that environmental conditions influenced the phenotypic pomegranate fruit attributes. Thus, the stability of pomegranate characteristics was different depending on fruit traits. None of the cultivars were stable for fruit weight and diameter. Some cultivars as Tounsi 6, Chelfi 1 and Chelfi 6 were considered as having high adaptability to the favorable environmental conditions and other cultivars could behave the best under unfavorable conditions. Juice pH, fruit weight, fruit diameter, fruit height, skin color and juice color had the highest broad sense heritability estimates. Total soluble solids, skin thickness and aril yield were the traits with the lowest estimates. High heritability along with high genetic advance for fruit weight, skin color, juice color and titratable acidity suggested that there is important additive gene action for such traits. Combining results of cultivars characterization and fruit traits stability showed that there are ample opportunities for improving several traits in pomegranate crop for adaptation to different environmental conditions.

**Keywords**: *Punica granatum*, pomegranate, cultivar, environment, fruit quality, multivariate analysis, heritability, improvement, Tunisia.

# IMPROVED VEGETABLE VARIETIES FOR CENTRAL ASIA AND THE CAUCASUS DEVELOPED FROM

# AVRDC – THE WORLD VEGETABLE CENTER GERMPLASM

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After the break-up of the Soviet Union in 1991, all countries in the region experienced difficulties in obtaining vegetable germplasm for breeding programs. The genebank at AVRDC – The World Vegetable Center conserves diversity of vegetable germplasm and, from 2005-2012 has introduced more than 1370 accessions and improved lines of 26 vegetable species representing 9 families to countries in Central Asia and the Caucasus through the Regional Network for Vegetable System Research and Development to foster faster variety development and dissemination. Partner research institutes have studied these vegetables in regional variety trials under various agroecosystems. Currently a total of 38 new varieties of 12 species are under state variety trials. Through collaboration, 35 new varieties of 8 vegetable crops including tomato, sweet and hot pepper, eggplant, vegetable soybean, mungbean, yard-long bean and cabbage have been released and registered in state registries. From 35 new varieties, 14 have been developed by conventional selection methods using germplasm received from the AVRDC genebank. All released varieties demonstrate economically valuable traits: early maturity, higher yield, resistance to diseases and pests, high nutrient content and other marketable features. Seeds of released varieties are multiplied to provide farmers. For the first time new varieties of non-traditional species such vegetable soybean, mungbean, yard-long bean and Chinese leafy cabbage have expanded the diversity of vegetables in the region, and have become popular for cultivation and consumption. Increasing the vegetable production will help diversify diets, increase farmers' income, and enhance the well-being of families throughout the region.

# INHERITANCE AND STABILITY OF SOME AGRONOMIC TRAITS OF AFRICAN YAM BEAN (*SPHENOSTYLIS STENOCARPA* (HOCHST EX. A. RICH) HARMS)

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African yam bean is an indigenous African pulse of immense nutritional significance with poor esteem. Owing to research neglect, fundamental information for its improvement is not available. Four phenotypic characters of thirty genotypes of the crop were evaluated for inheritance and stability in four locations in Nigeria. Analysis of variance identified significant ($P \leq 0.05$) genotypic variation among the thirty genotypes in each of the four locations (Ibadan, Ikenne, Mokwa and Ubiaja) for 100-seed weight (100SW) and seed weight per pod (SWP). Genotypic variation was significant ($P \leq 0.05$) for all characters except days to seedling emergence (DSE). Location and its interaction with genotype had significant ($P \leq 0.05$) effect on the four characters. Days to 50% flowering (D50F) had the least (10.26% and 11.05%) genotypic and phenotypic coefficient of variation (GCV and PCV). However, the highest (34.55%, 37.88% and 64.94%) GCV, PCV and genetic advance occurred in SWP. Broadsense heritability (%) ranged between 77.61(DSE) and 89.07 (100SW). Repeatability was highest (13.83%) in 100SW. The performance of TSs 87, TSs 91 and TSs 125 was highly significant for DSE and 100SW. The Joint Regression Analysis identified TSs24 and TSs82 as the most stable genotypes for DSE and SWP; their regression coefficient (b) were: 0.94 and 0.97 respectively and deviation from linearity ($S_{di}^2$) were 0.028 and -0.028 respectively. The most stable genotypes for D50F and 100SW were TSs 61 and TSs 84 with b = 1.015 and 1.017 respectively. The study reveals that arrays of genotype differ in their breeding value.

***Key words***: underutilized species, African yam bean, agronomic traits, heritability, joint regression analysis

# INVESTIGATIONS ON THE RESISTANCE OF SOME PROCESSING WHITE HEAD CABBAGE (*BRASSICA OLERACEA* L. VAR. *CAPITATA* SUBVAR. *ALBA*), GENOTYPES TO ROOT–KNOT NEMATODES [*MELOIDOGYNE INCOGNITA* (KOFOID & WHITE) CHITWOOD]

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This study was conducted during 2010–2011 as a field study in the field of Ondokuz Mayıs University, Agricultural Faculty, Horticulture Department and as a pot study in the acclimatized room under controlled conditions at Plant Protection Department. The main materials of experiment were *Meloidogyne incognita* (Kofoid & White) Chitwood infected soil and totally 27 white head cabbage (*Brassica oleracea* L. var. *capitata* subvar. *alba*), of which 4 were resistant and 23 was susceptible to root–knot nematodes. Roots gall were investigated according to 0–5 scale. In 2010 field experiment, 530-1 (2.2500), P33 (2.000), 173 (2.2500) and 183 (2,7500) cabbage lines have the lowest gall index. On the other hand, there was the highest observed in the roots of 195, 166, 542,115, 165, 148, 519, Yalova-1 and Bafra (5.000) lines. The results provide information on the resistant root-knot nematodes and breeding study of Turkish white head cabbage lines.

**Keywords:** cabbage, nematode, resistance

# STRENGTHS AND WEAKNESSES TRAITS FOR BRASSICA VEGETABLE CROPS PRODUCTION OF TURKEY

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*Brassicas* are widespread as wild, weedy and cultivated forms throughout Turkey. Vegetable brassica crops are an important and highly diverse group of crops grown world-wide that belong mainly to the species **Brassica oleracea** and **Brassica campestris.** Turkey has a significant place in world vegetable production. Turkey is fourth after China, India and the United States in world vegetable production. The total production of vegetable species in Turkey is 26.700.000 ton. In Turkey, cabbage is the most economically important member of the genus *Brassica*. The type of vegetables grown in Turkey has been diversified in the recent years. New crops include Brussels sprouts, Chinese cabbage, kohlrabi, Pak choi and aromatic vegetables. Among many factors that make Turkey a strong vegetable sector, appropriate ecological conditions, proximity to foreign markets, and implement new technologies quickly transferred into the country, include the fact that labor costs are still low compared to developed countries. In this study, it was given as comprehensive strengths and weaknesses traits for *Brassicas* vegetable production of Turkey.

**Keywords:** Brassica, vegetable, breeding activites, swot, Turkey

# THE DETERMINATION OF SALINITY TOLERANCE LEVELS AND THE EFFECT THE PLANT GROWTH AS USING ROOTSTOCKS OF TURKISH WINTER SQUASH GENOTYPES *(CUCURBITA* SPP.) FOR GRAFTED WATERMELON SEEDLING PRODUCTION

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Winter squash and pumpkins were recommended for use as a rootstock for the watermelon, melon and cucumber growing in the saline soils. Grafted seedlings recently are being used widely for vegetable growing in many countries of the world, recently. Practically, *Cucurbita* sp. (winter squash, pumpkin, *C. maxima x C. moschata), Lagenaria* sp. (Bottle gourds), *Benincasa* sp. and *Citrullus* sp. (watermelon) are used the most prevalent rootstocks for production of grafted watermelon seedlings. Winter squash (*Cucurbita maxima Duchesne)* and pumpkins ( *Cucurbita moschata Duchesne*) are two of the most important *Cucurbit* vegetable crops in Turkey. In a project that supported from TUBITAK, pumpkin and winter squash genetic material which are widely spread in the Black sea region were collected and characterized. In the other project that supported from Ondokuz Mayis University 2009-2012 among years all genotypes in the gene pool for 3 known races of *Fusarium oxysporum* f. sp. *niveum (0,1,2) and Meloidogyne incognita (R*ace-2) determined of resistance and sensitivity. In this study will be benefit from *C.maxima ve C. moschata* genotypes hybridized watermelon of rootstock breeding addition to this genotypes. In the gene pool and a sample group selected from these pumpkins and winter squashes will be hybridized (*C.maxima* x *C. moschata)* for expand of rootstock breeding genetic material. These materials were tested for 3 known races of *Fusarium oxysporum* f sp *niveum* and root knot nematode (*M. incognita R*ace-2) for determination of rootstock potential for watermelon. There are no data in terms of salt resistance genotypes. At the end of this research, it will be determined resistance levels at the different salt concentrations. In this study, the effects of different salinity levels (0, “control”, 4, 8, 12, and 16 dS $m^{-1}$) on seedling growth were researched. Seedlings grown under saline conditions were investigated for, plant length, root fresh weight, root dry weight, plant fresh weight, plant dry weight, leaf area, chlorophyll contents, diameter of the plant, leaf number, dry leaf number, relative water content and ion concentrations (Ca++, K+, Na+) in the leaves of winter squash genotypes. Results indicated that these local rootstocks responded different to some investigated parameters under saline conditions.

**Keywords:** Winter squash, pumpkin, genotype, rootstock, watermelon, grafting, salinity, tolerant

# USING DIFFERENT MOLECULAR MARKERS FOR BREEDING OF SOME HORTICULTURAL PLANTS

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Agricultural development in the national and international level to develop new products using innovative technology to provide the research and development activities are great importance today. For this purpose, in parallel with the developments in technology to perform high-quality new varieties of agricultural development as soon as possible to offer more relevant sectors, the use of biotechnology in plant breeding studies are of great importance. This study was carried out for this purpose and the work was carried out with different types of horticultural. Cherries, onions and peony breeding programs carried out by some individuals at the genetic level obtained from the studies were performed with different marker systems. As a result of laboratory studies some hybrid cherries obtained by hybridization incompatibility level were examined with different SSR markers. Self-fertile types have been determined. The genetic diversity within populations of onion in Yalova Atatürk Central Horticultural Research Institute examined again by SSR markers. Also in this study, a comprehensive study peony breeding crosses obtained from the same Institute identified herbaceous and woody species with suitable markers.

# BREEDING OF PEAR CULTIVARS RESISTANT TO FIRE BLIGHT DISEASE (*ERWINIA AMYLOVORA*): PROMISING GENOTYPES AND MOLECULAR CHARACTERIZATION

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With the aim of developing resistant varieties of pear to fire blight in Eğirdir Fruit Research Station have been initiated a pear breeding program in cooperation with University of the Mediterranean, Faculty of Agriculture, Department of Plant Protection in 2004. Starting from 2006, the genotypes from crosses with different combinations were tested to determine the level of fire blight in the greenhouse and those that have adequate levels of fire blight was transferred to land for observations of fruit. As a result of observations of the first fruit, commercially important candidates were grafted on clonal rootstocks and planted to land for trials as replications. Approximately 41 genotypes were planted to “a parcel of advanced observation” in five individuals and 231 genotypes were tested for fire blight tolerance in second time. 23 of these 231 genotypes were determined as high level resistant to fire blight. 21007 and 18045 types and their parents Williams and Kieffer were identified as molecular with the help of ISSR and RAPD markers. Dendogram showing the relationship was established with the data obtained from the genetic similarity.

# GENETIC CONTROL RESISTANCE TO YELLOW VIRUS IN MELON (*CUCUMIS MELO* L.)

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Yellow virus (YV) diseases cause severe damage to crops, inhibit plant vegetative growth and made total lost production in melon. Development of resistant variety is the most effective mean to control the diseases, since the vector of white fly is polyphagia, therefore difficult to control. The research consist of two field experiments, there were evaluation of resistance to YV and parent selection, and evaluation of resistance in P1, P2, F1 and F2 population. Twenty genotypes from three major melon groups of cantaloupe, inodorous and dudaim were evaluated and one line of dudaim group (MEV1) exhibits high resistance to YV, however other lines belongs to cantaloupe and inodorous showed highly susceptible performance. Resistance analysis on F1 from resistance x susceptible parents showed resistance of F1, subsequently resistance evaluation in F2 population revealed the disease severity score was not in normal distribution indicated that resistance to YV was controlled by a major gene. Chi-square ($\chi^2$) test result gave 13:3 as a suitable ratio, indicated that the resistance to YV was controlled by a pair of 2 gene with dominant and epistasis recessive action. PCR analysis showed virus existence in inoculated leaf of resistant genotype with lower scale compare to susceptible genotypes, indicated the possibility controlling resistance to the virus not to the vector.

**Keywords:** major gene, dominant, epistasis recessive

# IMPROVEMENT OF F1 HYBRID VEGETABLE VARIETIES AND QUALIFIED LINES PROJECT IN TURKEY

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The objective of this project supported by TÜBİTAK (The Scientific and Technological Research Council of Turkey) was to improve new lines and hybrid varieties consisting of high quality taste, color, nutrition content, and tolerance or resistance to abiotic and biotic stress conditions in tomato, pepper, eggplant, cucumber and melon. In this study, F4 and upper level lines available in gene pool owned by our institute were purified and characterized morphologically. Genetic materials were tested to abiotic and biotic stress conditions. Materials resistant or tolerant to stress conditions were used to develop new F1 vegetable varieties. Classical and biotechnological breeding techniques were used during these studies. As a result of this project, our institute will introduce to vegetable sector by improving 131 qualified lines and 15 new F1 varieties for vegetable species. The vegetable seed sector will benefit from the outputs of this project realized by collaborating universities and public sectors. At the end of the project, significant contribution to Turkish economy will be supplied by reducing external dependence in a strategic production input of F1 vegetable seed. Consequently, scientific outputs of project will be shared to all related sides.

**Keywords:** Vegetable, breeding, hybrid, abiotic stress, biotic stress

# LONG TERM ONION BREEDING PROGRAM IN TURKEY

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The edible Alliums are grown worldwide as fresh shoots for green salad and as bulbs to consume as fresh, pickled, dehydrated, cooked, or to produce onion seed or sets. Cytoplasmic-genic male sterility (CMS) is the most common method used to produce hybrid-onion (*Allium cepa* L.) seed in the world. A male sterile female, maintainer and pollinator lines are required in the cytoplasmic-genic male sterility system. It used to take six to eight years to select maintainer from an uncharacterized population or segregating family using classical selection and breeding methods. Today polymorphisms found in the cytoplasm and at nuclear *Ms* locus of onion can be used to identify normal (N) versus sterile (S) cytoplasm and recessive (*ms*) versus dominant (*MS*) alleles at the *Ms* locus, respectively. Identification of cytoplasms and nuclear genotypes using molecular marker method can be applied more accurately and in a shorter amount of time than classical breeding methods. With molecular characterization of the cytoplasm and nuclear genotypes, a breeder can determine genotypes in populations and significantly reduces the investment required to identify individual maintainer plants. Cytoplasms and nuclear genotypes in local commercial onion cultivars and breeding lines have been identified with this research. We had improvements in reducing split or multiple centered bulbs rates, increasing earliness and uniformity at harvest, firmness, and scale and neck tightness. Onion breeding program from 1998 to 2013 in Turkey along with housefly production will be discussed at the presentation. This work partially supported by MTN Seed Company and TUBITAK 110O665.

**Keywords:** Onion, *Allium cepa* L., Hybrid Seed, Cytoplasmic and Nuclear Characterization

# PREPARING RNAI CONSTRUCT FOR *FAD2* GENE FRAGMENT OF *BRASSICA NAPPUS* AS A STEP TOWARDS GENE SILENCING

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Manipulating the oil crops to improve the oil quality has been a field of interest for genetic engineering researchers during the last years. Increasing the oleic acid content of *Brassica napus has* been targeted to decrease the cardiovascular diseases meanwhile biodiesel production. *fad2* is a gene coding a key enzyme involved in oleic acid biosynthetic pathway in oil corps, named *fatty acyl desaturase.* Introducing a partial sequence of the aforementioned gene as an RNAi cassette in crops will increase the oleic acid ratio significantly in the oil extracted. Considering the start codon of the gene, the specific primers designed and following the genomic DNA extraction, the fragment of interest amplified by Polymerase Chain Reaction (PCR). After cloning in a desired vector, transformation to *E. coli* competent cells carried out. During the next steps the gene fragment underwent restriction and ligation reactions to achieve the desired orientation of sense and antisense fragments. At the end the prepared fragments of the gene transferred to a binary vector forming a cassette called RNAi construct.

**Key words:** *fad2,* Cloning*,* RNAi*,* Oleic acid, *Brassica napus*

# SELECTION BREEDING OF WILD *PRUNUS CERASUS* L. CLONAL ROOTSTOCKS FOR SWEET AND SOUR CHERRIES

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In Turkey, sour cherry is generally growth in Konya (Akşehir), Afyonkarahisar (Karacaören, Sultandağı, Dereçine), Ankara (Çubuk), Tokat and Kütahya. Sweet cherry is produced in Kemalpaşa (İzmir), Honaz (Denizli), Sultandağı, Dereçine (Afyonkarahisar), Akşehir (Konya) and Andırın (Kahramanmaraş) in long time (Kaşka, 2001). In Sweet and Sour cherry production areas, mazzard and mahlep seedlings are used as rootstock. *Prunus cerasus* wild plants are adaptable for different soils and climate conditions. Thus *Prunus cerasus* wild plants are wide spread in nature. Wild *Prunus cerasus* plants have different characteristics. This study was started in 2002. In project process, 38 genotypes were selected for different phenotypic characteristics which were as rootstock capabilities. These genotypes selected from Dereçine, Akşehir, Sultandağı, Doğanhisar, Şaphane, Kasımlar and Yenişarbademli. Selected genotypes were grafted on mahlep rootstocks and planted on selection orchard in research area. Vegetative propagation methods have been performed on these genotypes.

**Keywords:** *Prunus cerasus* L., clone, rootstocks, sweet cherry, sour cherry, breeding, selection

# THE ROOTSTOCK BREEDING AND SELECTION STUDIES FOR *CUCURBITACEAE* VEGETABLES IN TURKEY

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In many parts of the world, vegetable grafting is a routine technique used in continuous cropping systems. Use of rootstocks can enhance whole plant biotic stres responses by improving plant vigor through vigorous attainment of soil nutrients, avoidance of soil pathogens and tolerance of low soil temperatures, salinity, and wet soil conditions. The type of rootstock affects scion growth, yield, and fruit quality. The production of grafted plants first began in Japan and Korea in the late 1920s with watermelon (*Citrullus lanatus*) onto pumpkin (*Cucurbita moschata*) rootstocks. These countries have a long history of rootstock breeding. While the most current rootstock cultivars are old releases from 15 years ago, these rootstock breeding studies for cucurbits are a new topic in Turkey. All of the rootstock seed for watermelon, cucumber, and melon which is necessary for Turkey are imported. Thus rootstock breeding studies are required in order to reduce rootstock seed import. Grafting in vegetables was introduced to Turkey in the late 1990s. The first experiment on grafting was conducted on eggplant by grafting on tomato in Turkey in 1989 and following years in watermelon. Recently, rootstock breeding programs belonging to the Cucurbita and Lagenaria genus are ongoing for watermelon and cucumber. This review discusses vegetable grafting with a focus on the genetics and breeding of the rootstock studies in Turkey.

**Key words:** Rootstock, breeding, cucurbita, grafting, resistance

# AUTHENTICITY OF TURKISH OLIVE CULTIVARS USING SNP MARKERS

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Olive (*Olea europaea* ssp. *europaea* L.) is one of the oldest fruit trees in cultivation. The fruit of the olive tree is used both as table olives and for oil production. Historically, olive has been widely grown in Mediterranean countries. However, since the nutritional benefits of olive oil consumption is recognized, olive cultivation is spreading worldwide. Quality and authentication are important topics for international olive oil trade. Olive oils that meet certain quality standards such as PDO, PGI and TSG, which are recognized in the European Union, are traded for higher prices in the international market. High quality varieties of olive oil may be subject to adulteration with low quality ones and such an adulteration is very common. DNA-based analyses hold promise for their ability to distinguish among varieties within the same species. The development of reliable assays to analyze and distinguish genuine olive oil have become extremely important. Such tests will allow registration of oil as authentic which is important for both the consumer and producer. The goal of this project is to develop a reliable test method for the analysis and authentication of Turkish olive oils. To reach this aim, DNA sequences of olive varieties that are commonly used for oil production are screened to identify SNPs (Single Nucleotide Polymorphisms) which will be used to develop a DNA-based test for the authentication of the varietal origin of Turkish monovarietal olive oils. Testing and verification of authentic Turkish olive oils will increase the value of Turkish oils in the international market and increase their competitiveness.

# CARROT BREEDING STUDIES AND CHARACTERISTICS IN TURKEY

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According to the TUIK (2011), Turkey produced 602,078 tons of carrots in 31 000 hectares. Konya (373 thousand tons), Ankara (110 thousand tons) and Hatay (65 thousand tons) are the main carrot producing provinces. Carrots are high in carotenoid content which is the precursor of vitamin A and carrot consumption is important for fighting against the vitamin A deficiency in humans worldwide. The use of the seed of hybrid cultivar for carrot production in Turkey has reached to 90% and this hybrid carrot cultivar seed has been imported from abroad. The reasons why hybrid cultivars have been preferred for carrot production are high yield and uniform root size, shape, color and taste. In this research It is aimed at providing criteria for breeding which has an important place in carrot breeding.

**Key Words:** Carrot, breeding

# CHARACTERIZATION, SOME AGRONOMIC TRAITS AND Β-CAROTENE CONTENTS OF ORANGE FLESHED ALTINBAŞ MELON DIHAPLOID LINES GROWN IN ANTALYA AND BURSA LOCATIONS

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The objectives of this presented study were characterization of orange fleshed Altınbaş melon dihaploid lines that widely grown in most part of Turkey. The study was conducted in greenhouse condition in Antalya, Turkey and in open field in Bursa, Turkey. The pure lines obtained by irradiated pollen techniques were characterized according to modified UPOV descriptors for 63 characters. β-carotene content of the dihaploid lines were also determined. Some quantitative characters as fruit weight, fruit diameter, fruit lenght, diameter of seed cavity, lenght of seed cavity, thickness of flesh, total soluble solids and β-carotene content were also measured on the plants. According the research results, orange fleshed melon pure lines showed different level of variation in case of morphological characterization as well as fruit traits and β-carotene contents.

**Keywords:** Melon, dihaploidization*,* β-carotene, UPOV

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# DETERMINATION OF $F_1$ HYBRID ABILITY OF SOME SQUASH LINES

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Higher total yield is one of the most important criteria in under protect growing. Moreover, smoothness of fruit shape, fruit color and tendency to branching were important criteria for selection. In order to improve suitable variety for under protect growing, 92 pure lines which obtained after six inbreeding, hybridized as male parent with two tester lines according to top-cross method. Most important cross lines obtained with first tester parents were 73, 15, 120,226, 171, 82, 123, 262, 62, 223. Moreover, most important cross lines obtained with second tester parents were 302, 261, 328, 15, 189, 360, 172, 112, 3, 308. Furthermore most important cross lines obtained from both of the testers parents were 328, 15, 189, 112, 477, 26, 19, 297-A, 73. Consequently, specific combining ability test of twenty-five pure lines which obtained general combining ability test were determined.

**Key Words:** Summer squash, top cross, specific combining ability.

# DETERMINATION OF GENETIC DIVERSITY ON GENOTYPES OF TOMATOES BY SSR (SIMPLE SEQUENCE REPEATS) MARKERS

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The study covering allele profile, genetic definition and genetic similarity between twenty one local and three commercial tomato genotypes collected from different regions of Turkey were investigated with the aim of identifying genetic variability in tomatoes (*Solanum lycopersicum*) population by forty SSR loci. Number of alleles per locus ranged from 13 (LEat018) to 3 (SSR50, SSR80, SSR9, LEtat002). Expected and observed heterozygosity values were between He: 0,753 and Ho: 0,714 respectively. The mean of Polymorphism Information Content (PIC) value of these loci was found as 0,694. This shows that SSR loci used for this study were high level polymorphic. Considering distribution of alleles at loci, the highest allele frequency was observed from SSR75 with % 62,5 LEat014 with % 58,3 LEga004 with % 50,0 locus, while the lowest was in AI491065 with % 16,6 LEta024 locus. UPGMA (Unweighted Pair-Group Method Using Arithmetic Means) method was conducted for cluster analysis. The dendrogram was consisted two main groups, group two was the largest and it contained many sub-groups. Genetic similarity rate of genotypes from Bafra-Merkez and Sivas-Yukarıkale village was found as 0,776. The lowest similarity rate was observed between Sivas-Yıldızeli-Emirler village and ve Samsun- Çarşamba genotype with 0,136.

**Keywords:** Tomato (Solanum lycopersicum), Genetic relationships, SSR

# DETERMINATION OF ROOTSTOCK POTENTIAL FOR ROOT-KNOT NEMATODE RESISTANCE OF *CUCURBITA* SPP. GENOTYPES COLLECTED FROM THE BLACK SEA REGION, TURKEY

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Watermelon (*Citrullus lanatus*) and cucumber (*Cucumis sativus*) cultivars are highly susceptible to the southern root-knot nematode (*Meloidogyne incognita*), with considerable yield losses when this nematode is not managed. *Cucurbita moschata*, *C. maxima,* and their inter and intraspecific hybrids are used as rootstocks for cucurbit grafting, and they are more vigorous and more resistant to some soilborne diseases. One method to circumvent this problem is to graft susceptible scions onto nematode-resistant rootstocks. The objective of the present study was to evaluate the responses of 30 Cucurbit accessions collected from Black Sea Region of Turkey to *M. incognita* to identify genetic material that could be used as rootstocks or for breeding program. *C. moschata* (9), *C. maxima* (14) and *C. maxima* x *C. moschata* (7) genotypes were evaluated in greenhouse tests for resistances to *Meloidogyne incognita* race 2. It was found that all Cucurbit genotypes were susceptible to root-knot nematodes. However, no significant effects on growth performance between control and contaminated plants. It was concluded that Cucurbit rootstocks were not directly resistant to nematodes but they (M2, M5, K11, and K13) can tolerate nematodes with their rapid growing ability when nematodes are problem in the soil. The lines and hybrids selected will be grafted to watermelon and cucumber and later the performance of land condition infested with the root-knot nematode will be investigated. Thus, some lines were identified that may be useful as resistant rootstocks for managing root-knot nematodes in watermelon and cucumber

**Key words:** Root-knot nematode, resistance, rootstock, Cucurbita, grafted seedling, watermelon

# DETERMINATION ON MORPHOLOGICAL AND BIOACTIVE CHARACTERISTICS OF SOME WATERMELON LINES

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Total vegetable productionof Turkey is about 27,4 million tons and watermelon production consists of 14% of this production. Watermelon is produced in open field or under protected cultivation dependinding on climatic regions in Turkey. 95% of under protected cultivation production of watermelon is done in the Çukurova Region, while open field production is mainly done Southeastern Anatolia, the Mediterranean Region and the Thrace. Correct identification of the material to be used in watermelon breeding and well known properties of obtained individuals from crossbreeding is an important step for the successful execution of the study. For this study, from the gene pool of Alata Horticultural Research Station, 11 pure line selected that 1 female, 10 male variety as parents. In this way, morphological and bioactive properties of parents and hybrid individuals have been introduced.

**Keywords:** Watermelon, Morphological and Bioactive Characteristics.

# DETERMINE THE MORPHOLOGICAL CHARACTERIZATION AND SINGLE SEED DESCENT SELECTION BREEDING OF LOCAL TOKAT PEPPER *(CAPSICUM ANNUUM* L.*)* POPULATION

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This study was aimed to develop high yielding and quality standard varieties by collection of local populations of pepper *(Capsicum annuum* L.*)* that widely grown in Tokat and known as Tokat pepper that has elongated bell-shaped (lamuyo) with 3-4 lobs, thin exocarp and mesocarp with hot or sweet taste, making morphological identification and directed into selection of the correct name. This study, the scope of the pepper breeding were carried out at the Black-Sea Agricultural Research Institute, then local materials were collected from the areas of intensive cultivation of pepper in Tokat location. These materials were grown in the experimental field of the institute and plants and fruit characteristics of pepper genotypes were investigated for 5 years. Single seed descent selection was applied to local pepper genotypes that identified to morphological characteristics for determined the best representing of Tokat pepper. Homozygous inbred lines were composed utilizing from single seed descent selection method and then selfing 5 generations in the selected pepper genotypes. As a result, two inbred lines were determined as cultivar candidates that were kept out with uniformity, fruit quality and yield.

**Key Words:** Pepper *(Capsicum annuum* L.*)*, Local cultivars, population, Morphological characterization, Single seed descent selection, inbred line

# DEVELOPMENT OF DOWNY MILDEW RESISTANT MARKERS FOR CUCUMBER BREEDING PROGRAM

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*Pseudoperonos poracubensis* **(Berk.& M.A. Curtis) Rostovezis a species of water mould known for causing downy mildew on cucurbits such as cantaloupe, cucumber, pumpkin, squash and watermelon. To date, a downy mildew epidermic infected cucumber plants in worldwide scale is big problem in cucumber cultivation.** The outbreakwas evidence that some of the previously identifiedresistance genes (dm-1, dm-2, and dm-3) did not provide adequate disease control. Therefore, improving the genetic resistance of cucumberto downy mildew through plant breeding could be aneffective way to control this disease. To identify the downy mildew resistance gene(s) and integrate into the breeding lines, we are trying to QTL mapping. Recently WGS (whole genome sequencing) based GBS (genotype by sequencing) has been considered as a good QTL mapping tool. Therefore we made 20 mapping lines with double digested GBS libraries. Then HiSeq sequencing has been applied in these libraries. The subsequent GBS-based QTL mapping of downy mildew resistance of cucumber will be presented.

# DEVELOPMENT OF LONGER PEPPER LINES RESISTANT TO POTATO VIRUS Y (PVY)

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Pepper (*Capsicum annuum L.*), is one of the most important vegetable species produced both in the world and in Turkey. Turkey is in third place in pepper production in the world. There are many viruses affecting and limiting pepper production. Potato y virus (PVY), a member of the genus potyvirus, is one of the most common viruses infecting pepper crops. Improving resistant pepper varieties against the disease is more advantageous and easy way for producers. Recesses of PVY0, PVY1 and PVY1-2 are available in the world. The Pvr4 resistance gene in wild type SCM 334 pepper confers a complete resistance to the three pathotypes of potato virus. In this study, resistant genotype SCM 334 and susceptible inbred line Sera Demre 8 (SD8) were crossed to improve resistance in breeding lines. To eliminate the undesirable characteristics of the resistant genotypes, they were backcrossed three times with susceptible genotypes. Mechanical and molecular methods were used to determine the reaction of backcross progenies to the disease. The dominant SCAR markers were used to determine resistant and susceptible plants and results from the mechanical method were verified with the SCAR marker.

**Key Words:** Long-type pepper, *Pvr4*, CAPS marker, Mechanical inoculation

This study is part of TUBİTAK KAMAG 109G029 project.

# DEVELOPMENT OF QUALIFIED MELON LINES ACCORDİNG TO POWDERY MILDEW

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Powdery mildew is one of the biggest problems in melon cultivated areas in the world. The plants are infected by causal agent in hot and dry weather. The leaves are brownish and plant died in the advanced stages. Thus, the yield and quality is reduced. *P. xanthii* is the main factor of powdery mildew in *Cucurbitaceae* family. Chemicals used for the controlling this disease are creating adverse effects to the environment and human health and this method is expensive. The best solution for the control of the disease is use resistant cultivars. In this study developed tolerant melon lines according to powdery mildew. Two resistant genitor and 5 susceptible lines were used in this research. Powdery mildew disease agent was collected from areas that damage in our region commonly. Fungi were classified according to the structure under the microscope and used as the inoculum source. Backcrossing method is used for the development of tolerant lines. The lines used as female parent crossed with powdery mildew resistant genitors. F1 generation backcrossed with female parent again. Obtained $GM_1$ generations were tested with powdery mildew. Tests were conducted in in-vivo conditions for determination of resistance to powdery mildew. . In three-for true leaf stage, liquid suspension ($5x10^6$ spore/ml) containing the powdery mildew strain 5 spores was sprayed to the upper parts of the leaves and inoculation was realized. Resistant materials backcrossed with female parent again and tested. This process is continued until $GM_4$ generation and obtained tolerant lines.

# EFFECTS OF GRAFTING WATERMELONS ON *CITRULLUS LANATUS* VAR. *CITROIDES* GENOTYPES FOR PLANT GROWTH, YIELD AND FRUIT QUALITY

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The aim of this study is to investigate the rootstock potential of wild watermelon species *Citrullus lanatus* var. *citroides* genotypes which belong to the watermelon genetic resources collection of Çukurova University, Faculty of Agriculture, Department of Horticulture for watermelon and their effect on fruit quality (sugar content, carotenoid content). Argentario, a bottle gourd rootstock widely used for watermelon and Maximus, a *Cucurbita maxima* x *Cucurbita moschata* hybrid rootstock is used for comparison. Crimson Tide F1 is used as scion and non- grafted Crimson Tide plants are used as control. Time of first male and female flower initiation as well as time of 50% male and female flower initiation, diameter of main stem, length of main stem, number of nodes on main stem, total branch number, yield, fruit weight, fruit, length, fruit, diameter, fruit rind thickness, total soluble solids, flesh firmness, are analysed in 5 plants in each plot. Sugars (saccarose, glucose, fructose, maltose) and caratenoids (lutein, fitoen, fitofluen, α-carotene, β-carotene and ζ-carotene) are extracted and analysed as fruit quality parameters. Results will be presented in details during the congress.

**Key words:** Grafting, breeding, genetic resources, fruit quality

# FINE MAPPING OF SALT TOLERANCE TRAITS IN *SOLANUM PENNELLII* INTROGRESSION LINES

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Salt tolerance is a complex trait that is not easily bred into plants. Salt tolerance can be manifested in several ways such as the ability to increase shoot and/or root mass despite salt stress, a greater than normal accumulation of antioxidants like phenolic compounds and flavonoids, and an improved ability to exclude sodium ions. In this work, *S. lycopersicum* M82, *S. pennellii* LA716 and a *S. pennellii* IL population were evaluated for growth and their levels of antioxidant activity and content under both control and stress conditions. These data were used to identify QTLs responsible for controlling the antioxidant parameters under both control and salt stress conditions. Salt tolerance characteristics were observed in IL11-1, IL6-1 and IL7-4-1. This project aims to characterize the traits carried by these lines by fine-mapping the genes within the introgression. To this end, each IL was crossed with M82 to produce F2 populations of approximately 3000 individuals. These individuals were screened with molecular markers that delimit the 30-40 cM introgressions contained in each line. Recombinant F2 plants were self-pollinated to generate F3 recombinant families. Each F3 recombinant plant will be characterized with the molecular markers in the introgression region. Homozygous F3 plants will be self-pollinated and F4 individuals will be tested for salt tolerance. Thus, each effect (or gene) will be delimited to a particular chromosome region. Based on the results, a strategy will be devised for further breeding and marker-assisted selection of relevant salt tolerance traits in cultivated tomato.

# HYBRID SPINACH BREEDING-I

# CHARACTERIZATION OF NATIONAL SPINACH GENETIC RESOURCE AND IMPROVEMENT OF HIGH QUALITY PURE LINE

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This research was carried out for the purpose of purification and characterization of the gene pool in the short term, take place an important strategic interests of our country agriculture, national genetic resources collection, identification, preservation and production of these materials by developing new varieties, morphological characterization results were evaluated for 82 pieces of spinach line which obtained in 2013. Intensity of green color in leaf blade, the palm leaf, blistering lobe formation of the leaf blade, petiole adhesion, petiole length, cling to leaf blade, leaf blade shape, leaf blade edge, the apex shape on the leaf blade, elongate shape of leaf blade, rate of bisexual plants, rate of female plant, rate of male plant, flowering start time and mildew damage observations were investigated by using UPOV criteria.

**Key Words**: Spinach, morphological characterization, genetic material

# IDENTIFICATION AND ANALYSIS OF *MDSEF1* GENE FROM APPLE (*MALUS DOMESTICA*)

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Flowering in fruit trees like apple with a long juvenility is hindered and delayed by some inhibitor genes until their down-regulation by their controlling pathways. Shortening juvenility period could be achieved through identifying and silencing these flowering inhibitors via biotechnological methods. *SERRATED LEAVES AND EARLY FLOWERING* (*SEF*) is an Arabidopsis homolog of the yeast SWC6 protein, which is a conserved subunit of the SWR1/SRCAP chromatin-remodeling complex probably involved in the substitution of histone H2A and hence down-regulation of *FLOWERING LOCUS C* and *MADS-AFFECTING FLOWERING 4* and increasing *FLOWERING LOCUS T* and *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1* transcript levels. Here, we report the identification of three paralogs of *AtSEF* gene in apple (*Malus domestica*) which may have the same regulatory function in the genetic network of flowering in apple. One of these paralogs, *MdSEF1*, was analyzed further through bioinformatic approached as well as wet lab methods such as differential display techniques. Amino acid sequences and similarities of these homologs to their Arabidopsis counterparts have been shown. The expression pattern of the isolated gene in accordance with its downstream genes has been discussed.

**Keywords:** Apple, *AtSEF*, RT-PCR, Flowering

# IMPROVEMENT TO RESISTANT LINES FOR *FUSARIUM OXYSPORUM* F.SP. *RADICIS LYCOPERSICI*

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Tomato (*Solanum lycopersicum*) is considered as one of the most widely grown vegetable crop in the world. One of the most important challenges in tomato production is pests and diseases reducing yield and quality of the crop. Fusarium crown and root rot caused by the fungus *Fusarium oxysporum* f. sp. *radicis-lycopersici* (FORL), is the most important soil borne disease of tomato. In this study, 10 tomato pure lines and 2 resistant lines were crossed for improvement resistant lines with different types. F2 plants were tested against fusarium crown and root rot in root dip inoculation method. Four weeks after the inoculation, resistant and susceptible plants were scored 0 and 1, respectively. BC1 and BC2 plants were screened with molecular marker. The purpose of this study supported with TUBITAK KAMAG number of 109G029 project was to develope resistant lines for *Fusarium oxysporum* f. sp. *radicis-lycopersici*.

**Key words**: tomato, *fusarium*, backross,breeding

# MEIOSIS OF FERTILE AND STERILE SUNFLOWER AT THE CYTOLOGICAL AND MOLECULAR LEVEL

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The life cycles of all sexually reproducing eukaryotes are dependent on the process of meiosis. A detailed cytological description of meiosis has been built up over many years, based on studies in a wide range of plants. Meiotic process includes a number of important events as crossing over, synaptonemal complex and recombination nodules formation which is under the strict control of highly specialized genes. Molecular analysis of these genes leads to obtain new various information relating to the genetic mechanism, which is included in the functional activity of the meiotic process in plants, therefore the molecular study of meiosis gene represents fundamental and actual problem. The present study reports the meiotic behavior in fertile and sterile sunflower lines investigated at cytological level using light microscopy and at molecular level – through estimation of meiotic gene expression via quantitative PCR technique. Cytological researches have highlighted shape, size and degradation level of meiocytes in five stages of microsporocyte development. Expression level was estimated for some genes involved in meiotic control such as cyclins, histones, proliferating cell nuclear antigen and male sterility1. It was established correlation between male sterility, meiocytes degradation and specific gene expression. Obtained results extend knowledge about meiosis process of sunflower and offers useful information for breeders which could facilitate creation of $F_1$ hybrids.

# MICROSATELLITE ASSESSMENT OF GENETIC DIVERSITY AMONG JORDANIAN TOMATO (*SOLANUM LYCOPERSICUM* L.) LANDRACE

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Tomato landraces are considered valuable sources of genetic traits for crop improvement. Assessment of genetic diversity using simple sequence repeat (SSR) markers is a very effective means of targeting markers to marker scarce positions in the genome. This study was aimed to assess the genetic variability among 29 Jordanian tomato landraces collected from diverse environments. A set of functional SSR markers via *in silico* analysis of publicly available tomato DNA sequence was used. As a result, 22 SSR markers were developed and tested. A total of 32 alleles were scored and showed 100% polymorphic patterns with mean of 0.18 polymorphism information content (PIC) values. Mean of observed and expected heterozygosity were 0.19 and 0.24 respectively. The mean value of jaccard similarity index was used to clustering the 29 landraces. The value of 0.52 is separated the landraces according to their growth (determinant and semi-determent) type. These results are a part of funded project aimed to develop a landraces with good genetic variability values. In conclusion, microsatellite is a powerful tool to assess genetic diversity and these data will be used in genetic improvement of tomato landrace through national breeding program utilizing molecular approaches.

**Keywords:** Tomato (*Solanum lycopersicum* L.), genetic diversity, Microsatellite, *in silico* analysis

# NEW *LIMONIUM* SELECTIONS FOR CUT FLOWER SUMMER PRODUCTION

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Several off-type individuals of *Limonium,* identified in a germplasm collection, were selected for their aesthetic innovative traits for cut flower summer production. The selected plants showed a modification of the corolla color from blue/purple to white. In 2010, Explants were collected and *in-vitro* cultured on different media in order to set-up an effective protocol for large-scale micropropagation. The explants consisted of floral apices of immature stems collected 2 weeks before anthesis. The rooted plants were acclimatized in greenhouse onto heated benches covered by plastic tunnels. More than 120 plants were grown under greenhouse in spring 2011. At flowering stage, phenotype evaluations were performed in order to determine if the micropropagated plants had maintained the same color characteristics of the selected mother plants. Agronomic evaluations were also carried out in 2012 and 2013 by comparing the white-flowered off-type clones with the original blue-violet variety and two cultivars, used as a control, with white or blue-violet flowers, respectively. For each tested genotype the following traits were evaluated: length, rigidity and fresh weight of the stem, color and diameter of calyx and corolla, flowers drop, presence/absence of fragrance, number of flowers on the terminal spikelet, height and diameter of peduncle. By a commercial point of view, the most interesting aesthetic traits of the new white-flowered clones resulted in a significantly shorter length of the pedicle (which means an improved density of the inflorescence) and an increased weight of the stems in comparison with the control cultivars.

# PERFORMANCE OF SOME EGGPLANT GENOTYPES UNDER COLD STRESS

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To identify the performance to cold, generative and vegetative tests were performed on eggplant (*Solanum melongena* L.) genotypes. The study carried out both climates-controlled room and the greenhouse. The seedling planted in 4-5 leaf stage in the pots were exposed to 22/5 °C day/night for 24 h. Flowering fluctuation and pollen germination of plants released under cold stress were observed. Total 13 eggplant genotypes were selected as appears to be tolerant according to the test results performed in climates-controlled room. The yield per plant, average fruit weight, the average number of fruits, LAI value, first flowering dates, the distance between the plant nodes were defined for better understanding their performance under growing greenhouse conditions in winter season. The results were evaluated according to the weighting method. The genotypes 4, 29, 30, 17, 24 and 20 appeared to be more tolerant than the other. These genotypes can be used in eggplant breeding for cold stress tolerance.

# PRELIMINARY RESULTS OF GENETIC LINKAGE MAP IN EDIBLE FIG (*FICUS CARICA* L.*)*

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Fig (*Ficus carica* L.) is one of the most economically important fruit crops grown in Turkey and throughout the Mediterranean Basin. The long generation times hampers conventional breeding activities, hence fig cultivation is mostly based on empirical selection of adapted varieties. So far, no linkage map has been developed for *Ficus carica* using morphological or molecular markers. Therefore, the objective of this study was to develop the first linkage map of *F. carica*. The study utilized a pseudo testcross strategy with an F1 population from “Bursa Siyahı X Ak İlek” cross. One hundred and thirty-eight F1 plants along with the parents were scored with Amplified Fragment Length Polymorphism (AFLP), and Simple Sequence Repeat (SSR) markers. So far, AFLP primer combinations produced a total of 406 useful markers of which 223 were scorable on Bursa Siyahı and 183 were on Ak İlek parent. SSR primers identified a total of 40 loci on both parents. The female parent, Bursa Siyahı, had 15 linkage groups with a total of 235 markers. The male parent, Akilek, had 16 linkage groups with 198 markers. Total map distances for female and male parent were 1365 and 1220 cM, respectively.

**Keywords:** *Ficus carica* L, genetic linkage map, pseudo-testcross, AFLP, SSR

# STUDIES ON IMPROVING CUCUMBER (*CUCUMIS SATIVUS* L.) LINES FOR CHILLING TOLERANCE

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Cucumber (*Cucumis sativus* L.) is a tropical crop, but is also grown in temperate regions in late spring to summer. Cold temperature damage is a common problem for early-planted cucumber in temperate countries. Chilling temperatures (≤12$^0$C) can cause significant damage to cucumber plants. The objective of the present study was to identify chilling tolerant lines from a pool of 123 breeding lines and then select the lines improved. The approach was based on chlorophyll contents (Chl) and chilling injury index in cucumber seedlings at the cotyledonary and first true-leaf stage. Seedlings were exposed to chilling temperature at 5°C for 16 h, under 150 µmol $m^{-2}$ $s^{-1}$ photosynthetically active radiation (PAR) and allowed to recover at 26°C for 14 days using randomized complete block design with 2 replications in early spring of 2011. Chilling tolerance for the seedlings was evaluated by the severity of chilling injury (SCI) for cotyledon and the first true leaf stage. The scale values were quantified that ranged from 0 to 9. These results indicated that the chlorophyll contents of CH2, CH6, CH7,CH8, CH10, CH11, CH25, CH27, CH37,CH42, CH45, CH46, CH47, CH69, CH72, CH85, CH 90 and CH97 lines showed less variation than the other lines due to low temperatures. Consequently, these lines will be used to improve new hybrid varieties in cucumber breeding programs.

***Keywords:*** *Cucumis sativus*, cold stress, chilling injury, chlorophyll contents, Breeding

# STUDIES ON VARIETAL SELECTION IN WALNUT (*Juglans regia* L.) POPULATIONS OF ÇANKIRI PROVINCE

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In this selection survey that was performed to select the types with superior properties among the population of seedling walnut trees in Çankırı location, fruit samples were collected individually from 364 trees. Results of the study have been selected of Promising 8 walnut types. Than these types were evaluated for fruit and tree properties and 23 walnut types with fruit weight between 11.90-15.83 g, interior weight between 6.66-8.82 g, the interior ratio between %53.06-%60.41, shell thickness between 1.21 – 1.50 mm were selected as promising. On the other hand, the shell color was determined as dark in 2 types and tawny in 6 types also. The inner color was found light yellow in 4 types and dark yellow in 4 types. The selected types were in a good condition for full and sound interior ratio, 7 types gave 100% full and sound inner, whereas one type gave empty fruit proportionally 20%. 4 types showed homogamous blooming, 1 types showed protandrous blooming and 3 types displayed protogenous blooming.

**Keywords:** Walnut, varietal selection, Çankırı

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# STUDY OF THE INTERACTION OF *PHYSCOMITRELLA PATENS* AND PHYTOPATHOGENIC BACTERIA

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According to FAO, the world's total losses from diseases of agricultural crops is estimated some $25 billion in year. One of the principal ways to reduce the losses due to plant disease is the selection of resistant varieties and hybrids. Study of the interaction of plants and pathogenic bacteria is an important aspect of plant breeding for resistance to the diseases. Our goal is to study a model plant-pathogen interaction for *Physcomitrella patens* and phytopathogenic bacteria. Genome of *P. patens* was sequenced and there is a possibility to generate targeted knock-out mutants by homologous recombination. Many activated cellular and molecular defence reactions of *P.patens* are similar to those present in the flowering plants. The presence of haploid gametophytic phase in *P.patens* allows detection of mutant phenotypes without subsequent analyses segregation in the offspring. Therefore, *P. patens* is a convenient system for the study of plant-pathogen interactions and functional analysis of plant immune system genes and their evolution. We evaluated the virulence of several species of pathogenic bacteria to *P. patens* and optimized the method of inoculation *in vitro*. This work was partially supported by ISTC project #3431 and RFBR research project No.13-04-40104-H.

# THE DEVELOPMENT OF *XANTHOMONAS* AND TuMV - RESISTANT DOUBLED HAPLOID LINES OF *BRASSICA*

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Yield losses caused by bacterial and viral diseases on crop plants are increasing over the world. The problem is increased because of global warming and the appearance and spread of new aggressive strains of pathogenic bacteria and viruses. Turnip mosaic virus (TuMV) is the most important viral pathogen of many crops, including *Brassica* plants. Pathogenic bacterium *X. campestris* can reduce the yield of *Brassica* plants by 50%. Therefore, the development of *Xanthomonas* and TuMV- resistant DH-lines of *Brassica* is important task. Plant collection of *Brassica* species (64 accessions) was inoculated by 6 isolates of TuMV and 7 strains of *X. campestris*. Symptoms were recorded after visual inspection and leaves were sampled for testing for the presence of TuMV by DAS-ELISA test. Thirteen resistant samples to all isolates of TuMV, two of which are resistant to all strains of *X. campestris* were selected. These plants were used for the production of DH-lines through microspore culture. Isolated microspore culture was treated for 24 h at 35°C or 72 h at 33°C for the induction of embryogenesis. Embryos of 8 resistant to TuMV accessions of *B. napus* (№1, №417, Lugovskoy, Galant, Jp-8, Jp-4, Hanna and Griffin) and embryos of 2 resistant to TuMV and *X. campestris* accessions of *B.oleracea* ISA454.1 and *B. napus* №444 were obtained from the microspores treated at 33°C for 72 h. Also embryos of resistant to TuMV accessions Cobra, Center-1 and Center-2.1 were obtained after heating for 24 h at +35°C. The study was supported by ISTC project 3431.

# USING OF SELF-INCOMPATIBLE INBRED LINE AND DETERMINATION OF AGRO-MORPHOLOGICAL CHARACTERISTICS DEVELOPED $F_1$ HYBRID VARIETIES OF WHITE HEAD CABBAGE (*BRASSICA OLERACEA VAR. CAPITATA SUBVAR. ALBA*)

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Male-sterility and self-incompatibility are two systems in vegetable seed production that provide saving time and labor thus reducing the cost of seed. These two systems are widely used of producing $F_1$ hybrid seeds in *Brassicaceae*. This study was carried out between 2012 and 2013 on white head cabbage breeding test plot, under the 'White head cabbage $F_1$ hybrid cultivar improvement' project that began in 1998 at the Black- Sea Agricultural Research Institute-Samsun-Turkey. In this study there was used 145, 506, P 62-1, 4 and P 28 inbred line which determined by seed set analyze to check self-incompatibility and their partial hybrid combinations. The highest seed yields were obtain from the 145 X 506 combination with 18.37 seed/pod. This was followed by P 62-1 X 145, 145 X P 62-1 and 506 X 4 combinations with 9.20, 8.12 and 8 seed/pod, respectively. 145 and 506 inbred line were the prominent one in respect to both its self-incompatibility and hybrid seed yield. The line that determined as self-incompatible and their partial $F_1$ hybrid combination were investigated in terms of agro-morphological features. 145 X 4 hybrid combinations were determined as a candidate for cultivar registration with superior morphological features and high seed yield. Studies for cultivar registration were started.

**Key word**: Cabbage, Self-incompatibility, Morphological characterization, $F_1$ hybrid, Registration

# HIGH RESOLUTION MAP OF EGGPLANT (*SOLANUM MELONGENA*)

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A linkage map of eggplant was constructed for an interspecific F2 population derived from a cross between *Solanum linnaeanum* MM195 and *S. melongena* MM738. The map contains 400 AFLP® (amplified fragment length polymorphism), 348 RFLP (restriction fragment length polymorphism) and 116 COSII (conserved ortholog set) markers. The 864 mapped markers encompass 12 linkage groups, span 1518 cM and are spaced at an average interval of 1.8 cM. Use of orthologous markers allowed confirmation of the established synthetic relationships between eggplant and tomato chromosomes and helped delineate the nature of the 33 chromosomal rearrangements and 11 transpositions distinguishing the two species. This genetic map provides a two to three fold improvement in marker density compared to previously published interspecific maps. Because the interspecific mapping population is rich in morphological variation, this greater genome saturation will be useful for QTL (quantitative trait locus) analyses. The recent release of the tomato genome sequence will provide additional opportunities for exploiting this map for comparative genomics and crop improvement.

# GENOME POLYMORPHISM OF XANTHOMONAS ARBORICOLA

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Xanthomonas is a genus of phytopathogenic bacteria that includes up to 27 various species characterised by virulence specificity to the affected plants. Sometimes, the bacteria of certain species infect atypical host plants, for example, the strains of *X.arboricola* have been isolated from diseased plants of families *Asteraceae, Brassicaceae, Poaceae*, and *Solanaceae*. The collection of strains was studied, by MLST method, according to the procedure described by Young et al., 2008, Ignatov et al, 2007, including 7 conservative genes: *gyrB, dnaK, fyuA, rpoD, prpC, fabB,* and *nrdB*. Only pathogenic strains were used for this study. As a result of genetic analysis, we showed that strains, identified as *X.arboricola* by a number of biochemical and genetic tests, have alleles of genes *gyrB, dnaK, nrdB,* and *prpC* more similar to strains of *X.campestris, X.euvesicatoria, X.oryzae*. First, we assumed that putative horizontal gene transfer between the species of Xanthomonas can improve the bacteria adaptation to a new host plant. To check this hypothesis, we sequenced the genome of *X.arboricola* strain 3004 isolated from barley. The genome has a total length of 5,855,662 bp., consisting of 61 scaffolds, GC content is 65.3%. We annotated the assembled genome using the RAST server and detected 4,131 coding sequences. The gene order was most similar to *X.axonopodis* pv. *citri* strain 305. Sequence of a phage with reduced gene content most similar to Xantho Xp10 (*X.oryzae*) was found in the bacterial genome. The complete genome analysis showed that the *X.arboricola* strain 3004 in fact is close to an ancestral genome to all the known genomes of "core" Xanthomonas group, existed before it captured the Type 3 Secretion System and separate parts of its genome evolved in different directions towards adaptation to distinct host plants.

The work was supported by ISTC Project 3431.

# A NEW PROMISING FRUIT: CHERRY LAUREL (*PRUNUS LAUROCERASUS* L.) AND STEPS ON BREEDING

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Fruit breeding, the genetic improvement of fruit crops, has an ancient tradition that traces to the domestication process. The maintenance of genetic variance is the key issue in breeding and conservation. Conventional fruit breeding is based on continuous selection of superior phenotypes from genetically variable populations. For many years, breeding began with selection of superior types from natural seedling populations and then from seedlings that occurred naturally from grower fields with desirable genotypes fixed by vegetative propagation. Recently biotechnology techniques have been employed including **in vitro** propagation, embryo studies, genetically dissect traits e.g. molecular markers, genetic fingerprints characterizing of parents to determining genetic differences between types. *Prunus laurocerasus* L. (Cherry laurel), is a fruit native to the regions bordering the Black Sea in Southwestern Asia and Southeastern Europe. It is widely spread out in the North part of Turkey and there are many cultivars which show different characterization. The cherry laurel tree have reasonably pleasant fruits when fully ripe and also is a valuable ornamental plant for its attractive dark and evergreen leaves, and clusters of white flowers in the spring. The detailed information about characteristics and nutritional value of cherry laurel was obtained from earlier studies and served for breeding of new cultivars. Although breeding efforts in cherry laurel are more limited than the other major fruits, a continuous supply of new cultivars should result from ongoing studies. This review gives an overview of cherry laurel genetic resources, selection of superior types, challenges encountered in cultivation of cherry laurel, specialised techniques used in the development of new genotypes and propagation of the selected types.

**Keywords:** *Prunus laurocerasus* L., breeding, selection, biotechnological studies, propagation

## AEGEAN AGRICULTURAL RESEARCH INSTITUTE TOMATO BREEDING STUDIES

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Aegean Agricultural Research Institute Tomato Breeding Studies are aim to improve fresh market and processing tomato varieties. For this purpose, populations are generate to according to market, producer and consumers preferences, producer regions conditions. While The populations were developing, were also used to source of diseaes resistance such as Fusarium Wilt, Verticillium Wilt, Nematode, TSWV(Tomato spotted Wilt Virus), TMV(Tobacco Mosaic Virus),ToMV(Tomato Mosaic Virus) and TYLCV(Tomato Yellow Leaf Curl Virus). In the populations, have differences of fruit shape,colour and size among improved lines. Fresh market and processing tomato lines are examined in terms of plant habit, fruit size, fruit colour, fruit firmness, brix and yield.

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## CLEMENTINE × BLOOD ORANGE CROSSES

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Oranges and mandarins are two major citrus crops consumed worldwide. New cultivars are needed for consumer preferences. Hybridization experiments have been being continued different citrus growing countries. Cross-pollination experiments among ‘Clementine’ mandarin (*Citrus reticulata* Blanco) and blood oranges (*C. sinensis* Osbeck) were conducted in 2011. While monoembryonic and self-incompatible ‘Clementine’ mandarin was used as female parent, A1, A2, A3, H1, H2, H3, K1, and K2 local genotypes used as blood orange male parents. Before hybridization, anther numbers, pollen numbers, the ratios of pollen viability and germination tests were performed in 8 parent blood oranges parents. The pollen viability was found between 43.38% (H3) and 1.32% (A2) in TTC (2, 3, 5-triphenyl tetrazolium chloride) test. The pollen germination changed from 12.76% (H3) to 1.69% (A1) on 1% agar+ 25% sucrose medium. While the anther numbers were between 22.00 (K1) and 20.37 (H1, H2), the total pollen grains per flower was found between 139421 (A1) and 60500 (K2) on the hemacytometer. At hybridization experiments, 228 flowers were crossed, and 38 fruit, and 312 seeds were obtained. These local blood orange genotypes can be used as a pollen source for self-incompatible ‘Clementine’ mandarin orchards to increase fruit set.

**Keywords:** *Citrus reticulata*, *C. sinensis*, hybridization, pollen, TTC

# *IN VITRO* POLLEN VIABILITY AND POLLEN GERMINATION IN *PRUNUS LAUROCERASUS* L. (CHERRY LAUREL)

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In the fruit trees pollen quality consists of viability, morphological homogeneity, pollen germination and pollen tube growth rate which are very important component of fertilization and fruit setting and for this direction,. Study of pollen traits is one of the most important approaches for growers and breeders. The study was carried out to determine *in vitro* polen viability and pollen germination of 7 types (one is wild type) of cherry laurel (*Prunus laurocerasus* L.) in 2011 and 2012 years flowering seasons. Two pollen viability test (TTC and IKI) was used. Pollen traits of types were studied using *in vitro* medium containing 0%, 5%, 10%, 15% and 20% sucrose to determine best sucrose concentration for germination. The viability rates were different according to types and tests used. IKI test gave more clear and well-pointed results considerable. 15% sucrose gave the best germination rates for most of the types. Pollen germination rates was recorded periodically from one hour to 48 hours in 15% sucrose including media and the results showed that pollen germination rates was increased after 6 hours placed in to the culture media.

**Keywords:** *Prunus laurocerasus* L., pollen viability, germination

# STUDY OF OVULE FERTILITY IN THE MANDARIN GROUP (*CITRUS RETICULATA*) UNDER MANUAL AND OPEN POLLINATION CONDITIONS

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In Mandarin group, *Citrus reticulata,* the ovule fertility is complex under natural conditions. It could be influenced by several factors including the pollinator parent, the female variety, the stigma receptivity, the pollination date, the region and the used concentration of pollen grains. The number of seeds produced by a given variety is not reproducible in the absence of these data. The study of the female fertility and the distinction between the varieties of this group was therefore considered. The aim of this work is to study the ovule fertility of some mandarin varieties through the estimation of the number of seeds produced under manual and open pollination conditions. The study was conducted in two regions of Morocco, namely the Gharb, a sub humid region, and the Haouz, an arid continental region. The tests were conducted on 10 to 15 years old trees of Mandarin Nova and Mandarin Nadorcott as male, and Clementine Nules, Clementine Marisol, Mandarin Nova and Mandarin Nadorcott as female varieties. Saturation and 100 g pollen concentrations were compared one and six days after anthesis. The stigma receptivity was estimated 48h after pollination through the percentage *in vivo* germination of pollen. The number of seeds produced by fruit was counted one month before maturation. In the case of hand pollination, 100 fruits were used for each variety. The obtained results showed that the stigma receptivity decreases the further away you move from the anthesis stage. The seed number decreases when pollination was carried out six days after anthesis. In terms of pollen grain concentration, our results revealed an increase of seed number with the increase of concentration. The open pollination allowed a significant distinction between the ovule fertility degrees of the tested varieties, evaluated on the basis of seed number. Our results demonstrate the importance of the open pollination technique in the determination of ovule fertility in the mandarin group of citrus fruits. This technique is not influenced by pollen grain concentration or by the pollination physiological stage. In addition, it allowed a clear distinction between the varieties of this group.

***Keys Word:*** Citrus, ovule fertility, mandarin, open pollination, hand pollination, varieties distinction

# DEVELOPMENT OF BAC-END BASED SIMPLE SEQUENCE REPEAT (SSR) MARKERS IN APPLE

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A genome-wide bacterial artificial chromosome (BAC) physical map of the apple, *Malus domestica* Borkh., has been recently developed. This study addresses development of SSR markers from the BAC-end sequences in apple. Designed 187 BAC-SSR primer pairs were subjected firstly to gradient-PCR for amplification and to determine their optimum annealing temperatures. Then, the amplified primer pairs were tested in two F1 segregating populations: ‘Kasel-37’ x ‘Delbarestivale’, and ‘Kasel-41’ X ‘Williams Pride’. The PCR reactions were performed in 12 F1 progenies and in the parents to determine segregation types of the primer pairs. There was no amplification in 20 SSR primer pairs, and 87 of them were monomorphic in the two populations. As a result, 80 of the primer pairs showed segregation in the two F1 populations.

# AN EXAMPLE TO THE USE OF GENETIC RESOURCES FOR IMPROVEMENT THE RESISTANCE: THE DEVELOPMENT OF NEW POWDERY MILDEW TOLERANT GRAPE VARIETIES

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Powdery and downy mildew are the main threats for viticulture all over worlds and most *V. vinifera* varieties are susceptible to these diseases. The hybridization studies had been made with the use of disease resistant wild species or hybrid varieties as one of the parents. The native grape varieties to the very rainy Northeastern coastal area of Turkey are grown without any fungicide application. These varieties including some *V. labrusca* types had been collected at National Collection Vineyard and used for cross-breeding studies. As a result of elections, Özer Karası was registered in 2011 as powdery mildew tolerant wine grape cultivar. Quality and tolerance properties of this cv. and some candidates are presented in this study.

# ANTHER CULTURES IN DIFFERENT ORNAMENTAL PEPPER GENOTYPES

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Ornamental pepper (Solanaceae) has begun to gain its old popularity again in the last decades because of easy seed propagation, relatively short cropping time and heat-drought tolerance. The number of breeding studies on ornamental pepper has gradually being increased due to this renewed interest. Doubled haploid technology is a powerful tool to obtain pure lines for the breeding. This techonology has been applied successfully to vegetable pepper since 1973. However, there is almost no application of haploidy techniques in ornamental pepper as we know. This study highlights haploid performances of 48 ornamental pepper breeding lines tested via anther culture. The flower buds containing appropriate microspore stage determined by DAPI staining were collected in May and June 2013. Haploid responses of the genotypes were compared with two solid culture media, B5 and MS. The ingredients in the media were consisted of 1 mg/l BA, 4 mg/l NAA, 15 mg/l silver nitrate and 0.25% activated charcoal. Sucrose amount was 20 g/l in B5 and 30 g/l in MS medium. Anthers were exposed to a 35 ºC inductive heat shock for 2 days in dark, prior to culture at 25 ºC and 16/8 h photoperiod conditions. The percentage of androgenetic embryogenesis were changed between 0,07 and 7,67 among the 48 genotypes. Most of the embryos were obtained from B5 medium. 0,13-7,67 % embryogenesis were realized in 12 genotypes in B5 medium while 0,07-4,40 % embryogenesis were happened in 6 genotypes in MS medium. 5 genotypes gave response in both B5 and MS medium. The studies on embryo germination and acclimatization are currently underway. However, 2 haploid plants were transformed from the embryo till now and the ploidy levels of both were determined with Flow Cytometer.

**Keywords:** Haploid, Anther culture, Activated charcoal, Ornamental pepper, *Capsicum annuum*

# BIOTECHNOLOGICAL STEPS IN STRAWBERRY TREE (*ARBUTUS UNEDO* L.) BREEDING

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*Arbutus unedo* L. (Strawberry tree) belongs to Ericaceae family, is an evergreen shrub or tree, mostly known around Mediterranean region in natural habitat, has valuable medicinal and aromatic properties. The plant is mainly used for its edible fruits. In addition *A. unedo* have increasing importance in afforestration programmes, beekeeping facilities, ornamental purposes and elucidating plant physiology. Therefore, the species is seemingly a promising fruit plant. Orchards are very limited but increasing demand to plant will cause the starting new fruit orchards with superior genotypes viz., tolerant to the abiotic stress, resistance to pests and diseases, rich contents in terms of valuable compounds, convenience to postharvest operations, being visually preferable and suitable to target climate etc. Plant breeding is an important component to overcome elimination of unwanted features and to reach admirable characters. The main steps in breeding are good selection, succesfully adaptation and inheritace via transferring the features to subsequent generations. Studies on *Arbutus unedo* L. breeding via biotechnological approaches were reviewed. Just a few of the techniques have used in all known biotechniques for the purposes especially for selection and propagation of the determined best type. The mostly used techniques for *A. unedo* were consantrated on *in vitro* propagation and fingerprint analyses to determine genetic diversity and the favourite genotypes wherein the population with compared with pomological features for help in breeding programme. That sould not be ignored that *A. unedo* breeding is in its infancy when compared with numerous field and horticultural plants.

**Keywords:** *Arbutus unedo* L., strawberry tree, breeding, biotechnology

# BREEDING FOR SCAB RESISTANT APPLE VARIETIES

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Apple scab is an important fungal disease caused by *Venturia inaequalis* (Cke) Wint. that requires intensive control measures in most regions throughout the world apple production. It's a major problem, especially in temperate climates. Using of resistant varieties is the most effective method of disease control. Based on this phenomenon apple breeding studies have been started in Fruit Research Station to develop high quality new apple varieties resistant to apple scab. Hybridization studies were started in 2008 and so far approximately 15,000 genotypes were obtained. We used artificial inoculation, natural inoculation and molecular markers (SCAR primers) for selection of resistant apple genotypes. In 2012, the first flowers in 16 genotype**s** were observed. In 2013, 103 genotypes were observed flowering. Hybridization studies are made in different crossing combinations each year.

# COLLECTION AND EVALUATION OF *FRAGARIA* GENOTYPES FROM TURKEY

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Although cultivated strawberry, *Fragaria xananassa* Duch., is not native to Turkey, there are several related species exist in Anatolia. These include, *F. vesca*L., *F. viridis* Duch., *Potentilla micrantha* L. and *P. indica* (Andrews) Th. Wolf. Several trips were made to regions having these species and more than 200 populations were evaluated. Out of these, fifty genotypes were sampled and vegetatively propagated. These accessions were then evaluated for several taxonomic and horticultural traits on a replicated trial conducted on an unheated greenhouse. A broad range of variation was measured almost all traits evaluated. The principle components analysis of morphological traits revealed that the first three principle component explained 34%, 23% and 11% of the variation, respectively. The cluster analysis of the same variables indicated that all genotypes into three groups. The first group was constructed from mostly *F. ×ananassa* genotypes while the *P. michranta* and *F. virginiana* genotypes construed the other groups. The relationship of the representatives of Turkish octoploid strawberries and those of parental species were determined by using nine SSR primer pairs were. Ten RAPD primers were used in the molecular characterization of the genotypes; they generated 3-8 bands all of which were polymorphic for the population studied. Using all experimental results, a core collection which was composed from 16 genotypes of *F. ×ananassa* (6), *F. vesca* (9) and *F. viridis* (1) species representing Turkish strawberry genetic resources.

# CLONAL SELECTION OF CHERRY ROOTSTOCK CANDIDATES IN THE CENTRAL AND EASTERN BLACK SEA REGION IN TURKEY

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Turkey is one of the significant countries in the world from the plant genetic diversity/resources. Turkey encompasses areas major centers of crop diversity and center of origin for globally significant crops. This study was selected wild cherries genotypes with the ability to dwarf, semi-dwarf and / or vegetative reproduction in the natural flora of Central and Eastern Black Sea Region that can potentially be used as rootstocks for cultivars. A total of 459 wild genotypes were collected from Central and East Black Sea Regions (Amasya, Artvin, Giresun, Gümüşhane, Ordu, Rize, Samsun, Tokat and Trabzon provinces) in Turkey, during 2006-2009. Selected genotypes were recorded some features and the location data. Wild genotypes including 333 sweet cherry, 43 sour cherry, 77 mahaleb and 6 *Cerasus angustifolia* were selected from the towns and villages of the nine provinces in the project area. Sweet cherry was collected from all nine provinces, while sour cherry was selected other 7 provinces except Amasya and Tokat. Mahaleb was collected from 6 provinces, including the most number of Tokat. *C. angustifolia* was only gathered from Gümüşhane and Giresun. Genotypes were defined morphologically some features in their natural environment in the project area. The first three axes accounted for 65.21% of the variability among 459 accessions. The first axis was mainly related to variation in plant habit, branch angle, and one-year-old shoot: length of internode. The second axis was concerned with plant vigor and one-year-old shoot: branching, while the third axis was involved the number of trunk and tendency to suckering. In conclusion, the genotypes selected in this study may be useful for both breeders and rootstock breeding programs.

**Keyword:** Central and East Black Sea Regions, cherries rootstock, multivariate analysis, selection

# COMPARATIVE STUDY OF CALLOGENESIS OF TWO DATE PALM CULTIVARS

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The present work was realized in the department of research and development, of the nursery Tazdayt Biotech, to develop a micropropagation protocol of two rare cultivars of date palm with an important economic value, from the region of M'zab, south of Algeria, Dalla and Bentkbala, to contribute to the preservation of these two rare cultivars and making these cultivars more available for interested growers. We use the inflorescence explant, the medium was Murashige and skoog supplemented Gambourg vitamins and growth regulators, 2.4-D, 2iP, BAP, and NAA, different concentarion according the stage of Organogenesis or Embryogenesis; Casein Hydrolase was supplemented also. The explants start giving callus by the third week of the culture, and the first embryos could be obtained by the eight month; date palm plantlets obtained by eighteen month and they are in acclimatization stage now.

# TRANSCRIPTIONAL CHANGES OF TOMATO PLANTS INFECTED WITH *CLAVIBACTER MICHIGANENSIS* SUBSP. *MICHIGANENSIS*

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*Clavibacter michiganensis* subsp. *michiganensis* (*Cmm*) is a gram-positive bacterial pathogen causing bacterial wilt and canker of tomato (*Solanum lycopersicum*), producing economic losses worldwide. Host resistance is the most cost-effective means of controlling bacterial canker. For instance, no resistant cultivars are commercially avalaible. The resistance to *Cmm* is controlled by the several genes which are present in wild relatives of tomato including *Solanum pimpinellifolium*, *Solanum hirsutum* ve *Solanum peruvianum*. Host responses to *Cmm* and molecular mechanisms associated with the development of disease symptoms in tomato are unknown. The purpose of this research was to determine of resistance to *Cmm*, from either susceptible or resistant wild tomato to identify genes involved in disease response. 26 bacterial isolates performing high virulence among 107 bacterial strains isolated from various locations in Turkey between 1990-2012 were chosen for infection of plants. To analyze expression of genes related to induction of defense, we constructed cDNA from total RNA isolated from seedlings infected with *Cmm* and designed primers for Real-Time PCR. These new candidate genes of resistance would contribute to the development of more effective and sustainable bacterial canker disease control methods and breeding resistant, commercially acceptable, tomato cultivars.

**Key words:** *Solanum hirsutum*, *Solanum peruvianum, Clavibacter*, plant defense

# VVSTK1 ENCODES A PUTATIVE SERINE/THREONINE (S/T) PROTEIN KINASE EXPRESSED DURING GRAPE (*VITIS VINIFERA* CV. SULTANINE) BERRY DEVELOPMENT

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Serine/threonine (S/T) protein kinases are crucial components of diverse signaling pathways in eukaryotes. Protein phosphorylation regulates critical cellular functions. In eukaryotic cells, signal transduction, metabolism, movement, the circadian rhythm, and many other processes are controlled through protein phosphorylation and dephosphorylation by protein kinases and phosphatases, respectively. Together with tyrosine kinases, serine-threonine (S/T) protein kinases comprise a large class in the eukaryotic protein kinase superfamily. In this study, a full-length cDNA of a new serine/threonine (Ser/Thr) protein kinase gene, designated as *VvSTK1* (GenBank Acc. No. AF488697), was cloned from *Vitis vinifera* cultivar Sultanine by RT-PCR. The full length cDNA of *VvSTK1* was 728 bp and contained a 444-bp open reading frame encoding a protein of 147 amino acids. Homology analysis shows that *VvSTK1* strongly resembles plant Ser/Thr protein kinase genes, especially it shares 93% identity with calcium-binding protein CML13-like from *Cicer arietinum* and 89% identity with calmodulin, from *Ricinus communis*. Bioinformatic analysis shows that VvSTK1 protein belongs to a typical Ser/Thr kinase family.

**Key Words:** *Vitis vinifera*, Signal transduction, Serine/Threonine Kinase,

# INTRODUCTION TO PROTOPLAST CULTURE OF *ALLIUM URSINUM* AND *A. SATIVUM*

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The establishment of protoplast cultures of *Allium* species was tested as the prerequisite for somatic hybridization as a tool of increasing of genetic variability. Protoplasts were isolated from *in vitro* cultivated plants of bear's garlic - *A. usinum*, and *ex vitro* cloves of garlic – *A. sativum*. There were used two modified enzymatic solutions (Yamashita et al. 2002): 1% Cellulase Onozuka R-10, 0.5% Macerozyme R-10 and 0.5% Hemicellulase; 2% Cellulase Onozuka R-10, 0.5% Macerozyme R-10 and 1% Hemicellulase. The workflow of isolation was done according to protocol: http://www.vubhb.cz/_te.asp?F=institute/06dogr-protocols-mfpep.htm with washing solution by Yamashita et al. (2002). Kao and Michayluk cultivation medium (1975) was completed 0.2 M sucrose and 0.2 M glucose (Shimonaka et al. 2001) and 2 mM Putrescine dihydrochloride. The enzymatic solution of higher concentration was suitable both for *A. ursinum* and *A. sativum* with working time 21 hours and 9 hours respectively. The cultivated protoplasts maintained viability - application of Putrescine showed to be essential compare to control. Although there was observed cell walls regeneration and occasionally cell division, the major part of protoplasts kept spherical shape. Higher degrees of regeneration were not achieved. This is preliminary results, the work continues. Acknowledgement: This work was supported by the project LF 11012 EUREKA by Ministry of Education, Youth and Sports of the Czech Republic.

# SCREENING OF TEN CITRUS ROOTSTOCKS TO DROUGHT STRESS

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In Morocco, citrus orchards are planted in different areas with various soils and climates. The majority occurs in dry areas so that irrigation is necessary in order to assure adequate production. The spread of CTV in the Mediterranean Basin will soon prohibit the use of the traditional sour orange (*Citrus aurantium*) rootstock, which currently provides tolerance to soil drought, salinity and alkalinity. It is therefore imperative to develop and select new citrus rootstock. Our study sought to investigate the effect of different watering regimes on growth of ten citrus rootstock candidates. Ten citrus rootstocks, i.e. Citrumelo Winter Haven B2 31431, citrumelo 4475 B2G3, Mandarine sunki X *Poncirus trifoliata* 30591, Mandarine cléopâtre X *Poncirus trifoliata* 30585, sour orange (*Citrus aurantium*), Poorman B2 C3, Mandarine Sunki X *Poncirus trifoliata* B2 30581, citrange Carrizo ((*Citrus sinensis* x *Poncirus trifoliata* ), *Poncirus trifoliata* and *Citrus volkameriana* were subjected to different levels of drought stress to study their morphological and physiological responses. For each rootstock, three months' old seedlings were grown in plastic pots (0.5 L) in a greenhouse at El Menzeh, INRA Morocco. They were subjected to three watering regimes (100%, 75% and 50% of moisture field capacity ($H_{cc}$) of the substrate). The experiment was arranged in a split-plot design with three repetitions. Observations on plant height; dry and fresh matter accumulation, Relative Water Content (RWC), transpiration rate (T) and chlorophyll, soluble sugars (TSS) and proline contents were recorded. We recorded reduction in plant height and dry and fresh matter accumulation, relative water content (RWC), transpiration rates (T) and chlorophyll contents with increasing drought stress for all rootstocks tested. Drought stress significantly affects the physiological and morphological characteristics of citrus rootstocks and, in drought conditions a differential behaviour of the rootstock was found. Based on our results, rootstocks Mandarine Sunki X *Poncirus trifoliata* B2 30581, citrange carrizo, sour orange (*Citrus aurantium*) and Citrumelo Winter Haven B2 31431 present the best overall ability to withstand drought stress.

**Key words:** Eco-physiology, stress physiology, grafting, rootstock, vegetative propagation

# RED FLESH APPLES AND BREEDING STUDIES

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Apple can be eaten in a large region of the world, due to factors such as have a wide field of growing, length of storage time, the plenty of early and late varieties. The first that comes to mind is the colored skin when this mentioned apple redness, but fruits red fleshy have been studied recently by breeders. Anthocyanins that consist of the apple skin and of the apple flesh redness have many benefits in terms of health. *Md*MYB10 gene is responsible that is anthocyanin and the coloration of flesh and investigated numerous study about it. In this article, the introduction of apples fruit red fleshy, the benefits in terms of health, breeding studies and issues in future work were discussed.

**Key words:** Apple, fruit flesh, *Md*MYB10, anthocyanin, breeding.

# MOLECULAR MARKER ANALYSES OF ALMOND AND PLUM F1 PLANTS FOR RESISTANCE TO ROOT KNOT NEMATODES

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Almond (*Prunusdulcis Mill*.) is an important fruit species in the *Rosaceae* family and *Prunoidae* subfamilia. Except the Eastern Black Sea coastal regions and the high plateaus, almond is grown in large areas in Turkey. Almond could grow well in calcareous soils and dry conditions but not in heavy and clay soils and is susceptible to the root knot nematodes (*Meloidogyne* spp.).Myrobalan plum (*Prunus cerasifera*) govern resistance to root knot nematode species (*M. arenaria, M. incognita, M. javanica*) and marker systems linked to resistance genes have been developed. Its reported that 52% of the world agricultural areas contain the root knot nematodes. They invade the plant's root system, produce galls and give serious dame to transmission tissues. The root knot nematode-infected plantsexhibit reduced development, and leaf yellowing, flower and fruitdrop. Finally, duringsevere infection, plants may completely die. The use of toxic materials such as Methyl Bromide to control the root knot nematodes has been restricted in 2007, therefore breeding plant materials resistant to nematodes has gained importance. In this study, almond [Ferragnes and AB3 (*Amygdalus orientalis Mill*.*Type)*] and plum (*Myrobalan and Pissardi nigra*) F1 individuals were testedwith DNA marker systems in terms of resistance to root knot nematodes. The SCAR and SSR markers exhibiting tight linkage to root knot nematodes (*M.arenaria, M. incognita, M. javanica, M. floridensis*) resistance gene, *Ma,* in Myrobalan plum were used, and the results have been evaluated.

# FRESH APRICOT BREEDING AT ALATA HORTICULTURE RESARCH STATION

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An apricot breeding research was conducted to develop new varieties at Alata Horticulture Research Station for Alatayıldızı, Çagrıbey, Çagataybey and Sakıt-6 local varieties and Priana, Feriana ve Precoce de Colomer international varieties during the year 2003. Hybrid plants were planted to field in 2005 and 26 genotypes yielded fruits in 2012 and 18 genotypes in 2013. Pomological analyses (fruit weight, height, width, water soluble solids, acidity and flesh firmness) were performed over harvested fruits. Results were compared with the values of Ninfa and Precoce de Tyrinthe, the common varieties of Mediterranean. Some genotypes had larger fruits with higher water soluble solids than Ninfa and Precoce de Tyrinthe.

**Key Words:** Apricot, fresh consumption, breeding

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# THE NEW TABLE GRAPE CULTIVARS AND CANDIDATES

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Viticulture is characterized especially in Aegean Region with Sultanina raisin grapes in Turkey. Early or late maturing attractive hybrid table grape cultivars will be alternative for table grape growers. A new variety should extend the harvest season. Grapes with large, seedless and firm berries are also preferable. Stenospermocarpic genotypes were used as a pollinator in crossbreeding studies. The project was carried out at the Tekirdağ Viticulture Research Station to obtain new grape varieties maturing earlier or late season. Seeded genotypes are maternal while seedless ones are pollinator at conventional crossing techniques. The four new seedless table grape cultivars were released in 2011 and registration procedure was started in 2012 for eight candidates. Yield, growth and quality components of the new table grape cvs. and the candidates are presented in this study.

# STATUS AND PROSPECTS OF PISTACHIO, PRODUCTION, BREEDING AND ITS GOALS IN KYRGYZSTAN

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Pistachio (Pistacia vera L.) is one of the main tree species of walnut forests in Kyrgyzstan. The total area is 36,400 hectares, or 3.4% of the total forest area of Kyrgyzstan (Griza, 2008). Currently, pistachios are in extremely poor conditions, especially in the lower part of the area adjacent to settlements exposed, because of irrational human activities (tree cutting, grazing, which makes it impossible to recover naturally shoots pistachios, etc.).  Although the majority of these plantations are fully mature, at present the yields are low. In those cultures, pistachio nuts are small and heterogeneous and they do not meet international standards. One of the biggest challenges to the industrial cultivation of pistachios in Kyrgyzstan is the lack of proven zone-tested varieties and forms of pistachios. Therefore, an important research question is to analyze and study the introduced varieties and forms from other regions to grow them in the climatic zones of Kyrgyzstan. Despite the above mentioned, pistachios of Kyrgyzstan have huge gene poolthat allows to have a huge selection of the most economically valuable forms of pistachios. In nature, about 60 forms of pistachios are selected, and 5 of them are recommended for industrial growth. Researches have been carried out to spread selected varieties and foreigner selections. Fruits progeny from Iranian origin and others are under evaluation. In the laboratory, morphological description of pistachio fruits was based on the following criteria: weight, size, shape, detection and yield of the dry weight of the kernel.

# DEVELOPING CONFECTIONERY PUMKIN LINES AND HYBRIDS AND DETERMINATION OF THEIR SEED YIELD AND SOME YIELD TRAITS PERFORMANCES

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Pumpkin seed (*Cucurbita* spp.) are consumed as a snack in many cultures both in Turkey and also throughout the world. Pumpkin seed are rich in both oil and protein; oil contents are generally in the 40 to 50% range and protein content ranges from 30 to 40%. The first breeding studies were started in Trakya Agricultural Research Institute (TARI) in Edirne in 2007 to develop new cultivars on confectionery pumpkin because there is no registered cultivar and certified seed production in Turkey. After collecting materials from different part of Turkey and classifying them in three main groups as Urgup Sivrisi, Edirne type and Hanim Tırnagi in the breeding nursery, the single seed descent method was applied and selected plants were selfed in each generation based on morphological, seed quality and yield traits in following years. The major selection criteria have been small fruit, thin pericarp, high seed weight per kg fruit, high harvest index, vigorous growth at close spacing, good pollen production, and crown fruit set. Individual selections and selections within lines in $F_2$ and $F_3$ and further generations, exhibited improved germination under field conditions, more vigorous growth and good adaptation capability. Satisfied improvement on seed yields and they had generally much higher performance both in seed yield and some desired yield traits than previous years each generation. Experiments were conducted irrigated conditions at the institute fields in Edirne in 2013. The seed yields of hybrids changed between 865-1613 kg ha$^{-1}$ while average control yields (village populations) was 859 kg ha$^{-1}$. The average seed yield of candidate hybrids was 1243 kg ha$^{-1}$ so candidate hybrids exhibited 45% more performance than controls. Similarly, candidate hybrids displayed higher performance in other observed yield traits too on average values than controls such as 1000 seed weight (13%), seed length (10%) and seed width (6%). Based on these results, current snack seed pumpkin breeding lines developed at institute during the past 5-6 years show promising potential for confectionery market and after final evaluation of homogeneity in this year, some of them will be sent to registration.

**Key Words:** Confectionery Pumpkin, *Cucurbita pepo* L., Selection, Morphological traits, Seed yield.

# STUDIES ON CORRELATION AND PATH ANALYSIS OF TOMATO (*SOLANUM LYCOPERSICUM* L.) FRUIT SHELF LIFE ON ASSOCIATION WITH DRY MATTER CONTENT AND SOME QUANTITATIVE CHARACTERISTICS WITHIN UPOV TEST GUIDELINES (TG/44/11) IN UNDER GREENHOUSE GROWING CONDITIONS

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Long shelf-life and suitable for transportation are always wanted features by vegetable brokers and exporters. As of the date of September 2013, there are approxmately registered 1321 tomato variety and 962 varieties of these are listed in Turkey. Also aplication for registration amount is about 90 in every year. This research was carried out using 96 registered and candidate indetermined tomato varieties within DUS tests at 2013 spring growing period in greenhouse conditions in Antalya province. Trials were set up by UPOV directives, 2 replicants and in every plot has 12 plant. It was observed that firm fruit had generally long shelf life but not for all varieties. Other quantitative characteristics effects to shelf life to what extent were researched. As a related quantitative characteristics for fruit shelf life in the UPOV DUS test guidelines: fruit size, size of peduncle scar, size of blossom scar, diameter of core in cross section in relation to total diameter, thickness of pericarp, firmness were observed and measured. Dry Matter Content, one of the fruit quality features, was measured also. It was indicated from the research that the features were effective on fruit shelf life in addition to that it was important whether prericarp closed to peduncle scar or not for shelf life. This can be evaluated new morphological characteristic for UPOV DUS test guidelines.

**Key words**: Tomato, UPOV, DUS test, fruit shelf life, quantitative characteristic**,** path analysis.

# IMPACT OF THE CITRUS CULTIVARS AND PEEL FIRMNESS ON FRUIT INFESTATION BY *CERATITIS CAPITATA* WIEDEMANN (DIPTERA : TEPHRITIDAE) : A FIELDS TRIALS STUDY IN THE GHARB AREA (NORTH-WEST MOROCCO)

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In Morocco, the Mediterranean fruit fly, *Ceratitis capitata* Wiedemann (Diptera : Tephritidae) is a key citrus pest and annually requires several chemical treatments mainly for the early varieties. The purpose of this study is to investigate which citrus variety is resistant to medfly infestation and what are the main fruit physico-chemical characteristics involved. Field trials were conducted at different locations in the Gharb area (North-western part of Morocco). The field experiments were conducted in various citrus cultivars: sweet orange (*Citrus sinensis*, var. Washington Navel and Thomson), Maroc Late (*Citrus sinensis* [L] Osbeck), Clementine (*Citrus reticulate* Blanco var. Cadoux 1 and 2, SidiAissa, Ain Taoujdate, Nules and Marisol). There was a significant effect of citrus cultivars on fruit infestation for all field trials. The peel firmness and the number of essential oil glands were significantly higher in the lesser infested Clementine var. Ain Taoujdate than in Clementine var.SidiAissa, Clementine var. Cadoux 1 and 2. There was no significant effect of the other fruit physical characteristics, such as sugar, acidity, and maturity index on the infestation level. In general, peel firmness was negatively correlated with fruit infestation. The feasibility of the outcome of this work and its implementation in an integrated pest management strategy against *C.capitata* in citrus groves in Moroccoare discussed.

**Key words:** Citrus cultivar, *Ceratitis capitata*, physical and chemical characteristics, peel firmness, Integrated Pest management, Morocco.

# NATURAL FORMATION OF VOLATILE CHLORINATED HYDROCARBONS

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Biogeochemical cycle of chlorine is closely connected with carbon cycle. The formation of organically bound chlorine is partly due to enzymatic reactions, which bind chloride onto organic matter. During this process organic matter is hydrolyzed and when chlorination undergoes in the soil, humic substances can get smaller. Thus degradation of soil organic matter by chlorination leads to compounds with structures more easily degradable and water soluble. Chlorination of small molecules which are present in soil due to activity of microorganisms, fungi or plants, as these organisms can discharge enzymes into their surroundings and they act in the soil solution. In spruce forest soil chloride is present naturally and due to anthropogenic sources, road salting results in elevated concentrations as high as 2 M NaCl. In this work the effect of high concentrations of chloride and bromide on halogenation was studied by heme peroxidase enzymes (chloroperoxidase from Caldariomyces fumago and horseradish peroxidase) naturally occurring in soils. The emission of volatile chlorinated hydrocarbons was determined in the headspace by using solid phase microextraction (SPME) and gas chromatography with electron capture detector or mass detector (GC-ECD/MS). The formation of VOCl was confirmed in enzymatic experiments, where citric acid buffer, halogen ions (KBr, NaCl) and substrates (D-glucose, acetone, acetyl acetone) were present. Both enzymes formed chlorinated and brominated volatile compounds; mainly chloroform, bromoform, tri- and tetrachloroethylene, chlorinated and brominated methanes. An attempt has been made to identify unknown VOCl compounds, which were also formed as major products.

This work has been supported by the Grant Agency of the Czech Republic (13-11101S).

# DETERMINATION OF CHROMOSOMAL GARNISH WITH SOME TABLE GRAPE VARIETIES AND THEIR HYBRIDS GROWN IN R. MACEDONIA

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In this paper, investigations are performed in several table grape varieties grown in R. Macedonia with a few selections (hybrid crosses) from the same species. It is known that there are two Vitis genus and subgenus; Euvitis with 2n = 38 chromosomes and Muscadina with 2n = 40 chromosomes. All tested varieties fall into diploid varieties with 38 somatic chromosomes. It also showed that their hybrids are stable, diploid number of somatic chromosomes, do not have any defects in chromosome set in the first generation and are compatible with each other. Some of the tested varieties grapevine (Cardinal, Italy, etc.) are also obtained through conventional crossbreeding and according to their origin are hybrids, and some varieties are old and indigenous (red drenok) and raises a longer period in some orchards and vineyards in the Republic of Macedonia. The determination of the number of chromosomes or chromosome karyotype and set aims to produce data on the existence of some anomalies in the structure and number of chromosomes, and thus determining the change of some inherited characteristics. It is very important for further processing and breeding of the grapevine, especially when hybridization and clonal selection.

**Keywords:** number of chromosomes, chromosome set, hybrid, clonal selection, karyotype, diploid varieties, hybridization

# WINTERHARDY VEGETABLE PEA BREEDING FOR WYOMING, USA

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In Wyoming USA, vegetable production is challenging for vegetable growers, whether home gardeners or commercial producers due to a short growing season, high elevation and a relatively cool climate. A significant limitation to local vegetable production is that virtually no vegetable varieties have been bred in Wyoming for local adaptation. Development of local varieties could extend the growing season and increase yield. As a cool season annual crop, pea has potential for vegetable production in Wyoming. The objective of this study was to produce winterhardy vegetable peas that combine the characteristics of fresh, edible peas with the winterhardiness of feed peas. These could be planted in the fall, overwinter, and come on in the spring to provide produce earlier than spring-planted peas. Hybridizations between winter hardy feed pea (*Pisum sativum* ssp. *arvense*) and with all three types of food peas (shell, snow, and snap; *P. s.* ssp. *sativum*) were accomplished in the greenhouse in 2009. Natural selection began in $F_2$ and elite, surviving lines were advanced from the $F_2$ through $F_4$ generations using pedigree selection. The best hybrid-derived lines survived the 2010-11 winter, and their selected progeny performed even better over the 2011-2012 winter. A chi-square test for independence (a contingency test) comparing $F_2$ and $F_3$ survival indicates that the 23.2% of $F_3$ progeny of surviving $F_2$ plants (as evaluated in 2011-2012) was much higher than the 1.8% survival of $F_2$ progeny of $F_1$ plants (as evaluated in 2010-2011) with chi-square = 186.56, 2df, and significant at the $\text{Prob} < 0.001$ level ($\text{Prob} = 1.38 \times 10^{-40}$). Thus, we conclude that winterhardiness was heritable from $F_2$ to $F_3$ generations; even though considerable genetic segregation would still be taking place for what is apparently a complex polygenic trait. We were able to combine winterhardiness from *arvense* lines/cultivars with edible traits of *sativum* cultivars. $F_4$ seed will be distributed to Wyoming growers to identify best locally adapted winterhardy food pea varieties for Wyoming via a “participatory plant breeding” program.

# INFLUENCE OF GROWTH REGULATORS ON CALLUS INDUCTION FROM EMBRYOS OF FIVE CITRUS ROOTSTOCKS

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The aim of this work is to develop a protocol for callus induction of Moroccan Citrus rootstocks. Callus cultures were initiated from embryos explants of five *Citrus* rootstocks (*Cleopatra mandarin*, *Rangpur lime*, *Citrus volkameriana*, *Trifoliate orange*,*Citrus aurantium*) on (MT) basal media. Different concentrations of growth regulators were tested in order to obtain the best callus formation: 2, 4-dichloro-phenoxyacetic acid (2, 4-D) in combination with benzylaminopurine (BAP) at five levels (0, 0.5, 1, 2 and 3mgL-1) were used in this study. It was found that growth regulator concentration had a significant effect on the callus induction, the callus growth and callus physical appearance. The highest frequency of the calogenesis rate (100% and 83%) was observed with two combinations of 2, 4-D/ BAP : 1/ 0,5 and 2/ 1 (mgl-1). Medium containing only BAP (1mgl-1) resulted in the formation of large numbers of roots. Also, The callus induced on MT medium containing only 2, 4-D (1mgl-1) was brown in color and of low quality compared to that produced on MT media containing 2, 4-D/BAP. There was no callus formation on MT basal medium without growth. Also, the callogenesis depended on the genotype. It was maximal for *Cleopatra mandarin* followed by *Rangpur lime* and *Citrus volkameriana*, and then *Citrus aurantium* and *trifoliate orange*. Placed into light on gelosed MS medium, a budding was only observed on sour orange and Cleopatra mandarin in a fugace way.

**Key words:** Callus induction, Citrus rootstocks, 2, 4-D, BAP.

## BATEM SEKERI: A NEW ORANGE SELECTION FROM CV. WASHINGTON NAVEL

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The breeding activities on *Citrus* have been continuing for a long time in the world. In Turkey *Citrus* breeding activities particularly cultivar breeding studies started from 1979 year under the national program 'Citrus Cultivar Development Program'. In this study a new orange cultivar BATEM Şekeri, selected from cv. Washington Navel as bud mutation in Finike district, has been compared to cv. Washington Navel in terms of yield and fruit quality characteristics. The study conducted between 2008 and 2010 years at BATEM and obtained results evaluated cumulatively. The results revealed that cv. 'BATEM Şekeri' was better fruit characteristics than cv. 'Washington Navel'. It has bigger fruits, higher yield capacity, thinner rind and higher fruit juice yield.The yield, rind thickness and fruit juice yield was 80 kg per tree, 5,49 mm and 45.00% in cv. 'Washington Navel' and 120 kg per tree, 4,73 mmand 48.81% in cv. 'BATEM Şekeri', respectively.

**Keywords:** Orange, bud spots, selection breeding.

# INVESTIGATE OF SOME TOMATO GENOTYPES IN BREEDING OF TOMATO ROOTSTOCKS

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Use of rootstocks against soil-borne biotic and abiotic factors has increased tremendously in recent years. Rootstocks are preferred because of resistance against biotic and abiotic factors and plant vigor. Two tomatoes varieties (Çınar F1 and Azra F1) were grafted onto selected 15 tomato genotypes that its have high plant vigor and tolerant to low temperatures and grown between December 2011 with June 2012 in greenhouse in Erdemli. Fruit weight, average of fruit weight, fruit width, fruit length, and TSS of grafted non-grafted tomato varieties were compared. Grafted plants were superior to non-grafted plants are evaluated in terms of all the parameters. The highest yield was obtained from varieties grafted on Alata 57 genotype. It was determined 4 tomatoes lines for tomato rootstock breeding.

**Key words:** Tomato, rootstock, grafted.

# TOMATO VARIETIES WITH HIGH INDICES OF PRODUCTIVITY AND RESISTANCE TO ENVIRONMENTAL FACTORS

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In this paper, the results of the complex evaluation of valuable morphobiological and agronomic characteristics of tomato varieties, created at the Institute of Genetics and Plant Physiology of the Academy of Sciences are presented. In order to demonstrate the variability of agronomic characters and to specify the value of analyzed genotypes, their comparative evaluation was carried out by some of biological parameters: yield, production rate, average fruit weight, vegetation period, pericarp thickness, resistance to heat and cold stress. The varieties Jubiliar 60/20, Prestij, Elvira, Mihaela, Milenium and Tomiș have determined growth and are distinguished by plant height, precocity, yield and production. Also, these varieties differ by the important fruit characters as well as mass (large and medium), shape (round, flat –round and cylindrical), the number of lodge (2-3 and above), pericarp thickness (medium and large) and mesocarp thickness (medium, large and extra large). The evaluated varieties manifest increased productivity and good taste properties. The results attest the genotypes that combine precocity, high productivity and resistance to environmental factors. These can serve as initial material for breeding.

# **EFFECT OF PLANT DENSITY ON THE STRUCTURE OF THE MONOBULB (**SINGLE BULB GARLIC) **GARLIC HARVEST**

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Solo garlic, also known as single clove garlic, monobulb garlic, single bulb garlic, or pearl garlic, is a variety of *Allium sativum* and not of *Allium ampeloprasum*. Biological features of some varieties and forms of garlic allow improving of the cultivation technology of this crop through aerial bulbils. Their uses as planting materials contribute to accelerate the multiplication and improvement of varieties, as well as the growing of higher yields. The large range of seeding rates of air bulbils from 2 to 6 million units per hectare allowed following the plants growth and development and the formation of single bulb garlic at different areas and its impact on garlic yield. The highest yield was obtained at seeding rate of 3-4 million units per hectare, where the yield increase was about 1000 kg/ha. Increasing the seeding rate to 6 million units of aerial bulblets per hectare leads to an increase in the (small) fine fraction (26,5%) and reduction of the large fraction (16,4%). Based on the results, we can conclude that the optimum seeding rate of air bulblets is 750-950 kg/ha of air bulblets per hectare, that allows to obtain 7,000-8,000 kg/ha. The seeding rate 4-5 million units per hectare is the optimum for output products of single bulbs garlic (over 80%). Reducing the seeding rate contributes to increase the output of non-standard bulbs (dividing small bulbs). At low seeding, less than 2 million units of bulblets per hectare, the output of non-standard products is 20-25%.

# COLLECTING, IDENTIFYING AND CULTIVATION OF NATIVE *TULIPA ARMENA* IN THE FLORA OF TURKEY

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A primary national wide research project supported by TUBITAK (The Scientific and Technological Research Council of Turkey) titled 'Collecting, identifying and cultivation of native Tulipa and Hyacinthus species in the flora of Turkey' was conducted between the years of 2006 and 2009 at Black Sea Agricultural Research Institute. There are two sub species of *Tulipa armena* which is the one of the most important tulip species of Anatolia; *Tulipa armena* var. *armena* and endemic *T. armena* var. *lycica.* In this study, the plant samples represent the native populations from 26 different areas of Anatolia were collected. The sub species were identifyed and herbarium samples were prepared. The plants were morphologically characterized and phenological differences were determined for each species by multivariete analysis. In addition, DNA finger prints of present populations were determined, the levels of ploidy and phytochemical properties were investigated. The propagation studies were succeeded and the cultivation potentials were found to be quite high for most of the populations belong to *T. armena.* A following research project titled 'Breeding studies and developing new cultivars of Tulip (*Tulipa* L.) and Hyacinth (*Hyacinthus* L.) species for ornamental sector in Turkey' started in 2010 has been in progress. The performance of the selected candidate of the first cultivars of Turkey breeded and developed by selection from the populations has been investigated.

**Key words:** *Tulipa armena*, population, breeding, selection

# MECHANISM OF SEED TRANSMISSION OF TURNIP MOSAIC VIRUS STRAIN I2 IN BRASSICA PLANTS

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*Turnip mosaic virus* (TuMV) is one of the two most important viruses affecting crops worldwide. Seed transmission of the virus is the most dangerous ways to spread and conservation of a viral infection. This leads to large economic losses and increase primary infection in fields. Plant collection of *Brassica* was artificially infected by TuMV. Seeds of susceptible and tolerant to TuMV brassicas were collected to study of seed transmission of the virus. Presence of TuMV was diagnosed visually, ELISA, RT-PCR, real-time PCR and by indicator plant reaction by Holmes' method with modification. All diagnostic methods showed that up to 40 % of the seeds contained TuMV. Individual seed embryos contained virus infection as well that shows the possibility of transmission through inner seed contamination. For the first time, we found plant-genotype depended transmission of TuMV strain I2 through the seeds of brassicas. To identify mutations that allowed TuMV to be transmitted through seeds the complete coding sequence of the TuMV strain genome (GeneBank №KC297103) was determined. It was found that strain I2 belongs to the World-B group and the most similar to the isolate UK1. I2 and UK1 differed in 99 nucleotide substitutions distributed through the whole genome. One substitution in CP gene and four substitutions in P1 gene were non-synonymous and unique compared with the same genes of all known TuMV strains. We suppose that these discovered mutations enhance viral genome amplification, long-distance transport and the weakened the virus pathogenicity, that allows the plant to reach the flowering phase and get seeds infected by TuMV. The study was partially supported by ISTC project #3431 and RFBR research project No. 12-04-32084_mol-a.

## GENETIC RESOURCES PAPER LIST

1----EXPLOITATION OF RESISTANCE GENE ANALOGS ENCODING NBS-LRR DOMAINS IN WIDE HYBRIDIZATION   PRESENTATION.

2---GENETIC DIVERSITY ANALYSIS OF ANEMONE NARCISSIFLORA POPULATIONS COLLECTED FROM KUHKAMAR- ZONOUZ REGION OF IRAN US.DOCX”

3---ANALYSIS OF GENETIC RELATIONSHIPS AMONG ACHILLEA MILLEFOLIUM SUBSP. MILLEFOLIUM POPULATIONS BASED ON RANDOM AMPLIFIED POLYMORP.DOCX”

4---ASSESSMENT OF GENETIC DIVERSITY IN ELAEAGNUS ANGUSTIFOLIA POPULATIONS USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD).

5---ASSESSMENT OF GENETIC DIVERSITY IN LANDRACES OF FINGER MILLET (ELEUSINE CORACANA L.) GENOTYPES COLLECTED FROM DIFFERENT PARTS.DOCX”

6---CHARACTERIZATION OF DURUM WHEAT LANDRACES FOR COLD TOLERANCE AND AGRONOMIC TRAITS UNDER RAINFED CONDITIONS OF IRAN.

7----EFFICIENCY OF MICROSATELLITE MARKERS IN THE INVESTIGATION AND CONFIRMATION

8----EVALUATION OF DATA FROM AN OLIVE GERMPLASM COLLECTION.

9---GENETIC DIVERSITY OF CASSAVA BROWN STREAK VIRUS AND RESISTANCE OF CASSAVA BROWN STREAK DISEASE FROM UGANDA.

10---HETEROSIS STUDIES IN INDIGENOUS EGGPLANT GERMPLASM CONFERENCE.

11---SIMPLE SEQUENCE REPEATS ISOLATED FROM DURIAN (DURIO ZIBETHINUS MURR.) AND THEIR TRANSFERABILITY TO OTHER DURIO SPECIES.DOCX”

12---STUDYTHE EFFECT OF WASTEWATER NORTH REFINERY COMPANY-BIAGYIRAQ  IN ADIANTUM CAPILLUS VENERIS CHEMICAL AND GENETICS STUDY.

13---THE FORMATION AND STUDY IN THE CULTURE OF GENETIC RESOURCES OF FORAGE GRASSES BY THE EXPEDITIONARY COLLECTION OF WILD FORMS F.DOCX”

14----THE GENE POOL OF WILD FORAGE CROPS IN NORTHERN KAZAKHSTAN.DOCX”

15---THE VALUE OF GENETIC RESOURCES OF CROPS IN NORTHERN KAZAKHSTAN.

16---VARIABILITY IN MALE, FEMALE AND ANDROMONOECIOUS SIMAROUBA GLAUCA DC CULTIVARS AS ASSESSED BY MOLECULAR MARKERS.

17---AT LEAST TWO CYCLES OF SINGLE-PLANT SELECTION IN LENTIL LANDRACE ARE NEEDED TO REACH GENETIC HOMOGENEITY.

18---DEVELOPMENT OF DROUGHT TOLERANT TRIPLOID BERMUDAGRASS.

19---GENETIC ORIGINS OF CULTIVATED AND WILD GRAPEVINES FROM NEAR-CASPIAN ZONES OF AZERBAIJAN .

20---IMPROVED VEGETABLE VARIETIES FOR DEVOLPED GERMPLASM FOR ASIA.

21---RESISTANCE OF BARLEY ACCESSIONS FORM VIR COLLECTION TO HARMFUL ORGANISMS.

22---RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS.

23---A BREEDING SCHEDULE FOR IDENTIFYING THE VALUE OF LOCAL LANDRACE CV. EGLOUVI (LENS CULINARIS SPP) AS A SOURCE FOR RESISTANCE TO FUSSARIUM WILT.

24----AGRONOMIC EVALUATION OF BAMBARA GROUNDNUT (VIGNA SUBTERRANEA L) LANDRACE COLLECTIONS IN A DRY ENVIRONMENT.

25---CHARACTERIZATION OF GLUTAMIC ACID OF CORYNEBACTERIUM SP. AS A FOOD ADDITIVE DURING FERMENTATION.

26---FUTURE CHALLENGE TO IDENTIFICATION OF DROUGHT TOLERANCE AND RESISTANCE HIGH-THROUGHPUT PLANT PHENOTYPING.

27----GERMPLASM FOR SPRING DURUM WHEAT BREEDING ON ALTAI.

28---LANDRACE VARIETIES OF WHEAT IN UZBEKISTAN.

29---OCCURRENCE, ISOLATION AND DNA IDENTIFICATION OF STREPTOCOCCUS THERMOPHILUS INVOLVED IN ALGERIAN TRADITIONAL BUTTER.

30----ANALYSIS OF GENETIC DIVERSITY OF SRI LANKAN TRADITIONAL RICE VARIETY “HONDERAWALA” .

31----EVALUATION OF VARIATION OF KALE (BRASSICA OLERACEA VAR. ACEPHALA) POPULATIONS COLLECTED FROM BLACK SEA REGION, TURKEY .

32----GENETIC DIVERCITY IN BOTTLE GOURD

33----THE ADAPTIVE CAPABILITY OF SOME CEREALS FROM GEOGRAPHICALLY AND ENVIRONMENTALLY DIFFERENT AREAS OF AZERBAIJAN .

34---PCR IDENTIFICATION OF LACTOBACILLI STRAINS FOR POTENTIAL PROBIOTIC IN POULTRY.

35---PROTEIN CODING SEQUENCES OF AEGILOPS TAUSCHII CHROMOSOME 5D REVEALED BY IN SILICO ANALYSIS .

36----REACTIONS OF SOME TURKISH AEGILOPS AND TRITICUM MATERIALS TO PGT RACE RTKTC.

37---REACTIONS OF TURKISH WHEAT LANDRACES TO PGT RACE RTKTC.

38---RESISTANCE OF BARLEY ACCESSIONS FROM DAGESTAN TO POWDERY MILDEW AND BARLEY LEAF RUST.

39---REVALORIZATION TRADITIONAL DATE BTANA FOR PRODUCTION OF MICROBIAL POLYSACCHARIDES IN FOOD PURPOSES .

40---SEED COMPONENT DIVERSITY OF HYBRID MATERIALS ORIGINATED FROM WILD ANNUAL HELIANTHUS SPECIES .

41---SPONTANEOUS MUTATION EAM8 IN BARLEY ACCESSION FROM DAGESTAN MOUNTAIN

REGION.

42---THE DETERMINATION OF MORPHOLOGICAL AND AGRONOMIC PROPERTIES OF SOME CULTURE AND WILD PEA GENOTYPES .

43---THE ENVIRONMENTAL AND GENETIC MONITORING FOR CONSERVATION OF PLANT DIVERSITY.

44---THE GENE POOL OF SORGHUM CROPS FOR BREEDING FOR GRAIN QUALITY AND PRODUCTIVITY.

45---THE NEW IN THE WHEAT (TRITICUM L.) GENE-POOL OF NAKHCHIVAN AUTONOMOUS REPUBLIC.

46---THE STUDY GENETIC VARIATION OF BREAD WHEAT.

47---THE STUDY OF ADAPTIVE CAPABILITY OF THE VARIOUS RYE POPULATIONS FROM AZERBAIJAN.

48---VIABILITY TESTING FOR MRIZP GENE BANK ACCESSIONS OF LOCAL MAIZE (ZEA MAYS L.) LANDRACES .

49---APPLICATION OF MOLECULAR METHODS AS A MARKER IN BIOTECHNOLOGY IN BIOREMEDIATION STUDIES.

50---GENETIC DIVERSITY IN SOME WHEAT AND BARLEY GENOTYPES AS REVEALED BY AMPLIFIED FRAGMENT LENGTH POLYMORPHISM (AFLP) MARKERS.

51----IMPACT OF KASIB PROJECT GENETIC STOCK INTO SOLUTION OF PROBLEMS OF SPRING BREAD WHEAT BREEDING IN ALTAI TERRITORY .

52---URGENCY OF CARRYING OUT OF GENETIC CERTIFICATION OF VARİETİES OF THE GENOFUND OF GRAIN CROPS OF AZERBAIJAN.

53---MORPHOLOGICAL DIVERSITY OF ACHA (FONIO) GERMPLASM AND EVALUATION OF GENETIC VARIATIONS RAPD-PCR TECHNIQUES .

54----PLANT GENETIC RESOURCES ARE IMPORTANT FOR FOOD SECURITY IN CENTRAL ASIA AND THE CAUCASUS .

55---ASSESSMENT OF GENETIC VARIATION OF SALVIA SCLAREA L. BY RAPD .

56---DEVELOPMENT OF LOCAL POTATO VARIETIES WITH BREEDING METHOD .

57---TURKEY VEGETABLE GENETIC RESOURCES STUDIES .

58---EVALUATION OF WHEAT GENETIC RESOURCES IN AZERBAIJAN .

59---EVALUATION OF WHEAT GERMPLASM FOR RESISTANCE TO STEM RUST .

60---FOLIAGE AND TUBER STEROID GLYKOALKALOD CONTENTS OF WILD AND CULTIVATED SOLANUM SPECIES .

61---GENETIC RESOURCES OF CITRUS IN GEORGIA .

62----MOLECULAR AND PHYSIOLOGICAL CLASSIFICATION OF DIVERGENT CAMELINA SPP. GERMPLASM.

63---CHARACTERIZATION OF LOCAL OKRA (ABELMOSCHUS ESCULENTUS) POPULATIONS .

64---CONFESSED OF MORPHOLOGICAL VARIABILITY AT DOMESTIC DRY BEAN (PHASEOLUS VULGARIS L.) POPULATIONS COLLECTED FROM MIDDLE BLACK SEA REGION .

65---DETERMINATION OF MORPHOLOGICAL VARIABILITY OF LOCAL PEA GENOTYPES.

66----GENETIC MONITORING OF CROP WILD RELATIVES THEORY APPROACH AND VALUE FOR CONSERVATION .

67----MOLECULAR-GENETIC ANALYSIS OF UKRAINIAN BREAD WHEAT GENE POOL .

68----PRELIMINARY STUDIES ON THE BREEDING OF VACCARIA HISPANICA A NEW CROP SPECIES FOR TURKEY.

69----RAD SEQUENCING AND SNP DETECTION IN A PEARL MILLET GERMPLASM COLLECTION FOR USE IN GENOME WIDE ASSOCIATION ANALYSIS .

70----TRAIT ANALYSIS AND DIVERSITY IN SOME WHEAT LANDRACES AND ADVANCE BREEDING LINES EVALUATED UNDER DROUGHT AND HEAT STRESS CONDITIONS .

71----A CLONAL SELECTION IN ‘0900 ZIRAAT’ SWEET CHERRY CULTIVAR AND MOLECULAR CHARACTERIZATION BY AFLP ANALYSIS.

72---ANALYSIS OF HYBRID PROGENY OF DACTYLIS GLOMERATA FOR SUMMER DORMANCY AND PRODUCTIVITY TRAITS.

73---APPLE GENETIC RESOURCES OF TURKEY AND STUDIES OF EĞİRDİR FRUİT RESEARCH STATİON ON APPLE GENETIC RESOURCE.

74---ASSESSMENT OF HOST PLANT RESISTANCE TO STEM RUST IN PAKISTANI WHEAT GERMPLASM .

75---BRASSİCA GENETİC RESOURCES İN TURKEY AND THEİR İMPORTANCE FOR RAPESEED BREEDİNG .

76---COLLECTING OF WINTER SQUASH AND PUMPKIN GENETIC RESOURCES OF THE WEST ANATOLIAN .

77---COLLECTION AND AGRO-MORPHOLOGICAL AND GENETIC CHARACTERIZATION OF MOROCCAN FABA BEAN LANDRACES .

78---GENETIC VARIATION OF IRANIAN DURUM WHEAT LANDRACES.

79----GENETIC DIVERSITY STUDY OF SUMMER SQUASH LANDRACES (CUCURBITA PEPO) WITH NEUTRAL AND GENE-BASED MOLECULAR MARKERS XANTHOPOULOU ().

80---MORPHOLOGICAL CHARACTERIZATION OF THE NATIONAL MELON COLLECTION .

81----GENETIC DIVERSITY ANALYSIS IN CASSAVA FROM BAIXADA CUIABANA IN BRAZIL USING SSR MARKERS.

82---EVALUATION OF THE SAFFLOWER (CARTHAMUS TINCTORIUS L.) CORE COLLECTION UNDER ECOLOGICAL CONDITIONS OF SAMSUN .

83---SOME MORPHOLOGICAL AND AGRONOMIC CHARACTERISTICS OF SAINFOIN ECOTYPES OF EASTERN ANATOLIA REGION.

84---IMPORTANCE OF İNTERSPECİFİC HYBRİDİZATİON İN DEVELOPİNG 00-TYPE RAPESEED .

85---MISSING VALUES OPO SQUASH .

86---POSSIBLE ADDITIVE HARVEST PRODUCTS FROM EASTERN BLACK SEA TEA (CAMELIA SINENSIS L.) PLANTATIONS .

87---SELECTION AND CHARACTERIATION OF SUPERIOR BANANA TYPES IN TURKEY UNDER SUBPTROPICAL CONDITION.

88---FIELD MUSEUM OF AZERBAIJAN BREAD WHEAT (TRITICUM L.) VARIETIES.

89---EVALUATION OF RESISTANCE OF BREAD WHEAT GENOTYPES TO LEAF AND STEM RUST.

90---GENETIC VARIATION OF IRANIAN BREAD AND DURUM WHEAT LANDRACES.

91---GENETIC DIVERSITY AND POPULATION STRUCTURE IN A DIVERSE PANEL OF PERENNIAL RYEGRASS CULTIVARS AND WILD GENOTYPES.

92---POTATO GENETIC RESOURCES IN THE CZECH REPUBLIC .

93---TEA GENETİC RESOURCES AT THE EASTERN BLACK SEA REGİON .

94---THYMUS SERPYLLUM USED IN ARMENIAN HERBAL TEA CULTURE AND ITS .

95---TURKEY GARLIC COLLECTION .

96----RESPONSE OF ADVANCED, RELEASED, INDIAN AND LOCAL RICE GENOTYPES WITH BACTERIAL LEAF BLIGHT IN NATURAL FIELD CONDITION.DOCX”

97----EVALUATION OF IN VITROCALLI INDUCTION AND REGENERATION OF LAVANDULAANGUSTIFOLIA .DOCX”

98---CAN WE STILL FIND LANDRACES IN EUROPE AFTER 2000 INVESTIGATIONS IN LEMNOS AND LEFKADA .

99---RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS.

100---TOMATO GERMPLASM COLLECTION IN REPUBLIC OF MOLDOVA.

101---EXPLORATION AND COLLECTION OF TOMATO GERMPLASM IN NIGERIA.

102---FORM DIVERSITY AND SELECTION OF WALNUT IN KYRGYZSTAN.

103---ALLELOPATHY A BRIEF REVIEW.

104---RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS.

105---COLLECTING AND DOCUMENTATION OF TOMATO LOCAL FORMS IN REPUBLIC OF

MOLDOVA.

106---VARIABILITY IN MALE, FEMALE AND ANDROMONOECIOUS SIMAROUBA GLAUCA DC CULTIVARS AS ASSESSED BY MOLECULAR MARKERS.

107---SOURCES OF RESISTANCE TO STRIPE RUST (PUCCINIA STRIIFORMIS  F. SP. TRITICI IN WHEAT (TRITICUM AESTIVUM L.) LANDRACES.

108------DETERMINATION OF GENOME SIZE OF FESCUE SPECIES COLLECTED FROM EASTERN ANATOLIA OF TURKEY BY FLOW CYTOMETER.

109------USING AN INDEX OF MERIT FOR MULTITRAIT EVALUATION OF WINTERHARDY FEED PEA LINES

110---MOLECULAR AND PHYSIOLOGICAL CLASSIFICATION OF DIVERGENT CAMELINA SPP. GERMPLASM

GR-111---WHEAT ASSESSMENT ON THE CONTENT OF ZN2+, CU2+, CD2+ METALS

# EXPLOITATION OF RESISTANCE GENE ANALOGS ENCODING NBS-LRR DOMAINS IN WIDE HYBRIDIZATION OF COTTON

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Resistance gene analogs (RGAs) are one of the rich families of R genes that share conserved motifs and encode NBS-LRR domains. Based on this property numerous RGAs were isolated from Gossypium arboreum based on reported sequences from G. hirsutum L. in the database and subsequently cloned for nucleotide sequencing analysis. The isolated RGAs from G. Arboretum showed nucleotide and amino acid homology to the reported RGAs from G. barbadense and G. hirsutum but some of them were found to be unique in phylogenetic tree and they were considered as novel RGAs. There are two possibilities of their use either to as a probe for detection and isolation of full length R genes from crop plants or to use them as markers. So, the isolated unique RGAs were used as DNA markers in F1 generation and back crosses of G. arboreum × G. anomalum, and F1 of G. arboreum × G. capitis-viridis. The series of assays proved that G. arboreum is free of diseases and an important source that could be used for the development of disease resistant cotton plants. Due to this property G. arboreum is being used in inter-specific hybridization. The isolated RGA as a marker confirmed the inter-specific F1 generation and back crosses. The process of selection from inter-specific populations can be accelerated by the use of RGA markers and also could be used as an important tool to recover desirable plants containing resistance from G. arboreum.

# GENETIC DIVERSITY ANALYSIS OF *ANEMONE NARCISSIFLORA* POPULATIONS COLLECTED FROM KUHKAMAR- ZONOUZ REGION OF IRAN USING RAPD MOLECULAR MARKERS

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*Anemone* species has two subspecies named *narcissiflora* and *willdenowii* which the latest is recorded in Iran in 2010. Some samples (with 1-7 flowers) of *Anemone narcissiflora* were gathered from Kuhkamar-Zonouz region of East Azerbaijan province, Iran. Genetic diversity was evaluated by using 7 random primers with 10 nucleotides by using PCR-RAPD method. 39 polymorphic bands were produced from the six primers used in this technique that the maximum band is related to the RP1 primer, the lowest band is related to the RP7 and the average band for all primers were 6.5 polymorphic bands. Cluster analysis of samples was done by UPGMA method in NTSYSpc 2.02 software. Dendrogram resulting from migrating bands showed that the studied samples can be divided into two groups. The first group includes samples with one and two flowers and the second group consists of two sub-groups which the first subgroup consists of samples with three, four and five flowers, and the second subgroup consists of six and seven flower samples. The results of the comparison and analysis of the data obtained from RAPD technique and similarity matrix represent the genetic variation between collected samples. This study shows that RAPD markers can determine the polymorphisms between different genotypes of *A. narcissiflora* and their hybrids. So RAPD technique can serve as a suitable molecular method to determine the genetic diversity of samples.

**Keywords:** *Anemone narcissiflora*, Genetic Diversity, RAPD, Iran

# ANALYSIS OF GENETIC RELATIONSHIPS AMONG *ACHILLEA MILLEFOLIUM* SUBSP. *MILLEFOLIUM* POPULATIONS BASED ON RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS

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*Achillea millefolium* subsp. *millefolium* is a species of *Achillea* belongs to the Asteraceae family. The species *millefolium* has two subspecies which are called *millefolium* and *elbursensis*. According to this fact that the species *Achillea millefolium* subsp. *millefolium* belongs to the Kuhkamar region in East Azerbaijan, Iran, shows some different morphological traits according to the species identifying key, therefore five populations of this species were collected from different regions in order to study the genetic diversity of *A. millefolium*. In this study, RAPD marker was used to assessment of genetic diversity with the using four random 10 nt. primers. 27 polymorphic bands were produced from the 4 primers used in this technique that the maximum band is related to the RP6 primer, the lowest band is related to the RP2 and the average band for each primers were 6.7 polymorphic bands. Cluster analysis of samples was done by UPGMA method in NTYSYSpc 2.02 software. Dendrogram resulting from migrating bands showed that the studied samples can be divided into three groups. The results of the comparison and analysis of the data obtained from RAPD technique and similarity matrix represents the genetic variation between collected samples. The highest genetic distant according to the Nei genetic distant in GenALEX 6.5 software is calculated between pop.5 and pop.2 for equal to 0.356 and the lowest distant is located between pop.1 and pop.5. Also, molecular variation is %21 among populations and %79 within the populations. This study shows that RAPD markers can determine the polymorphisms between different genotypes of Achillea millefolium and their hybrids. Therefore, RAPD technique can be used as a useful molecular method to determine the genetic diversity of the studied samples.

**Key Words**: *Achillea Millefolium*, Genetic Diversity, RAPD-PCR

# ASSESSMENT OF GENETIC DIVERSITY IN *ELAEAGNUS ANGUSTIFOLIA* POPULATIONS USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS IN EAST AZERBAIJAN-IRAN

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*Elaeagnus angustifolia* is a species of *Elaeagnus* belongs to the Elaeagnaceae family. In Classification based on morphological characteristics, different populations with some various morphological traits are in one group as *E. angustifolia*. Thus, In this study, combination of random amplification of polymorphic DNA (RAPD) marker and morphological traits were used to investigation the presence or absence of an association between genetic variation and morphological features among populations of *E. angustifolia* collected from five different locations (Marand, Tabriz, Meianeh, Jolfa and Ahar) of East Azerbaijan province. RAPD analysis using 4 random primers generated 285 bands, as the average number of bands for each primer was 71.25 bands. The amplified products of the RAPD profiles ranged from 100 to 1500 bp. A matrix of genetic distances was employed to cluster the populations and UPGMA dendrogram was drawn using the (SAHN) clustering method as available in NTSYS-pc 2.02. Accordingly, the samples were placed in 4 groups. According to Nei genetic distance matrix, great genetic distance existed between Jolfa and Meianeh populations (0.167) and great genetic similarity existed between Jolfa and Marand populations (0.955). These results could be due to ecological conditions. Thus, our results showed that RAPD analysis is a suitable method to study genetic diversity and relationships among *E. angustifolia* populations. However, careful analysis of genetic diversity will be achieved by using more markers.

**Keywords:** *Elaeagnus angustifolia*, Genetic diversity, RAPD, Iran

# ASSESSMENT OF GENETIC DIVERSITY IN LANDRACES OF FINGER MILLET (*ELEUSINE CORACANA* L.) GENOTYPES COLLECTED FROM DIFFERENT PARTS OF MAHARASHTRA STATE (INDIA)

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A set of sixty-five finger millet (*Eleusine coracana* L.) accessions were screened for twelve morphological characteristics to study nature and magnitude of genetic divergence using Mahalanobis $D^2$ statistics during *kharif* 2009 and *kharif* 2010. Wide range of variation was observed for all the twelve characters under study. The analysis of variance exhibited significant difference among the genotypes for all the characters indicating substantial degree of variability. The estimates for genotypic coefficient of variation (GCV) were lower than the phenotypic coefficient of variation (PCV) for all the characters. The days to maturity exhibited the lowest GCV (7.37) as well as PCV (7.36) whereas, the iron percent had highest GCV and PCV (55.33 and 53.46 respectively). The highest difference between GCV and PCV values was observed for number of productive tiller per plant (3.84), whereas, iron content (0.13) showed the lowest difference between the GCV and PCV values. Heritability (b.s.) of all the characters in present investigation, was categorized as high to very high ranging from 61.52 to 99.52. The genetic advance was found ranging from 0.58 to 23.38. High heritability coupled with high genetic advance observed for the fodder yield per plant, days to 50 per cent flowering, days to maturity and plant height advocated high genetic progress for them. $D^2$ statistic indicated that the genotypes studied were genetically diverse. Based on genetic distances the 65 genotypes under study were grouped into five clusters. Cluster I contains highest 50 genotypes, followed by cluster II (11 genotypes) and cluster III (2 genotypes). The cluster IV and V were monogenotypic. In overall, $D^2$ analysis suggested KOPN 161, KOPN 370, VL 149, KOPN 387, PR 202, PES 110, KOPN 495, KOPN 892 and KOPN 926 were the most diverse parents could be utilized to improve, widen the genetic base and would be used as parents in breeding programme to enhance the productivity of finger millet.

**Key words:** Finger millet, Genetic diversity, $D^2$

# CHARACTERIZATION OF DURUM WHEAT LANDRACES FOR COLD TOLERANCE AND AGRONOMIC TRAITS UNDER RAINFED CONDITIONS OF IRAN

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A total of 641 durum wheat (*Triticum turgidum* L.) accessions, selected from durum wheat collection conserved at ICARDA gene bank, were evaluated at three highland research stations in cold and moderate cold rainfed regions of Iran. The main objectives were to (i) compare the different durum wheat populations for cold tolerance and agronomic performance in relation to their growth habit (spring, facultative and winter) and (iii) examine the potential of accessions to combine cold and drought tolerance with high yield and good agronomic traits, all towards exploring the potential for expanding durum wheat into cold and mild cold winter areas. Plant height, 1000-kernel weight and grain yield were among the best quantitative traits to differentiate the accessions, due to high phenotypic diversity index across locations. The results indicated that the resistant accessions were more originated from the populations of *Triticum turgidum* subsp. Durum and *Triticum turgidum* subsp. Carthlicum. The winter types had better agronomic performance and cold tolerance compared to facultative and spring types. Some of the accessions exhibited high level combination for high yield, and cold and drought tolerance, needed for the development of cultivars adapted to the highlands of Iran. The results indicated that selection for earliness and grain yield may express cold tolerance and adaptation to highland rainfed areas of Iran. In conclusion, the use of the selected cold resistant/tolerant accessions and tapping into wheat wild relative's gene pools could be used to improve winter hardness and cold tolerance in durum wheat.

**Key words:** Durum wheat, growth habit**,** phenotypic diversity, cold tolerance, agronomic traits

# EFFICIENCY OF MICROSATELLITE MARKERS IN THE INVESTIGATION AND CONFIRMATION OF INTROGRESSION IN BRASSICA SPECIES

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Microsatellite markers are believed to be a versatile tool in genomic and population studies. In the present study, thirty one microsatellite primers were employed to confirm the process of introgression in $F_2$ population of two interspecific crosses of three oleiferous brassica species viz *B. napus*, *B. juncea*, *B. campestris*. Thirty one microsatellite primers were used on introgressed hybrids of brassica from both $F_2$ populations that amplified 99 alleles of which 69 were polymorphic. The proportion of polymorphic loci was 69.7%. The number of amplified products ranged from 1 to 5. Polymorphism information content (PIC) of the primer sets ranged from 0.24 to 0.75. Dendrogram generated from cluster analysis revealed deviation of more introgressed hybrids towards female *B. napus* parent in both populations suggesting that C genome of *B. napus* has more contribution in the introgression process. Our results confirm the efficiency of microsatellite primers in the assessment of genetic analysis of brassica species.

**Keywords:** introgression, microsatellite markers, oleiferous brassica

# EVALUATION OF DATA FROM AN OLIVE GERMPLASM COLLECTION

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It is estimated that more than 2000 varieties of olives in the world. Both in terms of our country's abundant wild olive varieties and a great wealth of culture is well known. There are many olive type in Turkey which are not determined as botanically and not known characteristically as in other countries where olive growing. There are a lot of synonyms and homonymous in olive where are grown locally besides not much information about their adaptation abilities. Studies to determine the properties of olive varieties in our country dates are back to 1966. Works started in our Institution in 1968 and local varieties of olives grown zones has been scanned for morphological identification and 89 olive varieties has been registered. In this study, 84 domestic cultivars in the collection have been characterized on the basis of their morphological, pomological and agronomical characteristics. In conclusion, the results demonstrated a wide range of diversity among the examined cultivars.

**Key words:** Olive, Field Gene Bank, Characterization

# GENETIC DIVERSITY OF CASSAVA BROWN STREAK VIRUS AND RESISTANCE OF CASSAVA BROWN STREAK DISEASE FROM UGANDA

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Cassava (*Manihot esculenta* Crantz), an important root crop in Uganda is currently under threat from a diversity of constraints including pests and diseases. Cassava brown streak disease (CBSD), the latest outbreak of diseases attacking cassava in Uganda is widespread and devastating in many parts of the country. Cassava brown streak disease (CBSD), manifests as yellowing/chlorosis of the leaf vein and rotting of the edible roots which render it unfit for human consumption. Although, reported over a half a century ago, CBSD has remained less understood both aetiologically and epidemiologically. Yet, the development of resistant varieties requires knowledge of the genetic diversity of the causal organism. Studies were therefore conducted between April–September 2007 at the University of Bristol, UK to assess the genetic diversity of Cassava brown streak virus from Uganda. The results showed CBSD that induces a variety of symptoms on the secondary host *Nicotiana benthamiania.* Out of the total CBSV isolates assayed by RT-PCR, 9 gave the sequence size bands of 222bp. Overall, TBlastX sequence comparison with the NBCI database showed 94-100% and 80-83 % sequence identity with the Tanzanian, Mozambiquican and Ugandan CBSV isolates. In addition, a phylogenetic tree produced two distinct clusters. Cluster one consisting of isolates F1, F6, F12, F15, F20 and F26 were from Wakiso, Mukono, Mpigi and Luwero while Cluster two consisting of isolates F9, F17, F18, F19 and F28 from Mukono, Mpigi and Luwero. These were very distinct from the previous isolates from Tanzania, Mozambique and Uganda. Besides, the isolates previously sequenced from Uganda formed a separate sub cluster which is related to cluster one.

# HETEROSIS STUDIES IN INDIGENOUS EGGPLANT GERMPLASM

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Estimation of heterosis and combining ability are the important genetic attributes for eggplant breeders in anticipating improvement in productivity via hybridization and selection. Heterotic effects and genetic components of variation for qualitative and quantitative characters were estimated in eggplant (*Solanum melongena* L.). Forty hybrids generated by crossing four testers (males) with ten lines (females) were studied along with parents for studying heterosis and gene action for calyx length, fruit pedicel length, shoot borer infestation, fruit borer infestation, little leaf incidence, ascorbic acid content, total phenols content, number of fruit per plant and fruit yield per plant during rainy season of 2010-2011. The crosses obtained by L x T method possessed variation in terms of growth, yield and quality traits. Mean fruit yield per plant ranged from 2.85 to 1.04 kg. Among the 40 hybrids, the ones obtained from the cross 'Alagarkovil Local' x 'Annamalai' ($L_4xT_1$), 'Palamedu Local' x 'Punjab Sadabahar' ($L_5xT_3$), 'Palamedu Local' x 'EP 65' ($L_5xT_4$) and 'Keerikai Local' x 'KKM 1' ($L_7xT_2$) were suitable for heterosis breeding. Average performance of parents indicated that lines 'Alavayal local' ($L_1$), 'Sedapatty local' (Green) ($L_2$) and the tester 'Annamalai' ($T_1$) were good parents for further breeding to exploit high yield and low pest and disease incidences. Performance of these hybrids needs to be further evaluated in multiple locations or on farm trial prior to commercial use.

# SIMPLE SEQUENCE REPEATS ISOLATED FROM DURIAN (*DURIO ZIBETHINUS* MURR.) AND THEIR TRANSFERABILITY TO OTHER *DURIO* SPECIES

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Four hundred twenty four simple sequence repeats (SSRs) were isolated from eight microsatellite enriched libraries of durian (*Durio zibethinus* Murr. cultivar Matahari). Seventy nine microsatellite loci were screened. Eleven selected loci were further characterized and evaluated on a set of 17 durian germplasm from Kalimantan, Sumatra, Java, Sulawesi, Nusatenggara, and Papua Islands. All primer pairs produced an amplification product of the expected size and generally detected low to high polymorphism among the analyzed samples. All markers also showed across-taxa transferability in 3 other species of genus *Durio*. These SSR markers are expected to be an effective tool for marker-assisted breeding.

**Keywords**: simple sequence repeats, durian, across-taxa transferability

# STUDY THE EFFECT OF WASTE WATER NORTH REFINERY COMPANY-BIAGY/IRAQ IN *Adiantum capillus veneris*, CHEMICAL AND GENETICS STUDY.

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We record to first time growth fern *Adiantum capillus veneris* in polluted area with North Refinery Company wastewater in Biagy city and in non-polluted area Tikrit city(control station) in the middle of Iraq. Waste water, soil and plant samples collected from February2011 to February2012. HPLC analysis discover six Alkaloids compounds (Quanic acid,Kaemmpfertin,Isoquinoline, Adiantone, Astragalin, Fernadiene) and more phenols compounds(Caffeic acid, Thujone, Kaempferol, Ferulic acid, Isoferulic acid, Naringin, β-phellandrene, OH-adiantone, Leutoline and Coumaric acid) all Alkaloids compounds excepted Fernadiene recorded high values such as Quanic acid 50.42µg/ml;Kaemmpfertin 279.43µg/ml and most phenols compounds recoded high values such as β-phellandrene 3339.06µg/ml; Leutoline 1176.51µg/ml in polluted station on December 2011 with high COD value (107ppm) compare with control station (COD= 20ppm) Alkaloids compounds recoded values(Quanic acid 16.21µg/ml andKaemmpfertin 23.62µg/ml) and phenol compounds (β-phellandrene 69.15µg/ml andLeutoline 0µg/ml) relatively close to record values in polluted stationon September 2011(COD=28.9ppm) in Alkaloids compounds (Kaemmpfertin 25.19 µg/ml) and phenols compounds(β-phellandrene 29.3µg/ml and Leutoline 98.81µg/ml). With five nonspecific primer PCR analysis recorded different between plants plasmids which effects in chemical compounds.

**Key words:** *Adiantum capillus veneris*; Alkaloids; Phenols; Iraqi oil refinery.

# THE FORMATION AND STUDY IN THE CULTURE OF GENETIC RESOURCES OF FORAGE GRASSES BY THE EXPEDITIONARY COLLECTION OF WILD FORMS FROM THE NATURAL LANDSCAPES OF KAZAKHSTAN

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Flora of Kazakhstan has a unique diversity of ecotypes and species composition of forage crops that are of interest for use in breeding. Addition of donor samples to the existing gene is a valuable source of subsequent expansion of the collection of forage crops. In evolutionary terms, many forage crops maintained their wild relatives and, of course, they can become a valuable source and a culture improving wild for certain economically valuable attributes. These are the carriers of valuable features and their incorporation into the selection process can be a starting point for achieving breakthrough success in breeding. There are many examples in the world practice where wild-growing samples (ecotypes) or local ecotypes in the territory of Kazakhstan became the ancestor of many commercial varieties. For instance, known varieties of Lucerne grown in America, take their origin from Turkestan's Lucerne. Samples (ecotypes) of yellow Lucerne (Medicago falcate L.) from the territory of the former Semipalatinsk region, Russian wild rye (Psathyrostachys Juncea) and wheatgrass (Agropyron desertorum) collected by Canadian scientists in the last century (1930) became the basis of genetic plasma in breeding offset varieties of Lucerne of the type Rambler, drought-resistant varieties of Russian wildrye - Bozoysky improved. The territory of Kazakhstan, in contrast to other countries, covers different areas, the subzone of the steppe, semi-desert terrain, as well as mountain ranges - Tarbagatay, Tien Shan, Altai, Mugadzharskaya and various soil - climatic conditions of its environmental pressures have contributed to the formation of a wide variety of ecotypes. Mobilization of the genetic resources of wild-growing plants is still quite topical area. This approach is very important in the selection to enhance nitrogen-fixing ability of legumes and thus to stabilize the environmental situation in agriculture by reducing the consumption of such vehicles in the soil mineral nitrogen. The problem of collecting wild species of forage grasses drew the attention of many researchers around the world. It should be noted that, in the context of the conservation interests of the world is increasing. Collection of wild ecotypes of forage grasses and their study in the culture with the release of domestic sources - valuable attributes and properties have a significant impact on the development of selection - genetic science with the expected effect on the breeding of new varieties. By variety, in turn, will have environmental and social effects of food security.

# THE GENE POOL OF WILD FORAGE CROPS IN NORTHERN KAZAKHSTAN

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The use of food resources of wild plants is of great importance in creating hayfields and pastures. Wild plants are a source of valuable species and forms for the selection and replenishment of the gene pool. Their value lies in the fact that they have deep environmental and genetic factors, having been formed in the course of a long evolution in different soil and climatic conditions. The diversity of soil and climatic conditions of Kazakhstan entails a lot of species and population diversity in cultivated and wild flora. Over the past 10 years, scientists and breeders of the Baraev Centre have organized 6 expeditions to survey the natural flora and collected 557 types of wild perennial grasses in Northern, Central and Eastern Kazakhstan. The surveyed areas are characterized by a wide variety of soil and climatic conditions, which contributed to the formation of the plants’ valuable biological properties (tall growth height, cold and heat-resistance, early maturity and late ripening, high productivity and quality, and resistance to pests and diseases). In the North of the Kazakh Upland vegetation consists of: couch grass, brome, alfalfa, yellow clover and sweet clover, meadow grass, etc. The alkaline complexes contain clover (yellow and white), wheat grass (desert and Siberian), wheat grass (creeping and blue-grey), and alfalfa (variable and yellow). In the steppe zone, where the limiting factor is moisture, the following plants are concentrated- wheat grass, narrow wild rye, Russian wild rye, sand sainfoin, and yellow clover. Research and evaluation of wild specimens was carried out on normal zonal soils. As a result, the study identified the samples in terms of productivity and crop seeds that are resistant to drought, low temperatures in winter, frost, and disease. Selected samples are used in practical breeding as components for hybridization with the best local varieties and hybrids. The use of wild populations in the North of Kazakhstan created more than 30 drought-tolerant, high-yields, high-quality crop varieties of perennial grasses with various economic applications (hay-making, grazing, and integrated). At present, the gene pool of perennial grasses at the Baraev centre numbers more than 1,500 samples. The collection is annually updated with 30-50 samples of perennial grasses through exchange with scientific institutes in Russia, Belarus, Kazakhstan and Ukraine. Wild populations are important for the conservation of plant biodiversity and as sources in breeding for yield and resistance to stress factors.

# THE VALUE OF GENETIC RESOURCES OF CROPS IN NORTHERN KAZAKHSTAN

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In modern conditions, the role of gene pools capable of responding to changing environmental conditions, while consistently realizing its potential is one of growing importance. Genetic resources are valuable and strategically important capital for any state, ensuring the food security of the country and reducing loss through genetic erosion. The provision, retention, and management of genetic collections consitute the main source of crop improvement for the next decade. The contemporary Scientific Production Centre named after A. I. Baraev has a gene pool of around 4000 spring wheat samples, over 1,000 of spring barley, and more than 300 of oats. Every year the collection is supplemented by 40-60 samples of grain and forage crops by exchange with scientific research institutes of Kazakhstan, Russia, Ukraine, Belarus, international organizations, etc. The gene pool comprises locally breed varieties that represent unique genetic material, adapted to the agro-ecological conditions of North Kazakhstan, and varieties and lines of diverse eco-geographical origin needed to create competitive commercial varieties of wheat, barley, and oats. The study and assessment of initial material is carried out using field, laboratory and combined laboratory-field methods in both conventional natural and artifically created challenging conditions. As a result of the study indicative collections have been established, and catalogues published of the gene pool of five grain and forage crops from the Baraev Centre, including information about the genotypes of high productivity potential and grain quality, pathogen resistance, drought tolerance etc. A databank is being set up. In terms of increasing genetic diversity primarily, expand types represents of potential species *Triticum, Hordeum*, and *Avena* in particular are of great interest. In Northern Kazakhstan the global collection of crops played a significant role in the creation of drought-resistant, productive and high-quality varieties of crops. More than 50 varieties of grain and forage crops have been established using local genotypes. The presence of a wide range of genetic variants in the original genotype determines the effectiveness of selection when creating new varieties of crops.

# VARIABILITY IN MALE, FEMALE AND ANDROMONOECIOUS *SIMAROUBA GLAUCA* DC CULTIVARS AS ASSESSED BY MOLECULAR MARKERS

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*Simarouba glauca* DC, apart from being medicinal, is a versatile multipurpose oil-yielding tropical tree belonging to family Simaroubaceae, commonly known as “Paradise tree”, is a native of EI Salvador, Brazil. To understand genetic relationship, a comparative study was conducted to evaluate genetic diversity among 96 female, male and andromonoecious plants of *Simarouba*, collected from various geo-graphical location of India, employing 67 RAPD and 22 ISSR primers. The two data sets were analysed to calculate the total number of bands, the average number of bands per primer, the number of polymorphic bands, the percentage polymorphism, the effective multiplex ratio (EMR), the polymorphic information content (PIC), the marker index (MI) and the genetic similarity coefficients. In RAPD analysis, polymorphism percentage ranged from 9 to 100 with average percent polymorphism of 42.3% while for ISSR is from 11 to 77 with average of 38.8%. The mean PIC value (DI) for both marker system (0.92 for RAPD and 0.90 for ISSR) suggested that both the marker system is effective in determining polymorphism. The ISSR marker produced more information than the RAPD markers due to their higher EMR, as well as the MI values (5.04 and 4.58) compared to RAPD (3.31 and 3.04). The value of Jaccard similarity coefficient ranged from 0.78 to 0.97 and 0.78 to 0.95 based on RAPD and ISSR similarity matrix data. The UPGMA dendrogram obtained from the RAPD and ISSR data gave different clustering pattern with some level of similarities. The results indicate the effectiveness of these two marker system for demonstrating genetic relationship among *Simarouba* genotypes.

# AT LEAST TWO CYCLES OF SINGLE-PLANT SELECTION WITHIN A LENTIL LANDRACE ARE NEEDED TO REACH GENETIC HOMOGENEITY

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Lentil is predominantly self-pollinated, so landraces cultivated in the long-run represent valuable gene pools to directly derive pure-line cultivars. The objective was to assess the required selection cycles to reach the genetic homogeneity. A landrace of commercial interest was studied in Orestiada, Greece. Ultra-spaced single plants were selected on their yield performance, with seed of each selected individual constituting a separate progeny line. Thus, two plants selected in the fist cycle formed two first generation lines (coded 8 and 15). Each of the two initially formed lines led to respective four second-generation lines, and each second-generation line gave six third-generation lines (i.e. 8 → 8-1, …, 8-4 → 8-2-1, 8-2-2, …, 8-2-6). Concerning mean yield per plant, there were still significant differences within both groups of second generation lines, i.e. relative to check population varying from 1.81 up to 2.36 for the 8- group, and from 0.88 up to 1.23 for the 15- group. However, significant differences ceased to exist within the third generation groups, i.e. relative yields of 1.46-1.72 within the 8-2- group, and of 1.13-1.27 within the 15-3- group. As far as the CV values are concerned, they were consistently lower than the respective CVs of the check population, and more dispersed within the second- rather than the third-generation groups. Conclusively, the results were supportive of previous studies indicating that at least two rounds of selection within natural populations of autogamous species are required to reach a genotype that represents a pure-line cultivar.

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# DEVELOPMENT OF DROUGHT-TOLERANT VEGETATIVE (TRIPLOID) BERMUDAGRASS [*CYNODON DACTYLON*]

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To meet increasing demand on green space without further straining water resources requires use of water-efficient landscape plants. Hence, declining water resources necessitates development of drought-tolerant turfgrass cultivars. There is a great deal of variation for drought-tolerance among native bermudagrass germplasm originating from Mediterranean region. The aim of this study is to develop drought-tolerant, vegetative (triploid) bermudagrass cultivars. Native tetraploid bermudagrass genotypes were crossed with a diploid C. *transvaalensis* Burtt-Davy that originated from South Africa, and that possesses high turfgrass characteristics. The crosses were made at Akdeniz University, Antalya, Turkey, greenhouses in 2012. The seeds were germinated, DNA was extracted from the seedlings, and molecular markers were used to identify true hybrids. Phenotypic pre-selection was made among the hybrids and 400 hybrid genotypes were vegetatively propagated, and transplanted in the field with 3 (three) replications in June, 2013. Establishment rates have been recorded. Drought-tolerance and turfgrass characteristics (color, quality, texture, dormancy etc.) will be recorded until 2015. The preliminary observations indicate that triploid (vegetative) bermudagrass cultivars with superior turfgrass characteristics can be developed. New cultivars are expected to combine the drought tolerance of native tetraploid bermudagrass with that of superior turf characteristics of diploid C. *transvaalensis.*

**Key words:** bermudagrass, vegetative, triploid, drought-tolerance

# GENETIC ORIGINS OF CULTIVATED AND WILD GRAPEVINES FROM NEAR-CASPIAN ZONES OF AZERBAIJAN

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For determining of phylogenetic relationship between aborigine cultivars and wild forms of grapevine accessions originating from the Near-Caspian zones of Azerbaijan 3 chloroplast microsatellite loci (ccmp3, ccmp5, ccmp10) have been studied. At these loci 7 types of alleles (at ccmp3 two, at ccmp5 two and at the locus of ccmp10 three type of alleles) were defined combinations which have revealed 6 haplotypes in genotypes. Only D haplotype were observed in all studied populations. Also, this haplotype differed for its least difference (on the base of its alleles sizes) from other haplotypes and this is apparently connected with its primary origin. The distribution of haplotypes in grape genotypes explains the variability within and between populations. The results of cluster analysis determined that most of cultivated and wild accessions have the same haplotypes. It showed that the aborigine cultivars originating from the Near-Caspian zones of Azerbaijan were close related to wild accessions from this area. Results of the researches allow to conclude, that the Near-Caspian regions of Azerbaijan is one of the important center of the domestication of grapevine. The existing diversity in wild samples is very significant as the domestication pressure on cultivated samples has caused considerable losses of many useful genes, such as those responsible for resistance to different types of diseases and environmental stresses (drought, salinity, cold, heat, etc). Therefore, wild samples are very valuable reservoirs of useful genes which can resolve many of our present and future problems.

# IMPROVED VEGETABLE VARIETIES FOR CENTRAL ASIA AND THE CAUCASUS DEVELOPED FROM

# AVRDC – THE WORLD VEGETABLE CENTER GERMPLASM

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After the break-up of the Soviet Union in 1991, all countries in the region experienced difficulties in obtaining vegetable germplasm for breeding programs. The genebank at AVRDC – The World Vegetable Center conserves diversity of vegetable germplasm and, from 2005-2012 has introduced more than 1370 accessions and improved lines of 26 vegetable species representing 9 families to countries in Central Asia and the Caucasus through the Regional Network for Vegetable System Research and Development to foster faster variety development and dissemination. Partner research institutes have studied these vegetables in regional variety trials under various agroecosystems. Currently a total of 38 new varieties of 12 species are under state variety trials. Through collaboration, 35 new varieties of 8 vegetable crops including tomato, sweet and hot pepper, eggplant, vegetable soybean, mungbean, yard-long bean and cabbage have been released and registered in state registries. From 35 new varieties, 14 have been developed by conventional selection methods using germplasm received from the AVRDC genebank. All released varieties demonstrate economically valuable traits: early maturity, higher yield, resistance to diseases and pests, high nutrient content and other marketable features. Seeds of released varieties are multiplied to provide farmers. For the first time new varieties of non-traditional species such vegetable soybean, mungbean, yard-long bean and Chinese leafy cabbage have expanded the diversity of vegetables in the region, and have become popular for cultivation and consumption. Increasing the vegetable production will help diversify diets, increase farmers' income, and enhance the well-being of families throughout the region.

# RESISTANCE OF BARLEY ACCESSIONS FORM VIR COLLECTION TO HARMFUL ORGANISMS

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The resistance of barley to frit fly (*Oscinella frit* L.), bird cherry oat-aphid (*Rhopalosiphum padi* L.), leaf blights (*Blumeria graminis*, *Cochliobolus sativus and Puccinia graminis spp.)* has been estimated. We founded 19 from 108 samples that have partial resistance to named harmful organisms, most them are from Dagestan. Has been researched the resistance of commercial barley varieties of Russian Federation to frit fly in 2000-2002 years and ten years later – in 2010-2012 years. Among 108 investigated accessions in 2002 year we distinguished 9 varieties that had low damage of frit fly. That is 8, 3 % of total quantity. As to 2012 year 4 accessions among 45 varieties were injured at the level of standard or lower than it (8, 8 %). Varieties from Siberian, Privolzhsky and Southern districts were less injured by frit fly, then varieties from other districts as well now as ten years ego. The tendency of decreasing of resentence to frit fly have place. It was determined different compensatory responses of the varieties to the damage of frit fly. We founded some varieties that much more tolerant while damaged by frit fly in contrast with others. That may provide the satisfied yield in the case of the significant frit fly's damage. Several mechanisms of barley's resistance to frit fly where determined that are morphology and biochemistry characteristics of the plant.

# RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS

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This project was conducted at GAP Agricultural Research Center of Turkish Ministry of Food, Agriculture and Livestock in Şanlıurfa-Turkey and a semi-arid region of Turkey. The aim was to determine the effects of water stress on 194 melon accessions collected from different region of Turkey. Different irrigation levels were imposed to determine potential water stress' effect on melon accessions. All plots at the beginning were irrigated with enough irrigation water for healthy seed germination. The plants received enough irrigation until the period of true leaves. After the true leaves, irrigation treatments were initiated. While $I_1$ treatment was received full irrigation based on depleted soil moisture in the root zone, $I_2$ treatment was received 50% of $I_1$. The formula, improved by Karipçin et al. (2008), was used to evaluate data as an indicator of drought tolerance. For each accession, changing ratio between $I_1$ and $I_2$ treatments was obtained. If any accession's changing rate ($I_1/I_2$) was near 1 that means that the accession was more tolerant to drought than the others. Physiologic/vegetative characteristics were measured such as Situation of growing, Date of the first branch, Condition of dehydration, Leaf temperature, Root length, Date of the first male flower blooming, Number of flowers bud, Number of male flower bud, Width of flower, Canopy diameter, Main stem length, Width of root, Fresh root weight , Dry root weight. The results showed that forty-three of tested accessions were tolerant ones. The highest score obtained from the formulae was 100 with accession number 41, 106, 183 and 248. Other tolerant 39 accessions were rated between 99 and 80 point. 21 accessions were placed between tolerant and intolerant group. The accessions were classified as tolerant if they had a rating above 80 out of 100 and intolerant if the rating was below 64. 130 accessions were classified as intolerant.

**Keywords:** Genetic resources, abiotic stress, melon, accession.

# A BREEDING SCHEDULE FOR IDENTIFYING THE VALUE OF LOCAL LANDRACE CV. EGLOUVI (*LENS CULINARIS SPP*) AS A SOURCE FOR RESISTANCE TO FUSSARIUM WILT

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In order to conserve biodiversity and ensure food quality, an interest is justifiably concentrated to local traditional varieties. This study aimed to characterize a landrace of *Lens culinaris* (i.e., cv. Eglouvi) originating from Leukada Island, Greece, and identify its value as source for resistance to *Fussarium wilt*. A comparative evaluation for yield and resistance, as well as DNA fingerprinting through SSR molecular marker analysis, were performed. Field experimentation was conducted at the Fodder Crops and Pastures Institute (Larissa, Greece) at a low input system, including two non-replicated honeycomb designs (NR-0) at 50 cm and 80 cm were established in the field. The single-plant yield CV ranged to 162% and 140% for the experimental layouts of 80 cm and 50 cm, respectively. For molecular marker analysis, genomic DNA was extracted from young lentil leaves, using the CTAB method. Moreover, DNA samples were qualitatively and quantitatively evaluated by agarose gel electrophoresis. Following a preliminary evaluation of SSR primers, 12 primer pairs were selected and used in PCR reactions. Our findings indicate that such traditional variety demonstrated as a valuable gene pool for resistance to Fussarium spp. and therefore, may be potentially exploited as an ideal starting material for breeding activities. Moreover, the existence of intra-cultivar variation provides the opportunity for direct utilization as pre-breeding lines. Further employment of molecular markers and carefully linkage with phenotype expression is expected to allow the genetic mapping of lentil as well as the association of markers with important agronomic traits.

**Acknowledgement**

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# AGRONOMIC EVALUATION OF BAMBARA GROUNDNUT (*VIGNA SUBTERRANEA* L) LANDRACE COLLECTIONS IN A DRY ENVIRONMENT

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Bambara groundnut (*Vigna subterranea* L.) is an African legume valued for its drought tolerance and resistance to pests and diseases. However, due to absence of improved cultivars bambara groundnut farmers continue to grow their own landraces, with very little exchange of planting material between growers. Consequently, the number of landraces will continue to dwindle and hence landraces with useful traits but low yielding might be lost. Therefore, collection, identification and characterization of local landraces from various bambara growing regions is necessary. The objective of this study was to evaluate the variability in growth and yield of 27 bambara landrace collections from different agro-ecological areas of north-eastern part of South Africa. A field experiment was conducted during 2012/2013 cropping season at Nelspruit ($25^0$ 26’ 25” S, $30^0$ 58’ 57” E and 676m a.s.l), South Africa using a randomized complete block design replicated three times. Phenological development was analysed by determining days to 50% flowering, and incidences of stem rot caused by *Scleorotium rolfsii* were scored on a scale of 1-5. Grain yield was determined at harvest maturity. The disease incidence and 100-seed weight did not vary with the landraces. There was variation amongst the landraces in days to 50% flowering (46 to 53 days; mean of 49.4 days) and grain yield (407 to 3311 kg $ha^{-1}$; mean of 1405 kg $ha^{-1}$). It is clear from these preliminary results that there is considerable variability amongst the landrace collections evaluated in this study. Such variability may be exploited in bambara crop improvement programs. However, further studies over several seasons and sites are recommended.

**Key words:** Growth, Phenological development, traits, variability, yield

# CHARACTERIZATION OF GLUTAMIC ACID OF *CORYNEBACTERIUM SP.* AS A FOOD ADDITIVE DURING FERMENTATION

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Glutamic fermentation using *Corynebacterium* sp., is a major industrial fermentation with annual production about 1500 000 T. Glutamate is an amino acid used mainly in food industry, as a riser of taste. *Corynebacterium* sp. produce glutamate following a thermal shock when temperature of the semi-continuous jet engine passes from 33° to 39°C. Immediately after the thermal shock, glutamate is excreted and the cell multiplication is strongly slowed down. When the cells are implemented in continuous reactor at 39°C, as in semi-continuous method, the growth stops and the production of glutamate starts immediately. However, after hundred hours, the growth of cells begins again and the production of glutamate cease completely. A nonproducing strain at 39°C was isolated under these conditions from culture. Thus we have on one hand the initial producing strain of glutamate at 39°C, and on the other hand a variant unable to produce glutamate at the same temperature. Intracellular measurements showed us that when cells produce glutamate, the activity of oxoglutarate deshydrogenase complex (ODHC) is completely abolished and the activity of pyruvate deshydrogenase (PDH) is strongly slowed down. When cells are not able to produce glutamate after hundred hours, ODHC activity took again its normal level. These two enzymatic complexes divide a common enzymatic sub-unit, the lipoamide deshydrogenase, probably from membrane since it's implied in the respiratory chain. Thus it is probable that structure and composition of *Corynebacterium* sp. envelope are modified when temperature is high until 39°C, so it could affect the activity of the 2 enzymatic complexes. This work proposes to compare cytoplasmic protein (gel 2d) and wall-lipid (thin chromatography layers) profiles of the two strains in growth (33°) and production (39°) conditions. This work should enable us to better understand and improve in a rational way the excretion of glutamate by *Corynebacterium* sp.

**Key Words:** Mycolic Acids – Temperature - Glutamate Excretion - Membrane Fluidity - Thin Layer Chromatography

# FUTURE CHALLENGE TO IDENTIFICATION OF DROUGHT TOLERANCE AND RESISTANCE: HIGH-THROUGHPUT PLANT PHENOTYPING

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Plant phenotyping is a rapidly evolving concept that the functional plant body originates during plant growth and development from the dynamic interaction between the plant genetic background and climate change conditions in which the plant develop. High-throughput plant phenotyping includes sensors, system technologies and algorithms which provide multi-trait assessment with automatic measurements and saving time. The hyper-spectral spectroradiometers and imaging processes such as spectral imaging, three-dimensional imaging, thermal imaging, fluorescence imaging, magnetic resonance imaging and near infrared imaging enables monitoring of several dynamic complex traits in high-throughput plant phenotyping. These different techniques offer new methods and traits to assess drought tolerance and resistance. The trait of stomatal conductance is related to leaf and canopy gas exchange and it responds rapidly and sustainably to changes in soil water potential, and provides the main limitation to photosynthesis and growth. In thermal imaging, closing stomata is an early and sensitive reaction of plants facing drought stress which cause of reduced transpiration leaf temperature is rising locally, producing a spatial temperature pattern that can be visualized by thermography. Chlorophyll fluorescence is commonly used in phenotyping to see the effect of different genes or environmental conditions on the efficiency of photosynthesises and it is related to photosynthetic activity under drought stress conditions. The trait of canopy temperature can be measured by imaging technology in different environmental conditions, time of day and plant developmental stage and these parameters can change according to canopy traits and drought tolerances. Spectral indices and IR-temperature were highly correlated with canopy water mass and able to show the different drought stress levels. The traits of leaf senescence, carbon isotope discrimination and root structure are also used for identification of drought tolerance and resistance with sensor technologies.

# GERMPLASM FOR SPRING DURUM WHEAT BREEDING ON ALTAI

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Breeding of spring durum wheat on Altai has an aim to develop a complex of complementary varieties adapted to the regional environments for different natural and climatic zones of the south of Western Siberia. Major method for the creation of initial genetic diversity is inter- and intraspecies hybridization using local varieties and advanced lines as a basis. Sources of new germplasm are Vavilov's Institute, direct material exchange with institutions of Russia, Ukraine, Germany, USA, Canada and KASIB program as well. Each year about 200 entries are under study in a collection nursery. Sources of high productivity, quality traits, drought tolerance, desirable morphological parameters, resistance to diseases and pests were selected after screening. On the base of many-year experiment parameters of ecological plasticity are calculated for 78 entries. Genotypes from Samara Research Institute of Agriculture, Siberian Research Institute of Agriculture, Research Institute of Agriculture of Sough-West, Research Institute of Agriculture of Central Chernozem Belt are of prime interest. Participation in the KASIB program helps both to material exchange and use in crosses promising forms of Siberia and Kazakhstan and to have an opportunity of wide ecological estimation of the material. KASIB durums are actively used in crosses. For the period from 2000 425 crosses with the entries were realized. In 2013 2726 lines derived from the crosses were studied in different breeding nurseries including 17 in a competitive yield trial. Intraspecies hybridization plays a great part in durum wheat breeding. *Triticum dicoccum, T.aestivum, T.turgidum, T. timopheevii, T.persicum, as well as T.bioticum, T.monococcum, T.turanicum* were widely used in breeding program in Altai. Screening of collections made it possible to single out sources of agronomically valuable traits. With the help of species diversity a level of drought tolerance, grain productivity and disease resistance was elevated in a new breeding stock.

# LANDRACE VARIETIES OF WHEAT IN UZBEKISTAN

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In a complex climatic background, for the hundred years it has been created landrace wheat varieties possessing adaptability to local soil and climatic conditions. These varieties were differed with their high tolerance to salinity, drought and heat to severe winter. Moreover, they have strong and deciduous ear of wheat, their flour with good gustatory quality that had been used for baking national Uzbek bread. Scientists in their works leans on invaluable experiences of many generations of national breeder, studying history of creations local landrace varieties. Since long ago and present time, created different wheat varieties suitable for local regions of Uzbekistan that they likely posses local landraces describable with high content of microelements and good gustatory quality. During expedition in distinct regions of Uzbekistan, it was collected samples from local landrace wheat varieties such as Baboki, Jaydari bugdoy, Kizil bugdoy, Kora kiltik, Tuya tish and etc. Morphological analysis of ear and grains of these samples demonstrated that many of them belongs to *Gracum* varieties with white ear and white grains, and to *Erithrospermum* varieties with white ear and red grains, though among them have red ear varieties belonging to *Ferrigenium*, but also ranging compact forms of wheat having admixture of *T. compactum L*. With the method of individual selection, it was created collection of landrace varieties consisting 120 samples as primary material for breeding and was created several lines differing from others with tolerance to lodging during watering and also having high content of gluten and its index of deformation. Diversity cultivated and related wild species is basic material for development of national seed farming. In the world, people pay attention to maintenance of landrace varieties of local cultivated plants that considering them as potential useful source of allele genes and polygene's responding for resistance and tolerance of wheat to different adverse abiotic and biotic factors of the environment.

# OCCURRENCE, ISOLATION AND DNA IDENTIFICATION OF *STREPTOCOCCUS THERMOPHILUS* INVOLVED IN ALGERIAN TRADITIONAL BUTTER

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Algeria remains dependent on the importation of bacteria involved in industrial fermentations. *Streptococcus thermophilus* is an essential agent in dairy technology, including the production of yogurt. *Streptococcus thermophilus* isolates from 'Smen', a traditional fermented milk product provided from steppe region were subjected to taxonomical investigations and tested for antagonistic activity, acidifying power and proteolyses properties for possible inclusion in a starter culture preparation. The identification procedure included phenotypic investigations, molecular characterization by using species-specific primers from *glcK*, *dnaE, thrS*, *proA* and *serA* housekeeping genes in order to distinguish among reference, and wild strains of *Streptococcus thermophilus* and for their differentiation from *Enterococcus* spp. The acidifying capacity was deduced from pH measurement, proteolytic activity was realised in SMY medium and the inhibitory activity against two pathogenic strains, namely *Staphylococcus aureus* and *Escherichia coli* was conducted. A collection of 20 isolates Gram-positive, catalase-negative and cell morphology with a long chain were presumptively identified as *Streptococcus thermophilus* on the basis of phenotypic characterization. A total of 14 strains were tested by PCR DNA identification analysis and these indigenous isolates were unambiguously characterised by their housekeeping gene sequences. Their performance and physical properties were not significantly different from commercial starters strains used in this study. To our knowledge, this is the first report on the isolation and molecular characterization of *Streptococcus thermophilus* strains from traditional fermented milk product in steppe area of west Algeria. It was therefore suggested that wild bacterial populations should be preserved in order to protect the traditional lactic fermentation and for product innovation.

**Key words:** Smen, *Streptococcus thermophilus,* DNA, steppe area, product innovation

# ANALYSIS OF GENETIC DIVERSITY OF SRI LANKAN TRADITIONAL RICE VARIETY *"HONDERAWALA"*

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There are approximately 2000 rice accessions at Plant Genetic Resources Center (PGRC), Sri Lanka with a wide morphological and days to flowering (DF) variation while there are claims on duplicates. Identification of distinct genotypes and elimination of duplicates is important in breeding program. Our objective was to analyze the genetic diversity of *Honderawala* accessions using selected morphological characters including DF. Twenty *Hondarawala* accessions from PGRC were grown at rice research and development institute, Batalagoda during *Maha* season 2012/2013 in a completely randomized design (CRD). Thirty eightmorphological characters and DF were recorded. In order to analyze the diversity of accessions, a Principal Component Analysis (PCA)was performed in which 5 principle components (PA) explained 89% of total observed variation (SPSS version 20, IBM, USA). Culm Number at maturity (CN), Culm Number at vegetative stage (CNV) and Shoot weight (SW) included in1st PA. Grain Width (GW), Root Length (RL) and Panicle Weight (PW) included in 2nd PA. Ligule Length (LiL) and Plant Height at vegetative stage (PHV) included in 3rd PA. Culm Diameter (CD) and Grain Length (GL) included in 4th PA and Culm Length (CL) included in 5th PA. According to the hierarchical cluster analysis, 6 clusters were observed at rescaled distance of 15. Accession number 3528 remained unique while accessions 3864 and 4243, 3977 and 6428, 6690 and 3521 formed 3 clusters indicating their close genetic relatedness or the duplicates. DF variation coincided with clusters. Our attempt will be useful for genetic purification and defining standard characters of variety *Hondarawala* in the future.

## Keywords

Days to flowering, genetic diversity, morphological characters, Sri Lankan traditional rice

## Acknowledgement

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# EVALUATION OF VARIATION OF KALE (*BRASSICA OLERACEA* VAR. *ACEPHALA*) POPULATIONS COLLECTED FROM BLACK SEA REGION, TURKEY

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Kale (*Brassica oleracea* var. *acephala*) is one of the most important crops in the Black Sea Region of Turkey. In the first experiment year, 127 kale populations were collected from different geographical areas in this region. All populations of native kale genotypes were examined for morphological characteristics. Phenotypic diversity in their plant characters was assessed. Data were analyzed using principal component analysis (PCA). PCA revealed that the first five PC axes explained 67.0% of the total multivariate variation. Data were subjected to cluster analysis and several groups were identified with most of the populations. Clustered into ten groups, a dendrogram was prepared to evaluate morphological differences among populations. It revealed high variation. The results provide information on the diversity and it can assist geneticists and breeders to identify the populations with unique characteristics for inclusion in future breeding activities.

**Keywords:** kale, genetic resource, diversity, PCA, Turkey

# GENETIC DIVERSITY IN BOTTLE GOURD [*Lagenaria siceraria* (Mol.) Stand.]

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An experiment was conducted at the experimental field of Olericulture Division, Bangladesh Agricultural Research Institute, Bangladesh during the winter season of 2006-07. Twenty bottle gourd genotypes were evaluated to genetic diversity. The genotypes were clustered into five distinct groups with the range of 1 genotypes to 8. The inter-cluster distance in all cases was larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The maximum inter-cluster distance was observed between genotypes of cluster III and IV (15.010) followed by cluster II and IV (12.841) and the minimum was found between genotypes of cluster II and III (5.318). The highest intra cluster value (0.933) was observed in cluster I due to the presence of variations among the genotypes.

**Key words:** Genetic diversity, bottle gourd [*Lagenaria siceraria* (Mol.) Stand.] and cluster analysis.

# THE ADAPTIVE CAPABILITY OF SOME CEREALS FROM GEOGRAPHICALLY AND ENVIRONMENTALLY DIFFERENT AREAS OF AZERBAIJAN

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The present research has included an environment and genetic monitoring of the adaptive capability of some wild and cultivated species of the cereals from the genera *Triticum, Hordeum, Avena*, and *Aeqilops* growing in environmentally and geographically different areas of Azerbaijan (Absheron and Mountain Shirvan). Leaves and seeds of the plants to be studied were collected *in situ*. Their adaptive capability was estimated by using a complex analysis of the spontaneous mutability, the intensity of peroxide lipid oxidation, and the antioxidant enzymatic activity of protective mechanism. It was found out that the wild species of the cereals, like the cultivated ones growing in the same environment, demonstrated a higher adaptive capability. According to the estimated data, *Hordeum spontaneum L.* was the most adapted of all the wild species, regardless of their area of origin. Against the background of normal metabolic adaptation, the species of *Avena* and *Aeqilops* were characterized with a relatively low level of genetic stability. It was revealed that there was a directly proportional correlation between the dynamics of intensity of peroxide lipid oxidation and the level of spontaneous mutability of the cells, on the one hand, and their activity of antioxidant enzymes of the protective mechanism, on the other. Considering this characteristics, we can assume that the intracellular mechanism of compensative protection plays an important role in the development of general adaptation of the plants to the environment.

# PCR IDENTIFICATION OF LACTOBACILLI STRAINS FOR POTENTIAL PROBIOTIC IN POULTRY

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Antibiotics use had its limitations due to the emergence of new strains caused by multi-resistant misuse of these compounds in the poultry sector, despite the antibioprévention is currently the only means used to control health problems and related economic avian pathogenic. The use of probiotics is necessary to promote healthy microflora antagonistic to pathogens and screws can register as an alternative strategy proposed to protect poultry pathogens and to replace antibiotics as growth factor. This work has focused on the identification methods of DNA intestinal poultry strain producing inhibitory active substances against enteric pathogens including *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi* and to characterize them clearly for eventual use as potentially probiotic strains to control pathogens in poultry production. A total of 22 strains were isolated from different compartments of the digestive two rooster's local breed. Use of 16S rDNA primers and sequencing of the amplified DNA fragments were utilised to identify isolates belonging to the *Lactobacillus* flora. *Lactobacillus acidophilus*, *Lactobacillus gallinarum*, *Lactobacillus crispatus* and *Lactobacillus johonossi* strains were most diagnosed by colony PCR. Other techniques have been used for the isolation and detection of strains producing prebiotics such as exogenous polysaccharides (EPS), in addition preparation of whey rich in exopolysaccharides (prebiotic) for the watering of chicks, could be a working character fight against pathogens or play a beneficial role in poultry feed.The study on antagonism cultures showed inhibitory activity during interactions opposite pathogens by measuring the clear halos in vitro. Twelve of these strains were selected due to their strong inhibitory action. In the long term, these strains, once the best characterized genotypically, could be proposed as probiotics in poultry feed.

**Key words**: *Lactobacillus spp*, ADN, PCR, probiotique, prébiotique, pathogènes, *Salmonella*

# PROTEIN CODING SEQUENCES OF *AEGILOPS TAUSCHII* CHROMOSOME 5D REVEALED BY *IN SILICO* ANALYSIS

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Sequencing of the entire wheat genome has been a magnanimous and laborious task given that the polyploidy of *Triticum* makes the genome is three times larger than the human genome. The D genome of wheat putatively arose from a wild ancestor *Aegilops tauschii* (goatgrass), thus the molecular characterization of the *Aegilops* genome particularly 5D chromosome has become all the more important in unraveling the wheat genome structure and function, for wheat improvement. In our present study, we identified protein coding sequences present on 5D by blasting 454 sequencing data against shotgun sequences of this species. This information is invaluable in unveiling the protein coding genes on wheat DD genome.

# REACTIONS OF SOME TURKISH *AEGILOPS* AND *TRITICUM* MATERIALS TO *PGT* RACE RTKTC

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Wheat (*Triticum* spp.) is strategic cereal crop of Turkey. Stem rust (*Puccinia graminis* f. sp. *tritici*) is a disease affecting wheat yield and quality in Turkey. Wild relatives of wheat are important sources of useful genes for cultivated wheat. Turkey is one of the centers of origin of wheat. In this search we tested various *Aegilops* and *Triticum* accessions with *Pgt* race RTKTC to find new resistant sources to stem rust at the Central Research Institute for Field Crops at under greenhouse conditions in March 2013. The accessions were represented by 6 *Aegilops* species (*Ae. biuncialis* (7 genotypes), *Ae. caudata* (5 genotypes), *Ae. columnaris* (6 genotypes) *Ae. crassa* (2 genotypes), *Ae. Triuncialis* (8 genotypes), *Ae. umbellulata* (2 genotypes)) and 4 *Triticum* species (*T. dicoccoides* (3 genotypes), *T. dicoccon* (4 genotypes), *T. boeoticum* (4 genotypes), and *T. urartu* (3 genotypes)). Inoculations were made at Zadoks growth stage 12 using race RTKTC (virulent to *Sr5, Sr21, Sr7b, Sr11, Sr6, Sr8a, Sr9g, Sr9b, Sr30, Sr17+13, Sr9a, Sr9d, Sr10, SrTmp, SrMcn*) obtained from a single pustule. Following inoculation, seedlings were placed in a dew chamber overnight at 20 to 22°C and then transferred to a greenhouse at 20 to 25°C. Disease reactions were scored on a 0-4 scale after 14 days. Only one accessions of *Ae. crassa* (TUR 01433) was found resistant. This genotype could be new source of resistance to stem rust.

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# REACTIONS OF TURKISH WHEAT LANDRACES TO *PGT* RACE RTKTC

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Wheat (*Triticum* spp.) is the most important and strategic cereal crop of Turkey. Turkey is one of the centers of origin of cultivated plants such as *Hordeum* and *Triticum* species. Landraces of wheat are important sources of useful genes for cultivated wheat important. Stem rust (*Puccinia graminis* f. sp. *tritici* ) is among of the important biotic stresses of wheat growing area in higher altitudes and coastal areas. Stem rust is affecting wheat yield and quality in Turkey. In this search we tested various wheat landraces against to *Pgt* race RTKTC to find new resistant sources to stem rust at the Central Research Institute for Field Crops at under greenhouse conditions in March 2013. Inoculations were made at Zadoks growth stage 12 using race RTKTC (virulent to *Sr5, Sr21, Sr7b, Sr11, Sr6, Sr8a, Sr9g, Sr9b, Sr30, Sr17+13, Sr9a, Sr9d, Sr10, SrTmp, SrMcn*) obtained from a single pustule. After incubation overnight under high humidity conditions at 20 to 22°C seedlings were transferred to a greenhouse held at 20 to 25°C and reactions were scored on a 0-4 scale after 14 days. Among 210 genotypes, only one line was resistant. This could be new source of resistance to stem rust.

***Acknowledgement:***

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# RESISTANCE OF BARLEY ACCESSIONS FROM DAGESTAN TO POWDERY MILDEW AND BARLEY LEAF RUST

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During 2012-2013 at Dagestan Experiment Station (Derbent) 265 barley accessions from Dagestan have been studied for the resistance to powdery mildew (*Blumeria graminis* (DC.) Golovin ex Speer f. sp. *hordei* Em. Marchal) and barley leaf rust (*Puccinia hordei* G.H.Otth). The resistance was estimated twice (during ear formation and at the milky ripeness stage) according to the scale from 1 (very low resistance) to 9 (absence of symptoms). The epiphytotic level of diseases was observed; the damage rate of standard varieties constituted 1-3 score. Five accessions resistant to powdery mildew (k-23787, k-25615, кk28211, k-28212, k-30781) and six accession resistant to barley leaf rust (k-10469, k-10471, k-13233, k-17436, k-17439, k-30781) with damage rate of 7 score have been selected at the extremely hard infection background. The selected forms were resistant (7 score) at the North-West (Pushkin branch of VIR, St. Petersburg, Russia).

The study was supported by RFBR (project 12-04-96503).

# REVALORIZATION TRADITIONAL DATE “BTANA” FOR PRODUCTION OF MICROBIAL POLYSACCHARIDES IN FOOD PURPOSES

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Polysaccharides aroused great interest among scientists over the past thirty years. These macromolecules from renewable and abundant sources such as plants (cellulose, starch, alginate...) animals (chitin, hyalauronique acid...), microorganisms (pullulan, dextran produced by Leuconostoc mesenteroides...), and these polysaccharides have taken an important place in the world of polymers as evidenced by the recent studies on them affecting the increasingly diverse applications in the food industry , cosmetics but also in paints and textiles due to their gelling properties , thickening, emulsifying moisturizer (especially sought food : cream, ice vinegar ..) Thereby, our goal is to upgrade our national products taking the case of the traditional date “BTANA”, selecting strains of lactic acid bio- preservative character and look for exopolysaccharide -producing strains. The results allowed us to isolated a total of 8 lactic strains of Leuconostoc group pre-identified by biochemical and phenotypic methods. These last showed an over -production of exopolysaccharides. The identification of strains producing biopolymers was performed using screening methods based on different tests: expression of the mucoid phenotype in hyper- sucrose medium, the high viscosity in liquid culture, fixing the specific staining of exopolysaccharides in presence of toluidine blue and red medium ruthenium. Moreover, a characterization of exopolysaccharides was performed by an alcoholic extraction, purification, lyophilization, also a characterization by thin layer chromatography which showed a similarity profiles with commercial dextran and colorimetric assay was determined to 1254 mg / l for the highest production of LGM -IL2 strain EPS .

New potential applications of polysaccharides yet emerge, especially in an area at the interface between the pharmaceutical and food world, such as prebiotics.

**Key words:** *Leuconostoc*, traditional date, exopolysaccharides, dextran, prebiotics.

# SEED COMPONENT DIVERSITY OF HYBRID MATERIALS ORIGINATED FROM WILD ANNUAL *HELIANTHUS* SPECIES

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This study presents the evaluation of hybrid forms, obtained as a result of interspecific hybridization between sunflower inbred lines and wild annual *Helianthus annuus*, *H. debilis* and *H. petiolaris* accessions, resistant to leaves pathogens, on various indices related to their seed oil content. The investigation included accessions from the wild species sunflower collection of Dobroudja Agricultural Institute, General Toshevo, used as paternal parents in the crosses. The indices 1000 seed weight (*g*), kernel and hull (*%*), oil content in kernel (*%*) and in seed (*%*) and potein content were evaluated. The results showed very good statistical authenticity on level $P$ = 0.001 of the analytical hypothesis that the investigated hybrid forms were with different genetic potential on the studied indices, pointing to the existence of high variability among the used wild germplasm.

# SPONTANEOUS MUTATION e*am8* IN BARLEY ACCESSION FROM DAGESTAN MOUNTAIN REGION

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The barley gene *Eam8* is an ortholog of the *Arabidopsis thaliana* circadian clock regulator Early Flowering 3 (*Elf3*). *Early maturity 8* (*eam8*) mutations, also named *mat-a*, affect the circadian clock and photoperiod response. Mutant plants are day-length neutral or photoperiod insensitive. Spontaneous and induced mutants have been used in commercial varieties Mari, Russian early, Kinai5, Kagoshima Gold. Some alleles possess mutations leading to the defective putative ELF3 protein and yellow-green color of seedlings caused by photothermal stress. We studied landraces collected in the mountain regions of Dagestan (Russia), as well as Mona, Mari, Kinai 5 varieties (genotype *eam8eam8*), Belogorskiy (*Eam8Eam8*) and early variety Bankuti Korai. Genomic DNA was isolated from barley samples with yellow seedlings, which have been identified by phenotypic screening. A fragment of 580 base pairs located between the positions 1302 and 1881 of the gene complete nucleotide sequence has been amplified, cloned and sequenced. A single nucleotide deletion in the sequence of the barley landraces k-14891 was found. This mutation leads to a frame shift and altered protein synthesis and possibly induces insensitivity to photoperiod and early maturation. Similar changes were observed in the photoperiod-insensitive mutant mat-a.11 (genotype *eam8eam8*), obtained in 1955 under treatment by gamma rays of the variety Bonus.

The study was supported by RFBR (project 12-04-96503).

# THE DETERMINATION OF MORPHOLOGICAL AND AGRONOMIC PROPERTIES OF SOME CULTURE AND WILD PEA GENOTYPES IN K.MARAŞ CONDITIONS

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This study was carried out to determine some morphological and agronomic traits differences among 4 peas genotypes obtained from the natural vegetation and culture, and in order to compare the genotypes in the view of examined of the characteristic, Kahramanmaras Sutcu İmam University, Faculty of Agriculture, Department of Field Crops in the years of 2010-2011 and 2011-2012. The study was carried out according to the randomized complete block design with four replications for two years between genotypes which were determined the morphological and agronomic differences. According to the results of the two-year combined the analysis of variance, genotypes between to the number of days to flowering, plant height, number of pods per plant, 1000-grain weight, grain yield per decare, in spite of the average rate was a statistically significant difference in terms of features, the genotypes of dry straw yield property the difference was statistically insignificant. It was determined that the wild pea genotypes could be used in the studies of development of breeding appropriate in the Kahramanmaras ecology of the food pea types.

**Key Words:** Pisum sativum, wild pea, breeding, genotypes, grain yield, yield component

# THE ENVIRONMENTAL AND GENETIC MONITORING FOR CONSERVATION OF PLANT DIVERSITY

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To develop scientifically grounded programs for the conservation of plant diversity, it is important to carry out the monitoring of plants and the estimation of their resistance capability to the environment. Thus, it is necessary to use research methods revealing mechanism of genetic adaptation of plant species to various environmental conditions. In this connection we have developed an analyzing method allowing a complex estimation of resistance level of cultivated and wild species to different environments. The monitoring carried out at the sub cellular level includes the research of cell genome and metabolites characterizing its resistance and survival capability. A major indicator including the complex information about the resistance of plant organism is the level of spontaneous cell mutability. Therefore, the frequency and characteristics of chromosomal aberrations in the root meristem of seedlings is taken as a basis of the researches. The condition of the cell metabolism inevitably influences on the genome mutability. As a key indicator of the metabolism reflecting the changes of environment, the intensity of free radical - malonic dialdehyde – was studied in the leaves. At last, the activity of antioxidant enzyme of peroxidase enables knowing the level of intracellular protoplasm protection against various xenobiotics and harmful factors of the environment. Using the complex analyzing method, we investigated some cultivated and wild species of the cereals and leguminous plants originated from environmentally different areas of Azerbaijan. We found out species that demonstrated their low resistance capabilities in specific environments. The analyzing method suggested by us for an estimation of plant resistance can be used for forecasting some plant species to be endangered, and therefore, we can recommend it *in situ* and *ex situ*.

# THE GENE POOL OF SORGHUM CROPS FOR BREEDING FOR GRAIN QUALITY AND PRODUCTIVITY

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The gene pool of sorghum crops studied extensively for greater effectiveness in conducting research on the breeding of sorghum . A more complete biochemical analysis at all stages of selection , from nursery and primary source material is selected feed and food areas with the given parameters of grain quality : high protein, starch ( sugar) , which combines resistance to cold , drought , productivity , and other valuable features . As a result, research on sorghum crops of 200 numbers for economically valuable attributes stood out especially for the active growth of the initial 47 rooms , they differ tall, long leaves and panicles , thick and succulent stem, high yield seeds, tillering . Collection sorghum crops is described by 7-12 parameters. Allocated for use in the selection of such samples as K -909 , K -40 , K -279 , K- 201, AZ- 63 , AK- 33, 175 Saharnoe , Donskoe 8 , ES -102 , K- 87, AZ- 341 , K -42 , K- 1826 , K- 08192 , K -1772, K-266 and K- 434, characterized by tall plants from 180 to 450 cm , the thickness of stem weight from 1.0 to 2.0 cm and a length of panicles 14 to 48 cm , length of leaves from 55 to 97 cm, the richness of stem weight , resistance to disease , drought and other valuable features. According to the content of protein in the grain of food allocated rooms 5 rooms, the sugar content in the juice of the stems (18 - 20%) on sugar sorghum - 2 rooms. By complex qualitative characteristics spun samples K-12, K-84, K-02, K-2315, K-176, K-63 56 K-8511, K-9081, K-2517, K-684, K-85031 , K-1678, K-214, K-1305, they also are resistant to disease, juiciness cormophyte supply and other basic features.

# THE NEW IN THE WHEAT (TRITICUM L.) GENE-POOL OF NAKHCHIVAN AUTONOMOUS REPUBLIC

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As a result of the both expeditions, 136 samples of durum wheat, compactum and interspecific hybrids and 492 genotypes of bread wheat were collected; a unknown before varieties and forms were revealed. From mixed cultivars and populations of species, 27 samples of durum wheat, 76 diverse, mostly rare varieties and forms of *T. compactum* Host. *subconvar. rigidicompactum* A. Filat. et Dorof., *subconvar. roshanum* (Korzh.) A.Filat et Dorof. and *convar. compactum* as also interspecific hybrids were collected. In the fields of Babek district, 165 samples mainly of Asian subspecies of bread wheat (*subsp. rigidum (speltiforme), convar. semirigidum*) and spelt (*subsp. kuckuckianum* Gökg.) were collected. In the Sharur district, 47 samples were collected, in the Sederek distr. - 26, in the Gulfa distr. - 135, in the Shahbuz distr. - 151 samples. A net fields of durum and other tetraploid wheat species not meet on the territory of the AR. As an admixtures, in wheat crops were collected varieties of wheat properly durum - *subconvar. durum: var. hordeiforme, var. leucurum, var. boeufii* etc.; durum wheat with compact ear - *subconvar. durocompactum: var. pseudohordeiforme, var. pseudomurciense, var. pseudoalexandrinum, var. pseudoalboprovinciale, var. serengei, var. aydinense* etc., and spontaneous interspecific hybrids between bread and durum wheats. Appearing spontaneous hybrids should be identified and studied as valuable forms adapted to local conditions. In order to collect them in the industrial crops and on private plots, it is need to organize immediately the expeditions also in other regions of Azerbaijan. The spelt samples of Azerbaijan origin stored in the Genebank of the Institute and in the collection of VIR, refer to the Asian subspecies. Although more than 25 varieties are collected from the territory of Azerbaijan, only 6 samples there are in the VIR collection at the present time, and they are similar by morphological and agronomic characteristics. However, it is a sample of Azerbaijan origin k-45366 which was characterized by the maximum value of the plant height - 160 cm. The collected material of tetra- and hexaploid species is planted on Gobustan Zonal Experimental Station of the Azerbaijan Research Institute for Crop Husbandry in conditions of unsecured dry land. The main objective is creation of the original breeding material of durum and bread wheat's, of a trait collections and genetic sources in the directions of winter- and drought resistance, high yield and grain quality. We express our gratitude to the Leadership of the Science Development Fund under the President of Azerbaijan, Leadership and Staff of Genetic Resources Institute of the National Academy of Sciences of Azerbaijan (NASA) and Institute of Biological Resources of Nakhchivan Department of NASA, professionals and farmers of Nakhchivan AR for support in organizing and carrying out the expeditions.

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# THE STUDY GENETIC VARIATION OF BREAD WHEAT

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Wheat (Triticum aestivum L.) is the largest grain crop in the world. Selection for grain yield has been an important focus of wheat breeding programs for decades but in recent years it looks that as a result of introduction of commercial and breeder varieties diversity of wheat varieties has been reduced. This study was conducted to evaluate genetic diversity of bread wheat genotypes using analyses on grain yield. Two hundred seventy nine genotypes were planted in a randomized complete block design with three replications on growing season of 2011-2012. Analysis of variance showed significant differences among genotypes for grain yield. Cluster analysis was used to assess the pattern of variation and to group the genotypes. Cluster analysis based on squared Euclidean distance and ward's method, categorized the cultivars into five groups. The highest genetic distance was observed between Ghods cultivar and line number186.Such differences in genetic can be applied as a new source of variation in other breeding programs for wheat improvement.

**Keywords**: Bread wheat, Grain yield, Genetic variation, Cluster analysis

# THE STUDY OF ADAPTIVE CAPABILITY OF THE VARIOUS RYE POPULATIONS FROM AZERBAIJAN

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The research made with using a complex technique (the frequency analysis of chromosomal aberration, the intensity of peroxide reactions, and the activity of protective enzymes) has estimated the adaptive potential of 4 populations of the *Secale segetale* rye from different areas of Azerbaijan (Lerik, Sheki, Nakhichevan and Absheron). All the populations demonstrated their high viability and resistance to a complex influence of the environment. The data of cytogenetic analysis of the seeds revealed their resistance of the cell chromosomes. The study of the intensity of peroxide reactions, made with calculating the amount of malonic dialdehyde and the activity of antioxidant peroxidase enzyme in the leaves of all the populations, allowed of drawing a conclusion that this rye species possesses the sustainable positive adaptable capability. We suggested that this capability was likely to enable the rye populations wide spreading in the highly environmentally differenced areas. On the basis of the final data, we may consider the Nakhichevan rye population to be most resistant to the environment. The Sheki population was characterized with the highest frequency of chromosomal aberrations and the high activity of peroxidase. The direct correlation of the data may be explained with the possible activation of protective enzymatic mechanism of peroxidase during the increase of the chromosomal apparatus instability in the plant cells.

# VIABILITY TESTING FOR MRIZP GENE BANK ACCESSIONS OF LOCAL MAIZE (ZEA MAYS L.) LANDRACES

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Large number of accessions, usually stored in gene banks, makes the regeneration very expensive. As the viability of seeds stored in the genebank decrease slowly during storage, decision on identifying the accessions and their necessary regeneration is based on continuous monitoring both for viability and seed quantity in order to avoid excessive deterioration or reduction in seed quantity. In 2013, monitoring for seed viability was conducted on 703 local maize landraces from Maize Research Institute Zemun Polje gene bank, previously regenerated 20 to 25 years ago. According to the results of germination test under laboratory conditions (BP, 20-30°C, ISTA Rules), conducted in 2001 and 2013, 49 local landraces were chosen for germination testing under field conditions. Due to significant differences between the germination test results obtained under laboratory and field conditions, additional germination test in soil, as a growing media, with extended period of germination monitoring (up to half of the prescribed period for maize), was applied. Although the germination test results obtained under laboratory conditions, using soil as growing media, revealed higher rate of similarity to the results obtained under field conditions, significant differences in germination rate still remained for a certain number of investigated genotypes. Dealing with the old seed and heterogeneous genotypes by their genetic composition (open pollinated varieties), we assumed that more precise and relevant viability results for MRI Gene bank accessions could be achieved by modification of ISTA Rules (substrate, duration of testing, criteria of seedling abnormalities, etc.).

**Key words:** gene bank, maize landraces, viability

# APPLICATION OF MOLECULAR METHODS AS A MARKER IN BIOTECHNOLOGY IN BIOREMEDIATION STUDIES

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In the present study, the biodegradation capacities of various bacteria towards petroleum-hydrocarbons were determined in laboratory conditions. The purpose was to isolate and characterize petroleum-degrading bacteria from contaminated soil in refinery of Arzew in Algeria. A collection of 15 bacteria was obtained by enrichment cultivation from oils-contaminated soil and an indigenous microbial consortium was developed by assemble four species of bacteria which could degrade different fractions of petroleum hydrocarbons. 16S rDNA gene was used to identify isolates of selected consortium. Sequences were then compared to those present in the Genbank database at the infobiogen website using BLAST (Basic Local Alignment Search Tool). A phylogenetic tree was constructed using MEGA 0.5 software by the neighbor-joining method. The sequences obtained were deposited in banks of (National Center for Biotechnology Information databases) NCBI / DDBJ / EMBL / GenBank with accession numbers defined and oils biodegradability was analyzed by Thin Layer Chromatography with Flame Iozination Detection that performs quantitative compositional analysis of oil samples. The Iatroscan TLC/FID system measure the relative percentages of the four major fractions of petroleum; saturate aromatic, resin and asphaltene. The results indicated the performance of isolated designed consortium comprising genera of *Pseudomonas, Shewanella, Enterobacter and Serratia* to use the hydrocarbons as sole source of carbon and biodegradation was defined by an initial rapid decrease in the compositional saturate and aromatic fractions to 51.77 and 27.77 % respectively, coinciding with an increase in the asphaltene fraction. The resin content remained relatively constant throughout the project. The selected bacterial consortium looks promising for its application in bioremediation technologies. *alkB, nahAc* genes were positively detected in *Pseudomonas* sp. by degenerate polymerase chain reaction (PCR). This functional gene can be used as a marker in biotechnology to assess the catabolic potential of bacteria in bioremediation.

**Keywords**: Bioremediation, Petroleum-hydrocarbons, Microbial consortium, 16S rDNA, Pseudomonas, TLC/FID, *alkB* genes.

# GENETIC DIVERSITY IN SOME WHEAT AND BARLEY GENOTYPES AS REVEALED BY AMPLIFIED FRAGMENT LENGTH POLYMORPHISM (AFLP) MARKERS

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Genetic diversity among 8 wheat and 13 barley genotypes consisting of landraces, improved varieties and mutant lines was estimated utilizing DNA marker based Amplified Fragment Length Polymorphism (AFLP). Using a set of 8 AFLP primer-pairs for barley and 7 for wheat a total of 2983 data points for barley and 1440 for wheat were scored over all of the genotypes. The scored data points corresponded to a total of 363 AFLP markers for barley and 265 for wheat of which 91,3 and 78,1 markers were polymorphic with a percentage of 33% and 37 % for barley and wheat, respectively. The average genetic diversity was 0,18 and 0,2 across all barley and wheat genotypes, respectively. The dissimilarity matrices were then used to cluster the data using the Unweighted Pair Group Method with an arithmetic average (UPGMA) algorithm. The resulting phenograms indicated a clear distinction between the *Triticum durum* and *Tritium aestivum* on one side and from landraces and improved varieties within durum genotypes. In barley, two mutant genotypes where separated in two clusters and the other two with their parent were grouped in a sub cluster. The other genotypes were sub grouped in four sub-clusters in which the Jordanian cultivated landraces (Rum and Acsad176) grouped in one, the two Jordanian promising genotypes Roho and SLB6 in the second, the two Syrian landraces in the third and the two Syrian cultivars in the fourth sub-cluster. The phenetic clusters of genotypes were supported with high bootstrap values, indicating the reliability and stability of the AFLP data used for diversity analysis. These results indicated that AFLP system is a very effective and suitable marker for the assessment of genetic diversity among wheat as well as barley genotypes and should be used in exploration in breeding programs.

**Key words:** Wheat, barely, genetic diversity, AFLP

# IMPACT OF KASIB PROJECT GENETIC STOCK INTO SOLUTION OF PROBLEMS OF SPRING BREAD WHEAT BREEDING IN ALTAI TERRITORY

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Altai territory is one of the largest grain producers in Russia. Yearly grain production makes up 4 – 5 million t. Share of grain for human nutrition is around 2,5 million t that is 27-30% of total in Siberia. Spring bread wheat of Altai territory occupies an area of 2,0 – 2,5 million ha. At this the wheat is cultivated in different soil and climatic zones characterized by wide variation of precipitation amount and sums of effective temperatures for the growing period. For the recent 12 years the average wheat yield in Altai territory was fluctuating and varied from 0,7 till 1,57 t/ha. Increased and stable yield of the crop from breeding point of view can be reached through the development of a complex of varieties adapted to a spectrum of agroecological factors limiting yield in a particular zone. An international program KASIB plays essential part in solving above-mentioned task. First of all it is a source of enrichment of local genepool and serves for the development of promising hybrid and line stock. In Altai Research Institute of Agriculture 392 bread wheat entries have been studied for the period of functioning of the program (2000-2012). Material from KASIB nurseries was used in crosses numbered 307. At this varieties and lines by Russian participants were used in 205 crosses (66,8%) and by Kazakhstan participants in 102 crosses (33,2%). Most competitive breeding material after a complex of valuable traits was obtained with entries from Siberian Research Institute of Agriculture, Omsk Agrarian University, Scientific and Production Center of Grain Industry (Shortandy) and Pavlodar Research Institute of Agriculture. In competitive yield trail top lines from crosses with KASIB entries exceed a check variety by 0,19 – 0,52 t/ha averaged for 2 years. The study of promising lines will be continued.

# URGENCY OF CARRYING OUT OF GENETIC CERTIFICATION OF VARİETİES OF THE GENOFUND OF GRAIN CROPS OF AZERBAIJAN

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During the last 8 years at varieties of a genofund of wheat and 3, at maize of local selection and introduction and genotypes widely used in republic genetic certification to the most various qualitative and quantitative traits representing economic resources that is the high guarantor of preservation of a biodiversity of each culture within a concrete subspecies on the one hand, is spent and can expediently be used as parental forms in practical selection on the other hand. By present time to the majority of varieties of domestic selection of common and durum wheats the genetic passport to such trait, as colouring of an ear, grains and awn, ear and grain colour, awnless-awnness, hairy glume an ear, growth habit, reaction to a natural short photoperiodic day, the duration vegetative period, a wax of an ear, a stem and least, height of a plant, resistance to fungoid illnesses. The genofund of varieties of the maize, consisting of 490 genotypes was investigated on plant height, grain colouring, duration of the vegetative period, number of ears on a plant, productivity, to resistance illnesses etc. The further certification of varieties and hybrids maize on another economic - to the important traits to that our future researches are directed is planned.

# MORPHOLOGICAL DIVERSITY OF ACHA (FONIO) (*Digitariaexilis* and *Digitariaiburua*) GERMPLASM AND EVALUATION OF GENETIC VARIATIONS USING RAPD-PCR TECHNIQUES IN NIGERIA

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This study evaluated thirty-five Acha or Fonio (*Digitaria*spp) accessions for morphological and genetic characterization in order to unlock genetic potential of each variety for breeding purposes. The accessions were planted in plots measuring 2m by 3m, and replicated three times in a randomized complete block design. Data were collected using a $1m^2$ quadrant across plots in determining some morpho-agronomic parameters. RAPD protocol was used in the molecular classification of the accessions. Data obtained was analyzed statistically using ANOVA, correlation and cluster analysis. Morphological variations and growth performance of the accessions were observed to have an influence on grain yield. Jakah variety had the highest yield of 176.24kg/plot which differed significantly ($p<0.05$) with other accessions while morphological features of peduncle length, internodes length, spikelet per panicle number and plant height were observed to have positive correlation ($P<0.05$) with grain yield. Also negative correlation was observed ($P<0.05$) between days to 50% flowering and grain yield, portraying an inverse relationship between the two. On the other hand, morphology and molecular cluster analysis gave different number of clusters which was indicative of the need to use the two techniques for classification of fonio in Nigeria. Therefore the study has established the existence of diversity in morphological/ traits of Acha accessions. Also, the study has also confirmed the use of RAPD-PCR in unraveling the phylo-genetic diversity of Acha accession.

***Keywords:*** accessions, breeding, genetic diversity, phylogeny, morpho-agronomic

# PLANT GENETIC RESOURCES ARE IMPORTANT FOR FOOD SECURITY IN CENTRAL ASIA AND THE CAUCASUS

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Plant Genetic Resources (PGR) is an area of considerable importance in Central Asia and the Caucasus since it is a part of the West Middle Asian Center of origin and diversity for many of the globally important agricultural crops. Among those crop gene pools that originated or were domesticated here are cereals, food legumes, forage legumes, vegetables, fruit trees, fiber and oil crops and many medicinal and aromatic plants. Currently, the countries of CAC region have 165,120 accessions of different agricultural crops. Cereals occupy the first place with 76,347 accessions (46.24%), followed by industrial crops (13.59%), forage crops (12.84%), vegetables (8.41%), and horticultural crops (8.34%). Other crops taken together compose 6.82 %. This gene pool is an important base for the development of new varieties of crops resistant to biotic and abiotic stress. The value of the PGR is continuously increasing due to global changes of climate, desertification, and genetic erosion or extinction of PGR in the context of the destruction of their habitats leading to immediate negative impact. Therefore, an important task of scientists, policy makers, private sector and other players in the region is not only conserving, but also promoting sustainable use of the existing PGR. The presentation will review recent collaborative activities undertaken in this area by ICARDA and other international agricultural research centers.

# ASSESSMENT OF GENETIC VARIATION OF *SALVIA SCLAREA* L. BY RAPD

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*Salvia* is an important and the largest genus of the *Lamiaceae*. *Salvia sclarea* L. are used as spices and flavoring agents in perfumery and cosmetics and have economical value. The essential oil composition is highly influenced by genetic and environmental factors. For these reasons, diversity analysis could provide useful information for genetic improvement. Selection assisted by molecular markers is useful tool for germplasm characterization and evaluation of genetic polymorphism in association with the interest characters. Random Amplified Polymorphic DNA (RAPD) technique is quick, easy and requires no prior sequence information. This procedure detects nucleotide sequence polymorphism using a single primer of arbitrary nucleotide sequence. The genetic variation for 13 genetic groups ($F_1$ and parental forms) of *Salvia sclarea* was evaluated by RAPD-PCR method. Detected polymorphism level represents high genetic distance at inter-species level and introduces the RAPD as efficient marker for genetic relatedness assessment in *Salvia*. The DNA profiles for 23 primers were scored visually from gel electrophoresis. Clear and reproducible amplified bands were chosen in the analyses. The data obtained by scoring the profiles individually with different primers as well as collectively were subjected to the calculation of similarity matrix using Jaccard's coefficients. The similarity values were used for cluster analyses. The most amplification fragments were obtained with *OPG10, UBC250, OPB03, A2, OPB01, OPG05, OPH15, A3.* Primers *OPG10, OPA2* and *UBC250* revealed amplification products for most genotypes. The results indicate the presence of genetic variability among different genotypes of *Salvia sclarea*.

# DEVELOPMENT OF LOCAL POTATO VARIETIES WITH BREEDING METHOD

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Numerous foreign originated potato varieties are produced in Turkey. However any national and common potato variety does not exist. In this research, it is aimed to develop local potato varieties using true potato seeds (TPS) which were obtained from 21 combination that comes from breeding materials in Potato Research Institute in 2007. This research was carried out in green houses (tulle and glass covered) and the experimental fields during 2007-2012 by Potato Research Institute. This research was founded by TÜBİTAK project (Development of National Seed Potato Production System) and then it was supported financially by The Ministry of Food Agriculture and Livestock (MFAL). In this research, developing local potato variety studies was initiated using 19.841 true potato seeds belongs 21 combination that comes from breeding materials in 2007 (Agria X Anais, Agria X Hermes, Agria X Soleia, Panda X Anais, Panda X Hermes, Panda X Soleia, Provento X Anais, Provento X Hermes, Provento X Soleia, Van Gogh X Anais, Van Gogh X Soleia, Granola X Anais, Granola X Hermes, Granola X Solenia, L. Rosetta X Hermes, Marabel X Hermes, Agria X Van Gogh, Provento X Hermes, Agria X Granola, Anais X Granola). Selection of 9.935 single tuber clones were done according to some criterias that are tuber shape, eye depth, stolon length, appearance of plant and tubers etc. and these selected clones are come from the plants which belongs true potato seeds planted in green houses. Selected clones were planted as single tuber to six tuber in 2008 (1635 tubers), six tubers to twenty tubers in 2009 (333 tubers), twenty tubers to one hundred and twenty tubers in 2010 (170 tubers). Selection studies were continued with 61 clones come from one hundred and twenty tuber planting for yield experiment. 61 clones which were selected in previous year in Niğde, were planted with standard varieties in yield experiments by divided in two groups in institution fields. Clones used in yield experiments were observed during vegetation period in terms of plant development (number of main stem, plant length, growing type, blooming status, maturation period). Tuber per plant, average tuber weight, yield, distribution of tuber size of potato clones were measured and quality analysis have been done during the harvest. Promising clones varieties were reproduced by tissue culture. As a result, promising clones which will be selected according to different located yield experiments, will be submitted for registration as candidate local varieties.

**Keywords:** Potato, *Solanum Tuberosum,* breeding, selection,

# TURKEY VEGETABLE GENETIC RESOURCES STUDIES

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Turkey’s local vegetable varieties and populations collection and conservation studies have been carried out as a “ Vegetable Genetic Resources Research Project” since 1976. These studies consist of collection of materials, multiplication, regeneretion and characterization of materials.In addition, during the these studies, materials have a desirable trait have been use in breeding studies and to obtain new populations consider to economic importance. Nowadays, in the collection programs have come across commercial varieties particularly tomato and pepper species. Melon and okra local varieties have been grown by farmers, also used protected their seeds. Local okra and melon seeds are produced by farmers. Becauce of this reason, different local consumer preference and custom. The second reason is easy to seed production and conservation.During the regeneration , multiplication and characterization studies of vegetable genetic resources have a good agronomic traits materials are used in the plant breeding programs. Depends on the material traits are used to selection methods furthermore in order to use their traits making cross. In the institute, registred melon, tomato, pepper, eggplant and okra have developed by as a result of these studies. Especially melon variety Kırkağaç 637 are grown in many region in Turkey. The variety Kırkağaç 637 which was developed by breeding of Kırkağaç population.

# EVALUATION OF WHEAT GENETIC RESOURCES IN AZERBAIJAN

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The region of Central Asia is rich in wheat genetic resources. The diverse agro-climatic conditions shelter wide variations of different plant species including wheat. Several national and international collection missions were organized in Azerbaijan that enriched Azerbaijan plant gene bank over years. This study was conducted to determine genetic variations for important agronomic traits among 48 randomly chosen bread wheat accessions from the gene bank of the Azerbaijan Genetic Resources Institute. The accessions along with two entries of a local check were evaluated at two sites in two years in Azerbaijan. One of the two sites represented wide spread saline soils in Azerbaijan. The field experiments were conducted in a replicated Alpha design with two replicates. Data were recorded on several morpho-physiological traits. The wheat genotypes showed array of variations for plant height (PHT), peduncle length (PED), peduncle as percent of PHT (PED_PHT), spike number per plant (SPNPP), spike length (SPKL), spikelet number (SPKLN), kernel per spikelet (KPSPKLT), kernel per spike (KPS), grain weight per spike (GWPS), grain weight per plant (GWPP) and 1000-kernel weight (TKW). There was a significant effect of year on all traits. The effect of location and year × location interactions were significant for all traits except SPNPP, SPLTN and HKW. Genotype × year interaction was significant for all traits except PEDL, PPPHT, SPNPP and SPLN. Genotype × location and second order interactions were non-significant for all traits. Principle component analysis revealed continuous variations; however there were six different groups of genotypes. Several superior genotypes were identified for medium saline soils used in the study. The study provides new information on important traits in bread wheat in a set of previously unexplored bread wheat collections from Azerbaijan, which could be valuable for national and international programs on germplasm improvement.

# EVALUATION OF WHEAT GERMPLASM FOR RESISTANCE TO STEM RUST

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As it is known, Georgia is a country of origin of wheat. Stem rust had represented a major threat to wheat production in the world including Georgia. Breeding for resistance to rusts is a major emphasis for most wheat improvement programs. The wild and domestic relatives of wheat are important sources for disease resistance. Therefore, the objective of this study was identification of resistant genotypes to Georgian races of stem rust. A collection of fifty wheat accessions including twelve endemic wheat species and subspecies, ten domestic varieties, seven advanced lines and twenty one introduced entries from different international nurseries was evaluated under the artificial infection of stem rust in the field conditions. The wheat germplasm was screened using the predominant stem rust races mixture of Georgia. Resistance was detected in 48.0% of the tested entries. The endemic species: *Triticum monoccoccum (Var.laetissimum Korn), Triticum timopheevi (Var.tipicum Zhuk-var.viticulosum Zhuk), Triticum georgicum (Var.chvamlicum Supat), Triticum dicoccum (Var.farrum), Triticum ibericum Men(Var. fuliginosum Zhuk), Triticum ibericum Men (Var.stramineum Zhuk), Triticum macha Dek et Men (Var.dekaprelevichi Dorof), Triticum macha Dek et Men (Var.colchicum ), Triticum macha Dek et Men (Var.palaeoimereticum), Triticum spelta (Var.icterinum Al.)* and old Georgian varieties: Khulugo, Tetri ipkli were resistant and moderate resistant to stem rust. Also, some introduced accessions (DBDI-2WWSRRN-17,Dorade/altay2000/4Bez/Nad//LZM,(es85.24)3/F900k-aalr-res5,Haurani/aegtaushi/ cham6-/mz/cno67/3Ifn/4/ant/5/Attila-19FAWWON, Sunco/pastor-19FAWWON, SRMA/ tui// babax/ 3JGR-11LR-Res-132, BTZ-18FAWWON-IRR-149, 18FAWWON-SA-49) showed moderate resistance; the remaining 52% of entries demonstrated moderate susceptible reaction. The results obtained from present study provided useful information for national and international breeding programs.

# FOLIAGE AND TUBER STEROID GLYKOALKALOD CONTENTS OF WILD AND CULTIVATED *SOLANUM* SPECIES

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Types of the family *Solanaceae* produce a wide spectrum of steroid glycoalkaloids. The two main potato steroid glycoalkaloids are α-solanine and α-chaconine, which represent approximately 90-95% of total glycoalkaloids. Aim of this research was to determinate steroid glykoalkalod contents of 23 wild and five cultivated *Solanum* species. The research included species: *Solanum acaule 00030, S. andigenum 00108, S. berthaultii, 00260, S. bulbocastanum PIS 06-17, S. chacoense 00230, S. demissum 00250, S. fendleri 00275, S. goniocalyx 00109, S. gourlai 00043, S. guerreroense 00280, S. incamayoense 00047, S. leptophyes 00048, S. microdontum 00049, S. mochiquense 00050, S. phureja 00308, S. pinnatisectum 00051, S. polyadenium 00290, S. polytrichon 00053, S. sparsipillum 00071, S. spegazzini 00060, S. stenotomum 00212, S. stoloniferum 00295, S. sucrense 00062, S. vernei 00234, S. verrucosum 00299, S. x chaucha 00134 and S. yungasense 00070.* By 0.25g freeze-dried grinded foliages and unpeeled tubers were used respectively. Samples were purified on Solid Phase Extraction column and analyzed by HPLC-MS/MS. The highest concentration of foliar steroid glycoalkaloids contents of dry weight was found in the *S. yungasense 00070* with 14870 mg/kg and lowest to the *S. pinnatisectum 00051* with 3.4 mg/kg. Whereas, the highest concentration of tuber steroid glycoalkaloids contents of dry weight was observed to the *S. vernei 00234* with 16825.0 mg/kg and lowest to the *S. pinnatisectum 00051* with 19.1 mg/kg. There was not found any correlation (r=0.07) between foliage and tubers SGA contents of dry weight within researched species, but steroid glycoalkaloids contents between species were statistically significant (p<0.01).

# GENETIC RESOURCES OF CITRUS IN GEORGIA

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According to the historical sources introduction of citrus plants in Georgia relates to the distant past. However, the first attempts of citrus rehabilitation in Georgia began in 1840s. The favorable soil-climatic conditions of western Georgia and the biological peculiarities of citrus plants provided the foundation for creating a rich collection in the country that in one time played an important role in the industrial development of the field as well as raising the standard of living among the population of the country. At present the citrus collection represented in Georgia counts 11 species, about 100 varieties**,** about **200** hybrids, perspective clones and forms of various species: *Citrus limon (L)Burm.f (16 varieties), Citrus Sinensis (L) Osb (17 varieties), Citrus Reticulata Blanco (6 varieties), C unshiu Marcow (27), Citrus deliciosa Ten (2 varieties), Citrus nobilis lour (6), Citrus Leiocarpa (2 varieties), Citrus Clementina hort. Ex Tanaka (2 varieties), Citrus Lumia Risso (2 varieties) Citrus Grandis Osb (5 varieties), Citrus Paradisi Macf (9 varieties), Citrus Medica L (4 varieties), Citrus Aurantium L (6 varieties), Citrus Aurantifolia (4 varieties), Citrus Wilsonii Tan (1 varieties), Citrus Ichangensis Svingle (2 varieties), Citrus junos. sieb (3 varieties)***.** In 1994 Georgia joined the Convention „On Biological Diversity“ and took international responsibility to protect and reserve for the future generations the unique gene pool of the country that represents one of the significant constituent parts of the world heritage.

# MOLECULAR AND PHYSIOLOGICAL CLASSIFICATION OF DIVERGENT CAMELINA SPP. GERMPLASM

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Camelina is a promising energy crop for the biodiesel industry, especially for production of airplane fuel. In addition, its distinctive fatty acid profile and high protein contents satisfy the nutraceutical and animal feed uses. About 250 accessionswere collected from all of world and evaluated during 2012 and 2013. Oil contents and fatty acid profile from harvested seed was determined by GC-MS. Genetic diversity was assessed by SSR (simple sequence repeat) markers. The sixteen SSR markers were applied to determine the genetic diversity among the accessions. The distinctive variation of oil content and fatty acid profiles observed among the accessions. Detail information about above observations will be presented and will be used camelina breeding program.

# *CHARACTERIZATION OF LOCAL OKRA (Abelmoschus esculentus) POPULATIONS*

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In this study, morphological characterization was carried out on 38 different populations of okra, conserved in Aegean Agricultural Research Institute National Gene Bank, collected from different regions of Turkey and an okra variety. Characterization studies were made by using the IPGRI descriptor list published for okra. All populations were characterized in terms of 19 morphological traits. Similarity and differences of among okra accessions were obtained.

***Keywords:*** Okra (*Abelmoschus esculentus*), morphological characterization, National Gene Bank

# CONFESSED OF MORPHOLOGICAL VARIABILITY AT DOMESTIC DRY BEAN (*PHASEOLUS VULGARIS* L.) POPULATIONS COLLECTED FROM MIDDLE BLACK SEA REGION

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Different geographical structure and diversity of climatic structure in the Middle Black Sea Region has enriched the biodiversity of dry beans, morphological characteristics at the local bean populations have allowed the collection of different populations of dry bean. In this study includes to the declaration morphological characteristics of 54 local beans variability's that at the provinces 15 districts and 41 village and Samsun, Tokat, Amasya and Çorum in the Middle Black Sea Region. Definition of collected local beans populations was made according to the criteria of IBPGR and the EU CPVO. In order to determine of the morphological varieties, characterized bean populations were established according to Cluster analysis. 35 features in cluster analysis were taken into account, at the sub-samples of beans were collected in 14 groups. 14 groups analyzed; Group N with the 12 sub-sample has been more sub-samples, Groups A, J, K and M has been found 2 of each sub-sample that the groups having at least subsamples. Sub-samples that as a result of cluster analysis of both qualitative as well as quantitative variation in the definitions of properties carried, can be taken into the variety development and breeding works have been revealed.

**Keywords:** Middle Black Sea Region, biodiversity, morphological variability, cluster, breeding

# DETERMINATION OF MORPHOLOGICAL VARIABILITY OF LOCAL PEA GENOTYPES

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This study was conducted to determine morphological variability of local pea genotypes collected from different parts of Turkey. Experiment material obtained from Plant Gene Bank of Aegean Agricultural Research Institute and collected from five districts of Black Sea Region consisted of 40 numbers pea genotypes that divided according to unit color and shape. These materials were planted in the trial ground of Agricultural Faculty of Ondokuz Mayıs University during the 2004-2005 rearing period and 45 different features were identified. 13 of these features are quantitative, 32 of them are quantitative and morphological identification list determined by UPOV and EU-CPVO was taken into account. Principal Component Analysis (PCA) was done in order to determine morphological variability of genotypes. 13 main component axes were obtained by the analysis of ABA. These components represent 85.61 % of total genotypes variation. Eigen value of the first 13 main components change between 1.12-7.60 and 41.97 % of the variation are met. Properties of seed coat color and leaf color in the varieties with the anthocyanin at the second main component axis and characteristics of dry leaf weight, dry stem weight, dry leaf / dry stem ratio at the third main component have larger values than 0.3. Because of the eigen value of the genotypes is greater than 1, dendrogram was created by using Cluster analysis. Clustering of genotypes in 11 groups was identified as a result of Cluster analysis. While Group A found to be having the most genotypes with 9 numbers, Group I determined as being the least genotypes with only one number in these 11 groups. Plant height, number of branch and pod, pod length, seed number in the pod, grain yield, 100 seed weight, crude protein content of the genotypes in the study were determined varied between 57.5-173.2 cm, 1.4-7.8 unit/plant, 10.6-43.0 unit/plant, 4.9-9.9 cm, 4.0-7.6 units, 5.3-30.0 g/plant, 10.3- 36.4 g, 16.3-23.6 %, respectively. This change range of the investigated features has been revealed the usability of the genotypes in the studies of variety development and breeding programs.

**Key words:** Local pea, morphological variability, cluster, dendrogram, PCA, eigen

# GENETIC MONITORING OF CROP WILD RELATIVES: THEORY, APPROACH AND VALUE FOR CONSERVATION

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Genetic monitoring is the quantification of temporal changes in population, genetics and dynamics metrics. It constitutes a method with a prognostic value and an important tool for the protection of biodiversity. The monitoring of the genetic resource has been recognized in several international agreements and documents, but has not been thus far comprehensively implemented in nature and crop wild relatives (CWR) in particular. Methods for the selection and prioritization of species and monitoring populations within species are presented. The geneecological approach is proposed as the background theoretical framework for monitoring. The proposed indicators are gene flow-mating system, genetic drift and natural selection. Genetic verifiers are proposed for the assessment of the two former and demographic verifiers for the latter. Minimum sample sizes, critical levels of differences among parameters and costs for temporal evaluation are discussed, particularly in the contrast between markering and phenotyping. The benefits of the immediate application of genetic monitoring are highlighted. Genomic monitoring can be directly applied in the temporal evaluation of any CWR population and especially in species where dynamic gene conservation schemes have been already established. Moreover, it can have a wider and more important application as an early warning system in marginal and vulnerable CWR populations that are highlighted in climatic change scenarios.

# MOLECULAR-GENETIC ANALYSIS of UKRAINIAN BREAD WHEAT GENE POOL

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Molecular-genetic polymorphism of Ukrainian bread wheat varieties from different periods of time and centers have been investigated by using SSR, STS and allele-specific markers. SSR-analysis has revealed the changes at the level of genetic polymorphism in Ukrainian wheat germplasm during last hundred years of breeding process. We have detected dramatic changes in distribution of alleles frequency that could be partially explained by extensive involving of the genotype Bezostaya 1 and varieties with dwarfing genes from CYMMIT and Bulgaria in breeding programs. The crossing with Bezostaya 1 permit to spread the predominant alleles – *Ppd-D1a* photoperiod insensitive and *Rht-8c* dwarfing genes in modern winter wheat genetic pool. There have been shown that the dwarfing genes *Rht-B1b, Rht-D1b* are distributed with the high frequency among modern winter varieties especially in the South region of Ukraine. The translocations 1RS/1BL and 1RS/1AL, that bring some agronomic advantages, were detected with the help of molecular markers in genotypes of modern wheat varieties from Forest-Steppe zone. Traditionally in Ukraine the storage proteins composition is subjected to strong pressure during the selection for the technological quality of grain. Thus, observed by polyacrylamide gel electrophoresis level of genetic polymorphism of storage proteins is not high among modern wheat varieties. The application of allele-specific *Gli-1* and *Glu-A3* markers, designed Zhang et al. (2003, 2004), have permitted to identify not higher level genetic polymorphisms among varieties and determine the conformity of molecular-genetic data and electrophoresis of storage proteins. According to results of analysis of puroindoline genes – 95% varieties have been classified as “hard” wheats with alleles *Pina-D1a*, *Pinb-D1b* and only few were “soft” and have *Pina-D1a*, *Pinb-D1a* alleles. At the same time the differences in “hardness index” for wheat varieties with alleles *Pina-D1a*, *Pinb-D1b* varied considerably from 51 to 84.4. The molecular analysis of *Wx*-genes, that are involved in control of amylose content in starch, have revealed that there are not null-alleles of *Wx*-genes in genotypes of Ukrainian varieties. Thus, for creation of new varieties with special quality characteristics (low amylose content) foreign sources of null-alleles have been involved in breeding programs.

# PRELIMINARY STUDIES ON THE BREEDING OF *VACCARIA HISPANICA* (MILL.) RAUSCHERT: A NEW CROP SPECIES FOR TURKEY

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*Vaccaria hispanica* (Mill.) Rauschert (Caryophyllaceae) has recently been studied for its economic potential owing to special properties of starch grains, triterpenic saponins and cyclopeptide content suitable for drug delivery. Apart from a few flora based investigations, there is scarcity of studies on *V.hispanica* in Turkey. This work highlights preliminary studies conducted as part of a conclusive scientific project that aims to lay the foundation for breeding and economic cultivation of this underused species as an alternative crop, which may lead to the introduction of a new species of medicinal plant in Turkey. As part of project activities, seeds of 54 wild genotypes were collected from different locations of Turkey according to Davis' grid square system. In a preliminary study with a genotype previously collected, the germination percentage up to 98% was observed under *in vivo* and *in vitro* conditions with the absence of dormancy in the seed, successfully producing flowers and seed throughout the year under Antalya conditions. Furthermore, high multiplication capacity (5-20 shoots/bud), *in vitro* flowering, very dense hairy root and somatic embryo developments were achieved under *in vitro* studies. A very well-constructed, honeycomb-looking and a-1µm-average size starch grains were observed in SEM as well as protein, fat and saponin content of respectively of 13.86, 2.33 and 2.80 g /100 g determined in dry seeds. Germination tests in petri dishes according to ISTA Rules with 54 new genotypes showed considerable variation in terms of percentage of the germination and hard seeds among genotypes. Experiments are currently underway to investigate germination requirements and characteristics of the genotypes. As part of studies under way agronomic, morphological and molecular characteristics, chemical structures and responses to haploidy will be investigated on 54 genotypes.

**Keywords:** *Vaccaria hispanica*, Cow Cockle, Saponin, Starch, Cyclopeptid

# RAD SEQUENCING AND SNP DETECTION IN A PEARL MILLET GERMPLASM COLLECTION FOR USE IN GENOME WIDE ASSOCIATION ANALYSIS OF AGRONOMIC TRAITS IN PEARL MILLET

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Pearl millet [*Pennisetum glaucum* (L) R. Br.] is grown as a grain and fodder crop by the poorest of the poor farmers in the harshest environments of South Asia and Sub-Saharan Africa. It has excellent tolerance to environmental stresses and high nutritional and therapeutic food value. To breed resilient cultivars, a number of genetic and genomic resources have been developed and utilised in pearl millet in the past. Most such resources included bi-parental crosses which enhanced understanding of traits genetics and physiology and also enabled their breeding into elite cultivars using marker-assisted selection (Yadav et al. 2011). Although bi-parental crosses were successful in detecting usable genetic polymorphisms, they are limited to the genetic variation present in the two parental genotypes. In comparison to bi-parental crosses, germplasm populations created from genotypes evolved at wider geographical locations offer access to wider genetic variation for traits in a particular crop species. Access of genetic variations present in germplasm populations is facilitated by the discovery of high-throughput sequencing such as restriction site associated DNA sequencing (RAD-Seq) which makes it possible to generate single nucleotide polymorphisms (SNPs) at large scale and in cost effective manner to use in association analysis.. This presentation will describe efforts made towards developing a germplasm population for pearl millet, use of RAD-Seq for detection of SNPs and their subsequent utilization in identifying global genetic variation associated with traits of economic importance in this crop. Advantages and disadvantages offered by association studies in comparison to bi-parental mapping will be discussed.

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# TRAIT ANALYSIS AND DIVERSITY IN SOME WHEAT LANDRACES AND ADVANCE BREEDING LINES EVALUATED UNDER DROUGHT AND HEAT STRESS CONDITIONS

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Drought is affecting about 32% of 99 million hectares area under wheat cultivation in developing countries and at least 60 million hectares area in developed countries. In India, nearly 80% wheat is cultivated under irrigated conditions 66% of which receives only partial (1-2) irrigations and the remaining 20% is grown under rainfed environments. Wheat yields are reduced to 50-90% of their irrigated potential by drought in marginal rainfed environments. Heat stress is responsible for decline in wheat production in many regions of the world, including the parts of India, Pakistan, United States, Australia and Mexico covering 36 m ha area. High temperatures during grain filling period adversely affect the plant growth, yield and grain quality. Global warming will cause more frequent extreme temperature events increasing the frequency and severity of environmentally limited production. Development of tolerant genotypes is on priority. One hundred and sixty-one wheat genotypes were evaluated in irrigated timely, rainfed timely conditions two hundred and thirty-one in irrigated timely and irrigated late field conditions for their response to drought and heat stress and four stress indices were calculated. Variability averaged over traits was highest under rainfed conditions. Grain yield, plant height and productive tillers were more sensitive and test grain weight as tolerant under drought. Under heat stress grain yield, grain weight, test garin weight and phonological traits were more sensitive. Productive tillers and grain number /spike were identified as important selection parameters for drought and grain weight /spike, test grain weight and CTD for heat tolerance.

# A CLONAL SELECTION IN ‘0900 ZIRAAT’ SWEET CHERRY CULTIVAR AND MOLECULAR CHARACTERIZATION BY AFLP ANALYSIS

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Sweet cherry is one of the most important fruit species in Turkey. ‘0900 Ziraat’ is the main cultivar in sweet cherry production of Turkey. In addition, the cultivar ‘0900 Ziraat’ is called with different names by the growers in different regions. This study was carried out to find clonal variations within ‘0900 Ziraat’ in İzmir, Denizli, Manisa, Isparta, Afyon and Konya provinces of Turkey and select the best clones during 11 years (1996-2006) based on their yield and fruit quality. They were also characterized by AFLP analysis at molecular level. In this study, 45 candidate ‘0900 Ziraat’ trees were firstly tagged and 15 genotype of them were selected for their superior fruit quality and yield , then they were budded on Gisela-5 rootstock, and planted in 1999 in Eğirdir Fruit Research Station in Isparta province. Among them, ‘4203’ and ‘4206’ genotypes had the highest (pomological) points in the evaluation study, whereas ‘4218’ and ‘4223’ genotypes had the earliest flowering and harvesting times with high fruit quality. In molecular analysis, four AFLP primer combinations produced 83 DNA fragments having 93.8% polymorphism. The ‘3502’ and ‘4203’ were the closest genotypes. AFLP fingerprinting showed that clones were different from each other and ‘0900 Ziraat’ cultivar. In conclusion, new candidate sweet cherry cultivars were selected and they were found better than ‘0900 Ziraat’ cultivar. ‘4218’genotyp was registered as “Davraz”.later

**Keywords:** *Prunus avium* L., 0900 Ziraat, Clonal selection, AFLP, DNA fingerprinting

# ANALYSIS OF HYBRID PROGENY OF DACTYLIS GLOMERATA FOR SUMMER DORMANCY AND PRODUCTIVITY TRAITS

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Desertification constitutes a significant risk for the persistence of native population. For forage plants growing in areas subject to prolonged and severe summer drought, the most important agronomic characteristic is not the ability to produce during drought but the ability to survive, recover in autumn, and grow actively during the rainy seasons. Dormancy is an adaptive response defined as an absence of growth in summer despite irrigation, is a very effective adaptation to drought which has been observed in cocksfoot. Nevertheless, summer dormancy in cocksfoot is associated with low vegetative productivity. The objective of this study is to analyse the genetical determinisms and heritability of summer dormancy and biomass production in cocksfoot. The progeny between a summer dormant genotype from the variety Kasbah and a summer active genotype from the variety Medly is under study. The preliminary results showed that dormancy is heritable since some hybrids had high level of summer dormancy as the dormant parent Kasbah cv and producing more biomass than the productive parent Medly cv, despite an expected negative correlation (r=-0.40) between summer dormancy measured by the level of senescence in summer under irrigation and biomass production under favourable conditions in spring.

**Key words:** cocksfoot, hybrids, summer dormancy, biomass production

# APPLE GENETIC RESOURCES OF TURKEY AND STUDIES OF EĞİRDİR FRUIT RESEARCH STATION ON APPLE GENETIC RESOURCES

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Turkey is a region which has genetic abundance in a good number of species. Turkey, which include both Mediterranean and Asia minor regions that are defined as two important genetic resources, is in a host position for many annual and perennial species. Apple, one of those species, is one of well-known fruit species in Turkey. Turkey is one of the most apple producing countries (Erişli, 2004). In Turkey, having rich genetic resources, protection and evaluation studies for many fruit species are being continued in research institutions allied to Ministry of Food, Agricultıre and Livestock. Within the scope of the project named “Protection and Evaluation of Fruit Genetic Resources Egirdir Fruit Research Station” which is one of those institutions, studies on 330 of local and foreign apple cultivars continue. Variety descriptions, phenological observations and pomological analyses are being carried out on Genetic Resources parcels in accordance with UPOC criteria and data are being logged. With this study, protection and evaluation of wild, local or developed varieties and types, spread in Turkey and collected in previously surveying studies, is aimed. Material and data supplying for breeding studies will also be provided.

**Key Words:** Turkey, Genetic Resource, Apple

# ASSESSMENT OF HOST PLANT RESISTANCE TO STEM RUST IN PAKISTANI WHEAT GERMPLASM

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Ug99 wheat stem rust (race TTKSK) is a threat to global wheat production as it exhibits broad virulence to wheat varieties including virulence to the widely used gene *Sr31*. By 2007, Ug99 had spread out of East Africa, into Yemen and as far North as Iran. The wheat productivity enhancement program (WPEP) was launched in 2010 as a collaborative project between PARC, USDA and CIMMYT to protect Pakistani wheat from the potential threat of Ug99. In 2010-11 a baseline resistance study (BRS) of wheat germplasm was initiated among WPEP partners. The 1st BRS set comprising 220 wheat lines was screened in 2011 showed that 36 lines (16%) were resistant (30MR/MS) and 184 (84%) susceptible to stem rust under field conditions in Kenya. Out of these lines 36 appeared to be protected with APR genes, although Sr2 was present in only 21 lines. Under glass house conditions only 10 lines (4.5%) were resistant against race TTKSK. The 2nd BRS set of 324 lines tested in 2012 indicated that 100 lines (44%) were resistant to Ug99 under field conditions in Kenya; out of those only 22 (7%) lines showed resistance at the seedling stage to race TTKSK. Molecular data showed that only 8% of the lines carried Sr2; the rest of the 36% lines probably carrying other unknown APR genes. WPEP helped wheat programs in Pakistan to increase the frequency of Ug99 resistance genes (including Ug99 effective gene *Sr25*) in the local varieties thus protecting wheat production against this menace before it arrives in Pakistan.

# *BRASSICA* GENETIC RESOURCES IN TURKEY AND THEIR IMPORTANCE FOR RAPESEED (*Brassica napus* L.) BREEDING

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The *Brassica* genus contains many agronomically important crop species with a range of adaptation for cultivation under varied agroclimatic conditions. Of these, oil seed rape (*Brassica napus* L. ssp *oleifera*), is an important oilseed crop grown in moist and cool climates throughout the world. The genomic relationship of the six cultivated *Brassica* species of economic importance has been determined (U, 1935). The genomes have been denoted as the A, B and C genomes, with three monogenomic diploid species, namely *B. rapa* syn. *campestris* (AA, 2n=20; chinese cabbage and turnip), *B. nigra* (BB, 2n=16; black mustard) and *B. oleracea* (CC, 2n=18; cabbage, brussel sprouts, cauliflower and broccoli). The remaining three cultivated species, *B. napus* (AACC, 2n=38; canola, swede), *B. carinata* (BBCC, 2n=34; Ethiopian mustard), and *B. juncea* (AABB, 2n=36; Indian mustard) are amphidiploid hybrid taxa, evolving through hybridisation between the monogenomic diploid species. Domestication frequently results in limited genetic diversity. Wide genetic diversity for improved crop productivity is largely unexplored in the wild relatives of *Brassica* crops. Turkey itself is underexplored regarding its rich Brassica genetic resources. As well known, Turkey is one of the world's important plant genetic resources centres. Therefore it displays a very rich flora with a remarkable diversity. This richness has different reasons. Turkey is a part of the overlapping Vavilonian centres of plant diversity, a meeting place of three phytogeograhical regions, a bridge between Southern Europe and South-West Asia, a centre of diversity for many genera and sections, a centre of origin for many cultivated plants and weeds in Europe and a country with a high level of endemism. Regarding Brassicas, Davis described that Brassicas are widspread as wild, weedy and cultivated forms throughout Turkey. Different Brassica species are distributed in different regions of Turkey. Different work were done about the characterisation, utilisation and breeding of different Brassica species in Turkey. This review focusses on the presence of different wild and cultivated Brassica material in Turkey and their potential use in *Brassica napus* L. breeding.

# COLLECTING OF WINTER SQUASH (*CUCURBITA MAXIMA* DUCHESNE) AND PUMPKIN (*CUCURBITA MOSCHATA* DUCHESNE) GENETIC RESOURCES OF THE WEST ANATOLIAN

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In this study, a total of 147 Winter squash (*Cucurbita maxima* Duchesne) species collected from the cities of İstanbul, Tekirdağ, Edirne, Kırklareli, Balıkesir, Çanakkale, İzmir, Aydın, Denizli, Muğla, Manisa, Afyon, Kütahya, Uşak, Bursa, Eskişehir, Bilecik, Kocaeli, Sakarya, Düzce, Bolu, Yalova, Ankara, Konya, Karaman, Antalya, Isparta, Burdur where 76% of winter pumpkin production is made in Turkey and, a total of 54 pumpkin species (*Cucurbita moschata* Duchesne) were compiled. The pumpkins were sown on 23th of May 2013 in Hacınuman Village, Altınekin Town-Konya to morphologic characterization and breeding works. Beside selfing works, the fallowing measurements and observations were made: length of sepal of female flowers (mm), length of flower branch of male flowers (mm), diameter of flower branch on male flower (mm), color of flower branch on male flower, days to formation of first male flower, days to formation of first female flower - during flowering period and, length of leaf (cm), width of leaf (cm), length of leaf branch (cm), thickness of leaf branch (mm), segment of leaf palm, color of leaf palm, bubble on leaf palm, color of leaf branch, thorn on leaf palm - were also determined after fruits occurred.

**Keywords:** Winter squash, breeding, morphological characterization, *Cucurbita maxima, Cucurbita moschata*

# COLLECTION AND AGRO-MORPHOLOGICAL AND GENETIC CHARACTERIZATION OF MOROCCAN FABA BEAN LANDRACES

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Faba bean (*Vicia faba* L.) is an important food legume crop of Morocco with a multitude of uses. It is grown as rainfed crop in many parts of the country. Although, Morocco is among the major producer of this crop in the WANA region, its yield is low and unstable, fluctuating from 180 to 1520 kg/ha. This situation is mainly due to biotic and abiotic stresses. Climate change further aggravated these problems. The small farmers in the marginal areas were greatly affected, where this crop is being grown, mostly using local landraces and under rainfed conditions. Genetic variability present in faba bean landraces is crucial to the development of this crop. Therefore, a collecting mission was undertaken during the 2011-2012 growing season, covering the most of the faba bean growing region. A total of 68 local populations were collected. These populations were morphologically, through ICARDA/IPGRI descriptors, and genetically characterized, through SSR, and they were also evaluated for principle agronomical traits. The genetic diversity is 0.3550 and 0.6381 for amorce VF52 and VFG55. These populations showed large variability in leaflet number, plant height, pod characteristics. Moderate variability was observed for leaflet size and shape, flower color. Growth habit, upper nodes branching, wing, pod and hilum color showed no variability. A set of Moroccan accessions held at the national Gene Bank were also screened for biotic stresses and identified tolerant landraces for chocolate spot. The identified useful variability is being deployed in conventional breeding for genetic improvement of faba bean.

# GENETIC VARIATION OF IRANIAN BREAD AND DURUM WHEAT LANDRACES

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In this study the genetic variation of 46 bread and durum wheat landraces collected from different regions of Iran using morphological traits were investigated. Fifteen morphological characters were recorded and analyzed using multivariate methods. High genetic variability was observed for many of traits in the landraces. These results also indicated that genetic variation of durum wheat was more than bread wheat. Furthermore, the results of this study will support efforts of conservation and utilization of landraces in wheat breeding programs. Morphological traits could be successfully used in genetic characterization and genetic variation in bread & durum wheat landraces that may be useful for wheat breeding programs as genetic resources.

**Keywords**: Genetic Variation, Bread & Durum Wheats, Landrace

# GENETIC DIVERSITY STUDY OF SUMMER SQUASH LANDRACES (*CUCURBITA PEPO*) WITH NEUTRAL AND GENE-BASED MOLECULAR MARKERS

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Molecular markers are the modern molecular strategy used to characterize the genetic diversity and redefine the plant genetic resources. We have estimated informativeness and efficiency of SCoT and ISSR molecular markers, in order to classify 36 Greek landraces of *Cucurbita pepo* germplasm. For that reason we calculated the marker's discriminatory power and the level of polymorphism as well as the genetic relationship among the 36 landraces using a dendrogram and Principal Component Analysis (PCA). PCA analysis explained 47.14% for SCoT and 47.02% for ISSRs of the total genetic diversity. Moreover, the identification of the 36 landraces was facilitated via the use of High Resolution Melting (HRM) analysis using EST-SSR markers. The six EST-SSR loci used s which were derived from ESTs (Expressed Sequence Tag), generated a unique melting curve profile for each genotype allowing their classification. Furthermore, HRM analysis enabled the construction of a highly informative dendrogram, with the 36 genotypes classified in 6 distinct clusters. Additionally, using bioinformatics tools we found that the EST-SSRs used were hybridizing to genes involved in stress response to heavy metals and biotic stresses. The results provide guidance for future efficient use of these molecular methods in genetic analysis and breeding of *C. pepo.*

# MORPHOLOGICAL CHARACTERIZATION OF THE NATIONAL MELON (*Cucumis Melo L.*) COLLECTION

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Turkey is a secondary center diversity of Cucurbitaceae family which includes species melon, cucumber, squash and watermelon. Turkey is also one of the most important producers of these crops.In addition to regional types which are grown throughout Turkey, small fields of local types are also found.Although these local types do not contribute to overall production, they are an important factor in the conservation of melon genetic diversity.Aegean Agriculture Research Institute National Gene Bank Melon Collection contains approximately 360 seed samples collected from 52 different locations throughout theTurkey.In this study, as part of TUBİTAK 1060170 project (Genetic Characterization of the National Melon Collection) and TAGEM's Vegetable Genetic Resources Research Project, 160 melon populations preserved in the national collection were morphologically characterized.The characterization was performed using the IPGRI Descriptors for Melon 2003).Overall 35 plant and fruit traits were analyzed.

# GENETIC DIVERSITY ANALYSIS IN CASSAVA (*Manihot esculenta* Crantz) FROM BAIXADA CUIABANA IN BRAZIL USING SSR MARKERS

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Cassava (*Manihot esculenta* Crantz), is the main crop cultivated in traditional farming system in Brazil. Studies indicate that the center of origin and domestication of cassava is in the Brazilian Amazon, but much of the genetic diversity of this crop is unknown. This study was based on the characterization of genetic diversity in the state of Mato Grosso (MT), specifically in the municipalities of Cáceres, Porto Estrela and Santo Antonio do Leverger. The genotypes originated from traditional farmer's swidden fields. In this study, we made a characterization of 211 genotypes collected in 40 swidden fields, in 10 communities, in the three municipalities mentioned above. This characterization was performed using 14 microsatellite loci. We found high levels of observed heterozygosity ($H_o$= 0.587) and gene diversity ($H_e$ = 0.525), whereas most of the genetic diversity was found in the swidden fields (92%). There was a separation between the city of Santo Antonio do Leverger and the municipalities of Cáceres and Porto Estrela. A high intravarietal variability (97%) was detected among the landraces sharing the same folk name. Finally, in the analysis of allelic richness, very high levels were observed in the study area. In the result of priority areas for genetic conservation we found that the municipality of Santo Antonio do Leverger would be considered as a priority area for in situ conservation due to the high genetic diversity found, and to the concentration of constant frequencies for the most common alleles and the presence of fixed private alleles.

**Keywords***: Manihot esculenta*; Genetic diversity; Microsatellites; Landraces; Mato Grosso.

# EVALUATION OF THE SAFFLOWER (*CARTHAMUS TINCTORIUS* L.) CORE COLLECTION UNDER ECOLOGICAL CONDITIONS OF SAMSUN

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Test safflower genotypes consisting of the safflower (*C. tinctorius* L.) core colllection and three certificated local safflower (*C. tinctorius* L.) cultivars were sown in winter during 2007-2008 at the Experimental Fields of the Agricultural Faculty belonging to the Ondokuz Mayıs University. 205 safflower genotypes provided from the Regional Plant Introduction Station in Iowa/USA and three safflower genotypes (Dinçer, Remzibey and Yenice) were used as seed material. Genotypes were sown in a field nursery design in 4 blocks and the local cultivars were sown at the top, in the middle and at the bottom of every block. The safflower (*C. tinctorius* L.) collection consisting of 205 genotypes were sown with three local cultivars in 3m long rows with a interrow space of 10 cm per hand. Phenological observations were done over whole rows, agricultural characters were determined using 10 plants. Using the characterisation tables of UPOV phenologic characters beginning from emergence up to harvest time and morphological characters such as plant height, number of lateral branches, lenght of lateral brach, head weight, number of heads per plant, number of seeds per head, thousand seed weight etc. were determined. Principal Component Analysis was performed to determine genetic variation based on obtained characteristics and the results displayed that big variation exists regarding inside the safflower (*C. tinctorus* L.) collection.

**Key Words:** Safflower, *Carthamus tinctorius* L., Adaptation, Phenological and Morphological Characters

# SOME MORPHOLOGICAL AND AGRONOMIC CHARACTERISTICS OF SAINFOIN ECOTYPES OF EASTERN ANATOLIA REGION

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The aim of this study is obtained breeding lines which will be used in sainfoin breeding by maternal line selection methods. Prominent 15 lines were used, as pasture and grazing type, heavy grazing againts of pest disease resistance which was collected from the natural flora of Eastern Anatolia Region and investigated agronomic performances were used in observation garden for two years. This study was conducted at Central Field of Agricultural Research Institute of East Anatolia. According to the observations, the harvested seeds of selected plant will be transferred to advanced breeding levels. Each of the harvested seeds of selected plant by maternal lines selection methods from the strains observed agronomic performance in observation garden was sown as single and taken required observations from them. Maximum and minimum values of these parameters were 36-103 cm for plant height, 3-8 for the number of branches, 2,43-9,02 mm for stem thickness, 17-103 for the number of stems, , were determined as unit respectively. In addition to initial flowering date ranged between 161 – 183 days. It was observed that numbered of 1-8 strains as vertical, others as semi recumbent

**Key Words:** Sainfoin *(Onobrychis Sativa),* Selection, Pasture, Resistance

# IMPORTANCE OF INTERSPECIFIC HYBRIDIZATION IN DEVELOPING 00-TYPE RAPESEED

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*Brassica napus* L. is a relatively young species that derived only some 500-1000 years ago, in a limited geographic region, from spontaneous hybridisationsbetween turnip rape (*B. rapa*) and cabbage (*B. oleracea*) genotypes. Genetic diversity of oilseed rape is considered to be low because of the short cropping history and the strong breeding focus on seed quality characters. As a consequence, genetic variability in this important oilseed crop is restricted with regard to many characters of value for breeding purposes. Resynthesis of novel genotypes through artificial crosses between the diploid parents, assisted by embryo rescue techniques, is a useful strategy for broadening the genetic basis of breeding material, particularly in terms of increasing heterotic potential through hybrid development. Both progenitor species exhibit an extremely broad genetic and phenotypic diversity that gives the potential for a huge variety of different resynthesized rapeseed forms. The resynthesis of novel *B.napus* through artificial crosses between the diploid parents assisted by embryo rescue has repeatly been shown to be useful for broadening the genetic basis of this plant. As well known, canola quality resources were also found in rapeseed (*B. napus* L.) and were transferred to breeding material via crossing and selection. Also, it is well known that conventional *B. oleracea* and *B. rapa* material display high erucic acid and high glucosinolate levels. The detection of low erucic acid mutants in *B. oleracea* opened the opportunity to develop 0-quality resynthesised rapeseed *(B. napus L.)* forms, which was established by different studies. This review is discussing possible tools to develop low glucosinolate *B. oleracea* forms for further use in developing 00-quality resynthesised rapeseed (*B. napus* L.) forms.

**Key words**: rapeseed, interspecific, hybridization

# MISSING VALUES: OPO SQUASH

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Nowadays farmers prefer the cultivation of species and cultivars on farmlands which are suitable for the market and give maximum profit. Therefore, genotypes which superior characteristics and advantages not discovered up to now are under the danger of extinction. Though we can be in need of these uneconomic valued genotypes due to new developments. Genotypes not fulfilling the needed requirements today can fulfill our requirements in future at the first place. Our country is the gene center of some species of the *Cucurbitaceae* family and most of the species belonging to this family can be grwon without problems due the the rich ecological diversity in Turkey. However, some of the member of this family are grown only for hobby because of economic unimportance. Some of them are named as “Kral Tacı Beyaz Sukabağı” belonging to the species *Lagenaria sicerari,* “Turk’s Turban (kavuk kabağı)” belonging to the species *Cucurbita maxima* and “Küçük Su Kabağı” belonging to the species *Cucurbita pepo var. ovifer*. Some opo squahes belonging to *Lagenaria siceraria* are used as ornaments. However, genotypes only grown for hobby and not used as ornaments or for consumption are under extinction risk. The collection and conservation of such material will enrich our genetic resources and will provide suitable material for further breeding purposes.

# POSSIBLE ADDITIVE HARVEST PRODUCTS FROM EASTERN BLACK SEA TEA (*CAMELIA SINENSIS* L.) PLANTATIONS

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Tea (*Camelia sinensis* L.) is an important plant species mostly grown for its leaves all over the world. One of the leading tea producer countries is China; followed by İndia, Kenia and Sri Lanka. Turkey ranks at the 8th place with a tea plantation area of 75.890 ha and at the 5th place with a production of 221.600 tonnes. Tea is grown wholely at thewith 11,3 % by Artvin and with 2,62 % by Giresun and Ordu. The tea plantations in Turkey are established by planting seeds. This signalizes a large genetic variation. This variation takes away the homogenity in tea production reagrading quality negatively on one hand and creates an important resource regarding the development of new varietesnon the other hand. In Turkey, tea production consists of Chinese tea (Camellia sinensis) crossings. The same can be explained for other countries and species like *C. oleifera*, *C. chekiangoleosa*, *C. reticulata*, *C. grijsii*, *C. vietnamensis*, *C. crapnelliana and C. gauchowensis* are cultivated due to the quality of edible oil in its seeds. The oil content in tea seeds rises up 63,3 % in the speices *C. chekiangoleosa. I*n tea the highest obtained oil content is about 34 %. Nowadays high quality edible oil and biodizel can be obtained from the tea plan, originally cultivated for its fresh leaves, and this gives the possibility to selects superior genotypes displaying high oil yield.

# SELECTION and CHARACTERIATION OF SUPERIOR BANANA TYPES IN TURKEY UNDER SUBPTROPICAL CONDITION

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Banana has been grown in some microclimate since 1937 in the Mediterranean region of Turkey. At present, the total banana production of Turkey is 209.000 tons. As local demand (domestic consumption) for bananas exceeds supply, Turkey has to import bananas from overseas. But if Turkey uses all valuable bananas growing areas, the local consumption can be provided by local production. The main banana cultivar of Turkey is 'Dwarf Cavendish', but so far 'Grand Nain', and Azman (Valery) have been grown economically too. The average bunch weight in the open-field condition and protected cultivation are 20 kg and 35 kg respectively. Under the same region, it can be observed bunch weight differences between 20 and 110 kg in both open-field and protected cultivation. Therefore the local selection efforts are an important potential for banana genetic improvement. The objective of this study was to select desirable off-types from 'Dwarf Cavendsish' 'Grand Nain', and 'Azman' (Valery) which have grown both in open-filed and protected cultivation in Turkey's condition. For this purpose, Stem circumference, stem height, number of hands per bunch, finger weight, finger length and bunch weight were measured in open-field and greenhouse cultivation at the different banana locations. There were big differences in terms of agronomic features among these types. Stem circumference varied among types and ranged from 83 to113, number of hands per bunch from 12 to 18, finger weight from to 83-213 g, finger length from 18 to 24 cm and bunch weight from 35 to 96 kg.

**Key words:** Banana, selection, characterization

# FIELD MUSEUM OF AZERBAIJAN BREAD WHEAT (*TRITICUM* L.) VARIETIES

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Hard wheat, soft wheat and other species have been grown for centuries in Azerbaijan and have a wide polymorphism in many morphobiological and agronomic traits. Therefore, to demonstrate the achievements of breeding and comparative study of the varieties produced in different years, we have organized a Field Museum of wheat. The other aim was to find out morphobiolocal, physiological, genetic, technological and other changes occurred in the modern varieties in a few decades. On this basis in 2010-2012 years 56 genotypes including landraces, new cultivars of hard, soft and emmer wheat were sown in the Gobustan Experimental Station of the Azerbaijan Research Institute for Crop Husbandry. The museum included 27 varieties of durum wheat, including well-known landraces Agh bugda, Sari bugda, Kara bugda and others-the first breeding varieties of 30th years - Arandani, Shark, etc., varieties created in 50-80th years - Jafari, Sevinj, etc., varieties until 2000 year - Karakylchyk 2, Terter, Barakatli 95, and modern varieties of scientific and methodical breeding - Karabagh, Mirvari etc. Four emmer wheat landraces were sown in museum as well. In addition, 26 soft wheat genotypes were included: varieties of 50-80th years - Arzu, Birlik Zerdabi, Grekum 75/50, varieties of 90th and 2000 year - Mirbashir 128, Azeri, Akinchi 84, Giymatli 2/17, modern cultivars Azamatli 95, Gobustan, Ugur, Aran, Tale 38, Murov 2, Kirmizi Gul, Zirva 85 etc. Analyzing morphobiological and agronomic performance it was revealed that durum wheat landraces having low productivity potential were more productive than intensive varieties. Reproduction ratio of some modern durum wheat varieties was equal to zero. It was supposed that, because of the deep location of the tillering node local varieties were resistant to storms and severe spring and summer drought and eventually stood out in terms of yield and other indicators. On the contrary, in soft wheat the new varieties of intensive type were more productive. But as in durum wheat a lifestyle was not a deciding factor - productive genotypes were among the spring, winter and semi-winter forms. Emmer wheat genotypes with lower indicators than durum and soft wheat - showed average values or extinct.

# EVALUATION OF RESISTANCE OF BREAD WHEAT GENOTYPES TO LEAF AND STEM RUST

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In this experiment we have done phenotyping and genotyping analysis of 77 bread wheat accessions to leaf and stem rust. Infection types (ITs) were recorded using the Stakman 0 to 4 scale at 12 days (leaf rust) or 14 days (stem rust) post-inoculation. Plants were inoculated with stem rust races - MCCFC (avirulence – *21, 9e, 11, 6, 8a, 36, 9b, 30, 9a, 9d, 24, 31, 38* / virulence – *5, 7b, 9g, 17, 10, Tmp, McN*), TPMKC (avirulence – *6, 9b, 30, 9a, 24, 31, 38* / virulence – *5, 21, 9e, 7b, 11, 8a, 9g, 36, 17, 9d, 10, Tmp, McN*), RKQQC ( avirulence – *9e, 11, 30, 17, 10, Tmp, 24, 31, 38* / virulence – *5, 21, 7b, 6, 8a, 9g, 36, 9b, 9a, 9d, McN*) and leaf rust races - BBBDB (avirulence – *1, 2a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, B, 10, 18, 21, 28, 39, 42* / virulence – *14a* ), MFBJG (avirulence – *2a, 2c, 9, 16, 3ka, 11, 17, 30, B, 18, 21, 39, 42* / virulence – *1, 3, 24, 26, 10, 14a, 28*), TTRSD (avirulence – *17, 18, 21, 28, 42* / virulence - *1, 2a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 30, B, 10, 14a, 39*), and MRDSD (avirulence – *2a, 2c, 24, 3ka, 11, 30, 18, 21, 28, 42* / virulence – *1, 3, 9, 16, 26, 17, B, 10, 14a, 39*). 16 markers were used for screening for 16 resistance genes. Fragment analysis was done using an ABI DNA 3730 analyzer. Results of phenotype screening indicated that most bread wheat accessions were susceptible to leaf rust. We have selected only four highly resistant and nine moderately resistant bread wheat accessions. However, a majority of bread wheat accessions were resistant or moderately resistant to stem rust. So, 29 of the bread wheats were classified as highly resistant and 33 as moderately resistant to stem rust. Only 13 bread wheat genotypes were susceptible. Results of the molecular screening revealed the presence of the T1RS·1BL rye translocation in nine bread wheat accessions and all were highly resistant to stem rust and most were highly or moderately resistant to leaf rust. Material identified as leaf and stem rust resistant in these experiments will be grouped into germplasm pools and incorporated into our breeding program as potential sources of resistance or tested for yield performance in target environments.

# GENETIC VARIATION OF IRANIAN BREAD AND DURUM WHEAT LANDRACES

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In this study the genetic variation of 46 bread & durum wheat landraces collected from different regions of Iran using morphological traits were investigated. Fifteen morphological characters were recorded and analyzed using multivariate methods. High genetic variability was observed for many of traits in the landraces. These results also indicated that genetic variation of durum wheats was more of bread wheats. Furthermore, The results of this study will support efforts of conservation and utilization of landraces in wheat breeding programs. Morphological traits could be successfully used in genetic characterization and genetic variation in bread & durum wheat landraces that may be useful for wheat breeding programs as genetic resources.

**Keywords**: Genetic Variation, Bread & Durum Wheats, Landrace

# GENETIC DIVERSITY AND POPULATION STRUCTURE IN A DIVERSE PANEL OF PERENNIAL RYEGRASS CULTIVARS AND WILD GENOTYPES

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Perennial ryegrass (*Lolium perenne* L.) is one of the most valuable grasses, widely applied as traditional fodder and amenity grassland, as well as bioenergy biomass producer. Amplified fragment length polymorphism (AFLP) analysis has been used to asses genetic diversity and population structure in a collection consisting of wild genotypes from Lithuania and Ukraine and cultivars of various origin (193 genotypes in total). All genotypes were diploid. The three primer combinations used in the AFLP analyses amplified 227 fragments, 224 of them were polymorphic. Two distinct clusters, one containing wild genotypes from Lithuania, and another – wild genotypes from Ukraine were identified in principal coordinate analysis. Cultivars did not group into separate cluster. Analysis of molecular variance revealed that 96.7% of the variation was within groups of Lithuanian, Ukrainian wild genotypes and cultivars. Similar amount of genetic diversity was found in all groups according to genetic diversity indices. Population structure analysis based on the maximum ΔK value confirmed PCA results indicating two groups in the perennial ryegrass collection.

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# POTATO GENETIC RESOURCES IN THE CZECH REPUBLIC

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Potato Research Institute Havlíčkův Brod, Ltd. is responsible for working with potato (*Solanum* ssp.) genetic resources within the National Programme of Conservation and Use of Plant Genetic Resources and Agro-Biodiversity in the Czech Republic. Potato germplasm collection has been long-term maintained and regenerated exclusively under *in vitro* culture. The strategy of long-term cultivation is based on modification of basic conditions affecting growth and plant development (temperature, light regime, culture medium constitution) in order to slow-down growth and stimulate *in vitro* tuberization. The *in vitro* gene bank involves 2.439 accessions – 1.258 *Solanum tuberosum* varieties, 478 tetraploid hybrids of *Solanum tuberosum*, 271 dihaploids, 313 genotypes from 5 cultivated and 23 wild potato species and 119 interspecific hybrids of *Solanum* genus. For evaluation of genetic resources, a field study collection is planted, consisting of a preparatory and a working plot. The basic evaluation of accessions is performed based on the approved methodology. Under field conditions between 100 and 150 accessions are annually evaluated. Data about continuous evaluation of the accessions are delivered to users of potato germplasm, namely in the form of two informative reports and a list of stored accessions with information about their health state. Between 1994 and 2012 in total 5.249 accessions were delivered to users. The biggest users are research and university workplaces – 4.262 accessions and also practical potato breeders – 607 accessions. The accessions are also presented during thematically focused exhibitions and in museum expositions – 221 accessions. Foreign users requested 154 accessions. National Programme on Conservation and Utilization of Plant, Animal and Microbial Genetic Resources for Food and Agriculture of the Ministry of Agriculture, ref. no. 206553/2011-MZE-17253.

# TEA (*Camellia sinensis* L. O. Kuntze) GENETIC RESOURCES AT THE EASTERN BLACK SEA REGION

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Tea, *Camellia sinensis* (L.) O. Kuntze, is an drink and food material obtained after the processing of its fresh leaves with different methods, and is highestly consumed after water all over the world. The tea plant is grown at the 42 º N and 27 º S latitude zone in the world. However, it is planted in high rainfall and warm climate regions places where tea production is done economically ara rarely. India, China, Sri Lanka and Indonesia are countries where tea plants are grown commonly and tea production is intensive. Tea production on economc level are performed in about 30 countries inclusively these countries and Turkey. Turkey is on the 7. rank regarding the extent of tea plantation areas, on the 5. Rank regarding dry tea production and on the 4. rank regarding annual individual consumption between tea growing countries. Tea, an conventional export product of our country, has an important place in the plant production of the Eastern Black Sea region and 203.000 farmers are labour with tea on 758.000 ha land. The Black Sea coastline beginning from the border of the Georgian Republic up to the border of Araklı, Karadere/Trabzon and slopes nearly up to 1000 m and partly reaching up to 30 km to the inner parts, are identified as first class tea regions because they are the most appropriate region for tea production. This region contains at the meantime very important tea genetic resource. This review explains the tea genetic resources of the Eastern Black Sea region, their conservation and exploration possibilities.

# THYMUS SERPYLLUM USED IN ARMENIAN HERBAL TEA CULTURE AND ITS NATURAL MULTIPLICATION AS A SUPPORT MATTER OF ECOLOGICAL BALANCE AND BIO-CONSERVATION

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The herbal teas are an essential part of a tasty and healthful diet in the Armenian culture. Wherever and whenever there has been a social gathering, herbal teas have been brewed to share with family and friends. The criteria used in choosing herbs for tea preparation is, first, great flavor; second, premium quality; and finally, their ability to enhance the overall enjoyment of a fine meal. During 15 years scientific studies we recognize that on of the main component that used in several herbal tea blends made in Armenia is Wild Thyme. Unfortunately, wild thyme varieties under serious threat of natural and genetic erosion, because of improper selection of thyme species for harvesting as well as unsustainable harvesting and exploitation of these resources by local people taken place. The presented system of wild crafted herbs natural multiplication, on example of Thymus serpyllum, is important for conservation and biodiversity and one of the solutions of the above mentioned problem. Studies on germination of different species of *Thymus (T.serpyllum, T.vulgaris, T.armeniacus, T.kochi)* confirmed their poor germination and growing ability. It is important to mention that previous year harvested seeds have a higher germination percentage than recent year ones. For natural multiplication of Thymus serpyllum in the field, were chosen 3 plots with 0,5 hectare of each in the forest. According from the result of analyzes of independent samples and comparative analyzes of test plots the conclusion was following: Current methodology of natural multiplication and/or rejuvenation of Thymus serpyllum in the filed are effective. It is important to made the *Thymus* seed collections in the year before starting natural multiplication In the second year of natural multiplication the growing rate of multiplication achieved up to 11,3% During the natural multiplication the higher crop index were identify during the fourth year and starting from that period the self rehabilitation and development of plant, without any anthropogenic factors, are registered and natural balance with the environment are achieved. Essential oil content do not much depend to the multiplication/or growing elevation, but depends from the harvesting time of crops, which is shown in the data of essential oil analyzes content of Thymus serpyllum from different elevation of the Odzun are.

# THE GARLIC COLLECTION of TURKEY

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The Garlic Materials are collected by different regions of Turkey and are preserved as vegetatively in the Aegean Agriculture Research Institute National Gene Bank. Morphological characterization studies of 100 garlic materials have carried out in 2011-2012. The collection is characterized according to the Descriptors for Allium spp.(IPGRI 2001) and has evaluated for 17 leaf and bulb characteristics.Topset bulbils, bulbils in the part of the pseudostem and bulblets on stolons are observed in some populations. According to ability to flower characteristic, 4 populations have ability to flower. Violet and white colours of flowers are observed.

# RESPONSE OF ADVANCED, RELEASED, INDIAN AND LOCAL RICE GENOTYPES WITH BACTERIAL LEAF BLIGHT IN NATURAL FIELD CONDITION OF RARS KHAJRUA, BANKE, NEPAL

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Effective chemical control measures against the bacterial leaf blight of rice (caused by Xoo) are not available even though it is one of the major constraints of rice production in Asian countries particularly in Nepal. Therefore search of resistance source and its deployment in the breeding program is the best option to manage this disease both ecologically and economically. Therefore, a field screening of rice varieties with the disease was undertaken at Regional Agricultural Research Station (RARS) Khajura, Banke, Nepal in main rice growing season of 2012-13. Two hundred fifty three advanced rice lines obtained from National Rice Research Program; Hardinath, 25 landraces collected from farmers fields of Kailali and Bardiya, 3 Indian rice varieties popular in Kailali and Bardiya were tested in bacterial leaf blight nursery of RARS, Khajura under natural condition. Disease was scored in 0-9-scale. The results showed that all the three Indian rice varieties (Sarju 52, Indrasan & PR 202) which are gaining popularity in Kailai and Bardiya districts were found susceptible whereas among the tested 25 landraces, 10 found resistant, 11 moderately susceptible and remaining 4 susceptible. In case of tested 253 advanced rice lines including Sabitri ( resistant check) and TN-1 (as a susceptible check) 6 lines including Sabitri found highly resistant, 125 moderately resistant, 97 moderately susceptible and 24 including susceptible check TN-1 found susceptible with the disease in natural disease infestation condition of Kahjura. The results obtained in this initial study reveal the future research thrust, potentiality and directions for the deployment of resistance source in rice breeding program in mid and far western Nepal.

# EVALUATION OF *IN VITRO* CALLI INDUCTION AND REGENERATION OF *LAVANDULA ANGUSTIFOLIA*

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*Lavandula angustifolia* is one of the most important medical and aromatic plants. It was propagated by root cutting or seeds in traditional methods. Those are time consuming with low efficiency. So, *in vitro* cultivation provides possibility to increase propagation rate and helps in its transformation process. *In vitro* cultivation of *L. angustifolia* always faced to some problems because of existing plant phenol substrate. For *in vitro* culture optimization of *L. angustifolia,* different combinations of growth regulators were used. In order to determination of best callus induction medium, factorial experiment with completely random design with 2 factors and 4 replications were used. The factors were 2,4-D in 3 levels(0, 0.2 and 0.4mg.l$^{-1}$) and Kinetinin 3 levels(0, 0.2 and 0.4mg.l$^{-1}$). The most callus percentage was gained in MS medium supplemented with 0.4 mg.l$^{-1}$ 2,4-D and 0.4 mg.l$^{-1}$ Kinetin. Produced Calli regenerated in MS medium supplemented with1.6 mg.l$^{-1}$ in BAP and 1 mg.l$^{-1}$Kinetin as a best medium.

# CAN WE STILL FIND LANDRACES IN EUROPE AFTER 2000? INVESTIGATIONS IN LEMNOS AND LEFKADA, TWO GREEK ISLANDS

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Islands are generally considered as areas potentially possessing rich biodiversity in plant genetic resources. Two case studies were carried out in Greece, (1) on Lemnos, an isolated island in the Northern Aegean Sea, and (2) on Lefkada, a well-known touristic island of the Ionian Sea. In both islands landraces are mainly conserved in home gardens or in small fields, usually by elderly people, and mainly used for local consumption. Several collecting expeditions have been organized in the two islands, especially by the Greek Gene Bank, focusing on landraces and crop wild relatives . The landscape of Lemnos is predominantly flat or hilly (highest elevation 430 m), while that of Lefkada is mostly mountainous (average elevation 500 m) with a diverse relief containing small basins and plateaus. Two collecting expeditions were organized in Lemnos, a minor one in April 2009 and a larger one in June 2010 which exclusively dealt with landraces. The results, especially of the second collection were very encouraging and led, apart from the main collection (112 accessions) in June, to posterior donations (in August and November 2010) reaching 142 accessions of crop landraces in total.  In Lefkada the collecting expeditions of September 2010 and October 2012 yielded in 65 and 36 accessions respectively, mainly from isolated mountainous villages. The collecting missions for both islands have been completed and demonstrated that Lemnos retains more or less its agricultural character in contrast to Lefkada where the touristic pressure is large and many inhabitants have relinquished agriculture to tourism. Nevertheless, our findings suggest that rescuing the remaining local varieties should be first priority and that despite the different character of Lemnos and Lefkada, both could become models of agro-touristic development in Greece.

# RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS

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This project was conducted at GAP Agricultural Research Center of Turkish Ministry of Food, Agriculture and Livestock in Şanlıurfa-Turkey and a semi-arid region of Turkey. The aim was to determine the effects of water stress on 194 melon accessions collected from different region of Turkey. Different irrigation levels were imposed to determine potential water stress' effect on melon accessions. All plots at the beginning were irrigated with enough irrigation water for healthy seed germination. The plants received enough irrigation until the period of true leaves. After the true leaves, irrigation treatments were initiated. While $I_1$ treatment was received full irrigation based on depleted soil moisture in the root zone, $I_2$ treatment was received 50% of $I_1$. The formula, improved by Karipçin et al. (2008), was used to evaluate data as an indicator of drought tolerance. For each accession, changing ratio between $I_1$ and $I_2$ treatments was obtained. If any accession's changing rate ($I_1/I_2$) was near 1 that means that the accession was more tolerant to drought than the others. Physiologic/vegetative characteristics were measured such as Situation of growing, Date of the first branch, Condition of dehydration, Leaf temperature, Root length, Date of the first male flower blooming, Number of flowers bud, Number of male flower bud, Width of flower, Canopy diameter, Main stem length, Width of root, Fresh root weight , Dry root weight. The results showed that forty-three of tested accessions were tolerant ones. The highest score obtained from the formulae was 100 with accession number 41, 106, 183 and 248. Other tolerant 39 accessions were rated between 99 and 80 point. 21 accessions were placed between tolerant and intolerant group. The accessions were classified as tolerant if they had a rating above 80 out of 100 and intolerant if the rating was below 64. 130 accessions were classified as intolerant.

**Keywords:** Genetic resources, abiotic stress, melon, accession

# TOMATO GERMPLASM COLLECTION IN REPUBLIC OF MOLDOVA

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The conservation of the genetic resources of the Lycopersicon is of great importance, due to the nutritional and economic value. Tomato is the most common vegetable crop in Moldova. Most of the tomato accessions are kept in the Centre of Plant Genetic resources of Moldova that plays the coordinating role in the activities on *ex situ, in situ* and *on farm* conservation at the national level.

Currently, the collection of tomato includes 673 accessions. The collection covers different types of accessions such as cultivars, landraces, wild relatives, hybrids. The largest part of collection is formed by the cultivated species *Lycopersicon esculentum* L. (622 accessions). Wild species include *L. hirsutum* Humb. (11 accessions), *L. chilense* (2), *L. cheesmanii* (1), *L. peruvianum* Mill. (33) and *L. glandulosum* (4). The tomato collection was extended with samples from expedition missions. The collection data are computerized. Information on collection maintained *ex situ* consists of common basic information – passport data that correspond to Multi-Crop Passport Descriptors (MCPD), elaborated by the Biodiversity International and FAO. Passport data includes thirty-three fields such as: institute code, accession number, collecting number, genus, species, accession name, acquisition date, country of origin, geographical description, biological status, collecting source, pedigree, donor institution etc. For evaluation and characterization of tomato germplasm were used IPGRI Crop descriptors.

# EXPLORATION AND COLLECTION OF TOMATO GERMPLASM IN NIGERIA

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The major constraints to vegetable production in Nigeria border around poor seed supply of acceptable and adaptable/locally developed varieties. This renders farmers totally dependent on the imported exotic varieties which are prone to local pests and diseases. Exploration for Tomato germplasm diversity was carried out in the Northern and Southern states of Nigeria. The Eight states which are the main growing areas of the Country: Ogun, Oyo, Plateau, Kaduna, Jigawa, Kano, Gombe and Borno states were surveyed for germplasm collection. Individual, random sampling methods and Questionaire were used . The local landraces were found mostly in the Southern states and collected during these exploration trips. It was observed that there is higher demand for improved seed by farmers in the Northern states than their counterparts in the South. The largest growing area for tomato is in Kadawa in Kano state and the period of growing is between October to January on ten thousand hectares of land. During these exploration trips, a total of 100 accessions of tomato germplasm with a wide range of genetic diversity include shape, sizes and color were collected. The local indigenous knowledge on production, storage and marketing practiced by the farmers was also recorded.

# FORM DIVERSITY AND SELECTION OF WALNUT IN KYRGYZSTAN

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In the mountains of Kyrgyzstan in the natural forests are forms of walnut, very different from each other.

According to researchers 11.2% of nuts are large, 85.1% the small and 3.7% very small. Weight of nuts in the following ranges from 2 to 19 g, are more common from 8 to 13 g, the average weight of a walnut, the 8.4 g. Core output ranges from 30 to 70% by weight of a nut, and more than 70% of the nuts with the release of the core of 41 to 60%. Walnut shell thickness varies from 0.2 to 2.9 mm. Most nuts have shells of medium thickness and about 30% of the nuts with a thick shell and about 20% of the nuts with a thin shell.

The fat content in nuts Kyrgyzstan is very high. Analyzes of samples of nuts, showed that the percentage of fat on a dry seed varies from 62 to 74, on average 71%. In natural forests of walnut and cultures are forms more resistant to frost, which later blooming, disease resistant and regular fruiting. Such forms of walnut deserve serious attention and wide propagation in production. Over the period 1999 to 2010 in the region of the walnut-fruit forests are selected more than 20 new forms of walnut. Selected forms differ on a range of agronomic traits and biological properties. In the selection of new forms of walnut task was to find trees that differ not only good quality fruit, and yields, the regularity of bearing, resistance to frost and diseases. These economically valuable traits and biological properties were identified during observation of selected forms in cultures and natural forests of walnut for a few years. Regularity of fruiting forms are selected from studying tree nut crop for 3 years. Resistance to low temperatures is determined annually, especially in years with late spring frosts. Stability of selected forms nut to disease, in particular to marconiya (Marconina juglandis) determined by comparison with other trees for 3 years. According to the results of assessments and the amount of points scored by complex biological and agronomic characters highlights the most promising forms of nuts. These forms include: 3A, 4A, 10A, 11A, 12A, 2R, 19A and AB. They regularly and good fruit, resistant to frost, and at the same time enjoy the high quality of the fruit. Among the selected forms as late-forms can be distinguished forms 2K and AB, self-pollinated forms 3A, 4A and 11A. Of great importance for the industrial cultivation of walnut have early-maturing forms of walnut. These forms into early fruiting season, different with productivity. Feature of the early appearance of forms is the formation of the fruit from the secondary flowering. Early appearance of the forms should be selected form with quality fruit and disease-resistant and external environmental conditions. From a sample of our forms, such as forms 7A and 15A are the early appearance, which regularly produce fruit, often produce fruit on new growth from lateral buds and secondary bloom.  The most promising forms of walnut are registered with passport.

# ALLELOPATHY; A BRIEF REVIEW

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Allelopathy is a well known area of active research in ecology. However, its importance in agro-ecology is still underappreciated. This review sets out to address this situation and introduce this new and developing field to a wider research audience and to stimulate new research in it. The review starts with an introduction, followed by discussions of allelochemicals, the role of allelopathy in crop production, Allelopathy related problems in crop production, and Suggestions for future research. It also describes broader research into allelopathy in agriculture and the biosciences, and literature resources on the subject. We hope that it will encourage more scientists to initiate research into this exciting new field.

# RESEARCH ON WATER STRESS EFFECT OF WILD AND DOMESTIC MELON ACCESSIONS

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This project was conducted at GAP Agricultural Research Center of Turkish Ministry of Food, Agriculture and Livestock in Şanlıurfa-Turkey and a semi-arid region of Turkey. The aim was to determine the effects of water stress on 194 melon accessions collected from different region of Turkey. Different irrigation levels were imposed to determine potential water stress' effect on melon accessions. All plots at the beginning were irrigated with enough irrigation water for healthy seed germination. The plants received enough irrigation until the period of true leaves. After the true leaves, irrigation treatments were initiated. While $I_1$ treatment was received full irrigation based on depleted soil moisture in the root zone, $I_2$ treatment was received 50% of $I_1$. The formula, improved by Karipçin et al. (2008), was used to evaluate data as an indicator of drought tolerance. For each accession, changing ratio between $I_1$ and $I_2$ treatments was obtained. If any accession's changing rate ($I_1/I_2$) was near 1 that means that the accession was more tolerant to drought than the others. Physiologic/vegetative characteristics were measured such as Situation of growing, Date of the first branch, Condition of dehydration, Leaf temperature, Root length, Date of the first male flower blooming, Number of flowers bud, Number of male flower bud, Width of flower, Canopy diameter, Main stem length, Width of root, Fresh root weight , Dry root weight. The results showed that forty-three of tested accessions were tolerant ones. The highest score obtained from the formulae was 100 with accession number 41, 106, 183 and 248. Other tolerant 39 accessions were rated between 99 and 80 point. 21 accessions were placed between tolerant and intolerant group. The accessions were classified as tolerant if they had a rating above 80 out of 100 and intolerant if the rating was below 64. 130 accessions were classified as intolerant.

**Keywords:** Genetic resources, abiotic stress, melon, accession.

# COLLECTING AND DOCUMENTATION OF TOMATO LOCAL FORMS IN REPUBLIC OF MOLDOVA

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The conservation of traditional local varieties is an essential component of sustainable agricultural development. The need for conservation of crop genetic diversity in the form of traditional crop varieties, or landraces is emphasized in the Convention of Biological Diversity, Agenda 21, and the International Treaty on Plant Genetic Resources for Food and Agriculture. Local forms act as a primary source of breeding material for modern varieties. In this context the local forms of tomato occupies an important place among the local agricultural products and serve as material for scientific researches.  This paper reports data about the collection and documentation of vegetable local forms in different region of Moldova. For this purposes expeditions in different geographical regions of the country are conducted and local varieties are collected. This activity was supported by SIDA in SEEDNet project. Data were collected using purposely development form. Information about collected material is store in the ReGen documentation system that has been developed in the Centre for Plant Genetic Resources of Moldova. The database consists of two parts: passport and collecting data that is determined by issues as identification and features of collecting place, sample identity, information about the cultivar's donor, cultivar distribution and cultivation manner, geophysics site description, selection and storage of collecting materials, cultivar uses etc.

# VARIABILITY IN MALE, FEMALE AND ANDROMONOECIOUS *SIMAROUBA GLAUCA* DC CULTIVARS AS ASSESSED BY MOLECULAR MARKERS

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*Simarouba glauca* DC, apart from being medicinal, is a versatile multipurpose oil-yielding tropical tree belonging to family Simaroubaceae, commonly known as “Paradise tree”, is a native of El Salvador, Brazil. To understand genetic relationship, a comparative study was conducted to evaluate genetic diversity among 96 female, male and andromonoecious plants of *Simarouba*, collected from various geo-graphical location of India, employing 67 RAPD and 22 ISSR primers. The two data sets were analysed to calculate the total number of bands, the average number of bands per primer, the number of polymorphic bands, the percentage polymorphism, the effective multiplex ratio (EMR), the polymorphic information content (PIC), the marker index (MI) and the genetic similarity coefficients. In RAPD analysis, polymorphism percentage ranged from 9 to 100 with average percent polymorphism of 42.3% while for ISSR is from 11 to 77 with average of 38.8%. The mean PIC value (DI) for both marker system (0.92 for RAPD and 0.90 for ISSR) suggested that both the marker system is effective in determining polymorphism. The ISSR marker produced more information than the RAPD markers due to their higher EMR, as well as the MI values (5.04 and 4.58) compared to RAPD (3.31 and 3.04). The value of Jaccard similarity coefficient ranged from 0.78 to 0.97 and 0.78 to 0.95 based on RAPD and ISSR similarity matrix data. The UPGMA dendrogram obtained from the RAPD and ISSR data gave different clustering pattern with some level of similarities. The results indicate the effectiveness of these two marker system for demonstrating genetic relationship among *Simarouba* genotypes.

# SOURCES OF RESISTANCE TO STRIPE RUST (*PUCCINIA STRIIFORMIS* F. SP. *TRITICI* IN WHEAT (*TRITICUM AESTIVUM L.*) LANDRACES

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Stripe rust caused by *Puccinia striiformis* is a severe foliar disease of wheat (*Triticum aestivum* L.) worldwide. Wheat landraces are valuable heterogeneous genetic resource for improving the genetic base for resistance to diseases in wheat. The objectives of this study are to determine the resistance in wheat landraces to stripe rust pathogen. Secondly, to isolate and characterize stripe rust isolates and lastly, to map the yellow rust resistant genes. About, 700 wheat Watkins collections from the UK are being evaluated for yellow rust (stem and leaf rust) resistance at Njoro and we will validate these in further trials and advance mapping. Stripe rust isolates will be collected from wheat growing areas in Kenya and races designated. Current study indicates that there is limited germplasm resistant to stripe rust and efforts to identify and characterize new sources of resistance are imperative to prevent future losses and to maintain diversity for resistance.

**Key words**: *Puccinia striiformis ,* landraces, stripe rust race, mapping

# DETERMINATION OF GENOME SIZE OF FESCUE SPECIES COLLECTED FROM EASTERN ANATOLIA OF TURKEY BY FLOW CYTOMETER AND USAGE IN PLOIDY ANALYSIS AND TAXONOMIC CLASSIFICATION

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Genome size is the total amount of DNA contained within one copy of a single genome. It is typically measured in terms of mass in picograms or total number of nucleotide base pairs. One picogram equals 978 megabases. Genome size is stable among individuals of a species and cells of a single plant. Therefore, it is species specific. However, it differs approximately 600 folds among species. Today, flow cytometer is the method of choice in genome size determination due to its speed and sensitivity. The objective of this study is to determine genome size of approximately 140 fescue populations collected from East Anatolian region of Turkey by using flow cytometer. Based on the results of this study, genome size of fescue populations varied between 4.41 pg and 14.97 pg. In conclusion, genome size determined by flow cytometer can be used to determine ploidy of fescue populations and facilitate their classification taxonomically.

# USING AN “INDEX OF MERIT” FOR MULTITRAIT EVALUATION OF WINTERHARDY FEED PEA LINES

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Winter feed pea (*Pisum sativum* ssp. *arvense*) is a nitrogen-fixing cool season annual legume that might serve as a partial or complete replacement for fallow in the winter wheat-summer fallow (WW-SF) system in the Central Great Plains (CGP) USA, thus making farming and ranching in the region more economically and environmentally sustainable, with all the benefits of a legume in the rotation and the potential to integrate cereal and livestock production. Benefits resulting from rotation with legumes include nitrogen credit, increased soil organic matter, reduced soil erosion, pest and pathogen control, increased soil water storage efficiency, economic diversity and, perhaps, sequestration of carbon via more intensive cropping in an age of climate change. Winter feed pea has successfully integrated cereal and livestock production elsewhere (e.g., Europe, southern Australia and the Palouse region of the U.S. states of Washington and Idaho). The objective of this study was to evaluate advanced breeding lines bred in the Wyoming environment in comparison with existing winter feed pea cultivars that were bred elsewhere. Diverse winter feed pea genetic lines/cultivars were hybridized in the greenhouse and artificial selection began with an $F_2$ spaced plant nursery. Natural and artificial selection began among single plants, and then among single plants within superior segregating families, and finally among bulked progenies of advanced lines. As breeding populations were advanced from the $F_2$ through $F_9$ generations, the number of lines retained was reduced, as seed of elite, advanced lines was increased. In the 2010-2011, and 2011-2012 winter annual growing seasons, and at two locations (Lingle WY and Laramie WY), seven elite Wyoming breeding lines were tested together with the three most available U.S. winter pea cultivars (‘Common’, ‘Specter’, and ‘Windham’, all from the Pacific Northwest). In large randomized, replicated experiments, we evaluated yield of lines/cultivars for forage and seed under both dryland and irrigated conditions. Results demonstrate that breeding for the Wyoming environment can produce superior locally adapted lines for the CGP. An “index of merit” that integrates yield potential for Forage Dryland, Forage Irrigated, Seed Dryland, and Seed Irrigated systems demonstrated that five Wyoming bred lines are the top five lines of ten tested in this evaluation. The three check cultivars were in the bottom five lines tested, along with two Wyoming lines that were lines that were retained because they exhibited morphological diversity, but not high yield potential, in early generation testing. We conclude that our elite lines, especially Wyo#11 and Wyo#13, proposed for release as ‘Archer’ and ‘Arrow’, respectively, are well-adapted to Wyoming and yield well under different conditions. We also discuss alternative “indices of merit,” related to “selection indices,” as ways of evaluating and graphically illustrating the value of lines/cultivars tested for multiple use (e.g., in our case, forage vs. seed, and dryland vs. irrigated) in sustainable agroecosystems.

# MOLECULAR AND PHYSIOLOGICAL CLASSIFICATION OF DIVERGENT *CAMELNA SPP*. GERMPLASM

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Camelina is a promising energy crop for the biodiesel industry, especially for production of airplane fuel. In addition, its distinctive fatty acid profile and high protein contents satisfy the nutraceutical and animal feed uses. About 250 accessionswere collected from all of world and evaluated during 2012 and 2013. Oil contents and fatty acid profile from harvested seed was determined by GC-MS. Genetic diversity was assessed by SSR (simple sequence repeat) markers. The sixteen SSR markers were applied to determine the genetic diversity among the accessions. The distinctive variation of oil content and fatty acid profiles observed among the accessions. Detail information about above observations will be presented and will be used camelinabreeding program.

# WHEAT ASSESSMENT ON THE CONTENT OF $ZN^{2+}$, $CU^{2+}$, $CD^{2+}$ METALS

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Various vegetations on terms genetic resources for carrying out preliminary selection on the general adaptability (GA) of cereals significantly accelerate breeding process. Metal resistance of initial forms is an important component of GA cereals in the conditions of anthropogenic pollution, as in Kazakhstan, and all over the world. The breeding wheat materials including winter, spring forms and facultative wheat in different ecological conditions on experimental sites of Kazakh Scientific Research Institute Agriculture and Plant Growing. Laboratory researches on influence of ions of $Zn^{2+}$, $Cu^{2+}$, $Cd^{2+}$ of metals (20 mg/l in a nutrient medium) on changes of physiological & biometric parameters growing of 7 day sprouts of wheat were carried out in 2010-2013. Comparison of metal resistance of plants carried out on the basis of Wilkins coefficient calculation. It was found that cereals resistance to the action of $Zn^{2+}$, $Cu^{2+}$, $Cd^{2+}$ metal depends on the content them in grain, the growth conditions (irrigation and rainfield), a varietal and genotypic specificity. A number of stability of cultivars of winter wheat to studied metals is constructed: $Cu^{2+}$: Progress (0,88) > Bogarnaja 56 (0, 66) > Bezostaja 1 (0, 64); $Zn^{2+}$: Bogarnaja 56 (1,16) > Progress (0,95) > Bezostaja 1 (0, 83); $Cd^{2+}$: Progress (0,97) > Bogarnaja 56 (0,85) > Bezostaja 1 (0,82); It is established that ions of $Cu^{2+}$ and $Cd^{2+}$ render stronger inhibiting effect for growing of roots and vegetative mass of all studied versions of wheat. The Wilkins coefficient was higher for facultative wheat in winter crops in comparison with spring at cultivars “Ruta” and “Kazahstanskaya 10”. Wheat cultivars Kazahstanskaya 10, grown up without irrigation, had at laboratory conditions a higher level of resistance to metals in comparison with the seed which has been grown up on an irrigation. Facultative wheat showed higher level of resilience to a metal stress, in comparison with winter and spring forms that testifies to their considerable potential for studying of GA and the subsequent involvement in crossings. As a whole the assessment of a wheaten variety on metal resistance will allow to reveal valuable initial forms for pre-breeding and breeding on GA.

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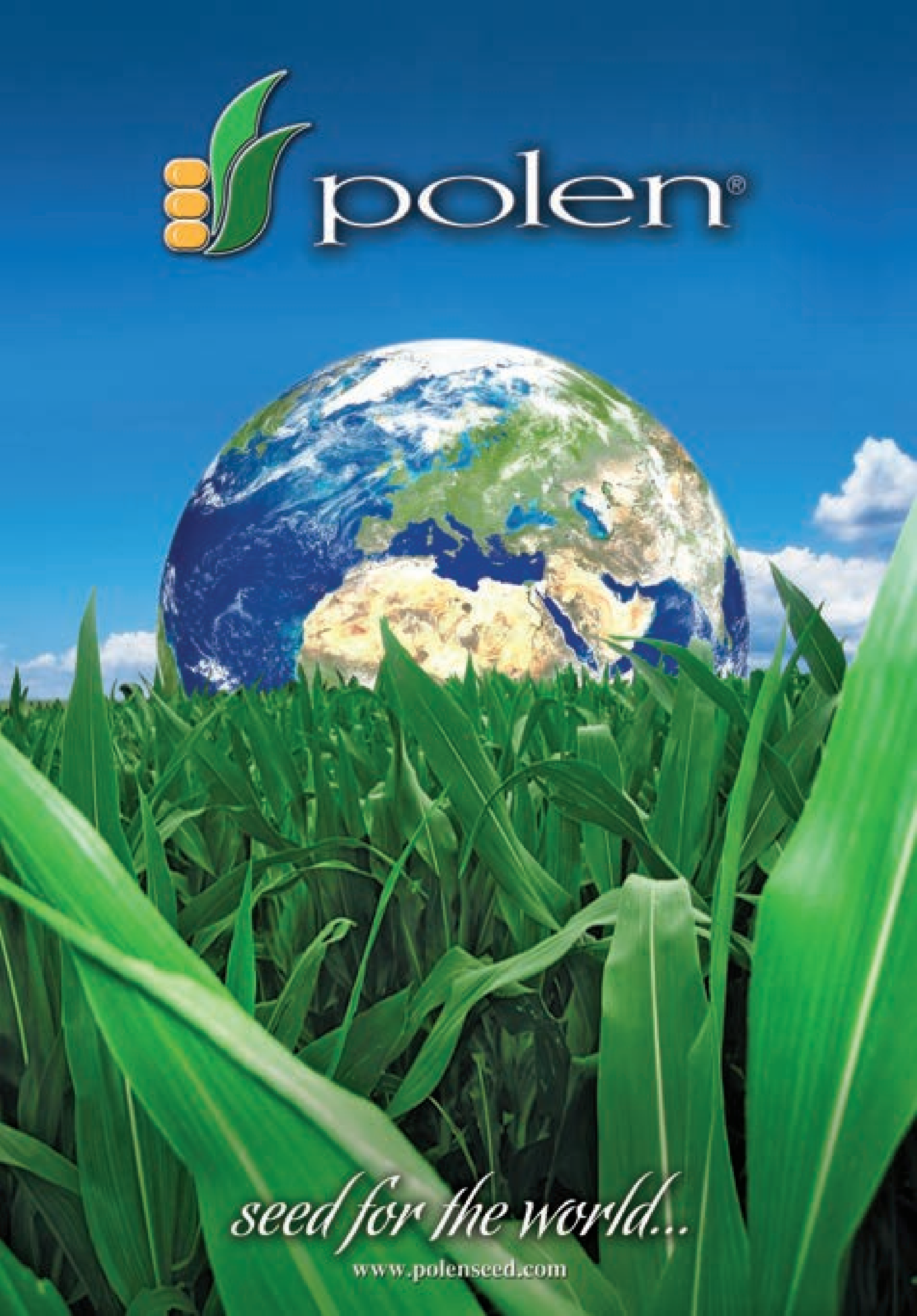
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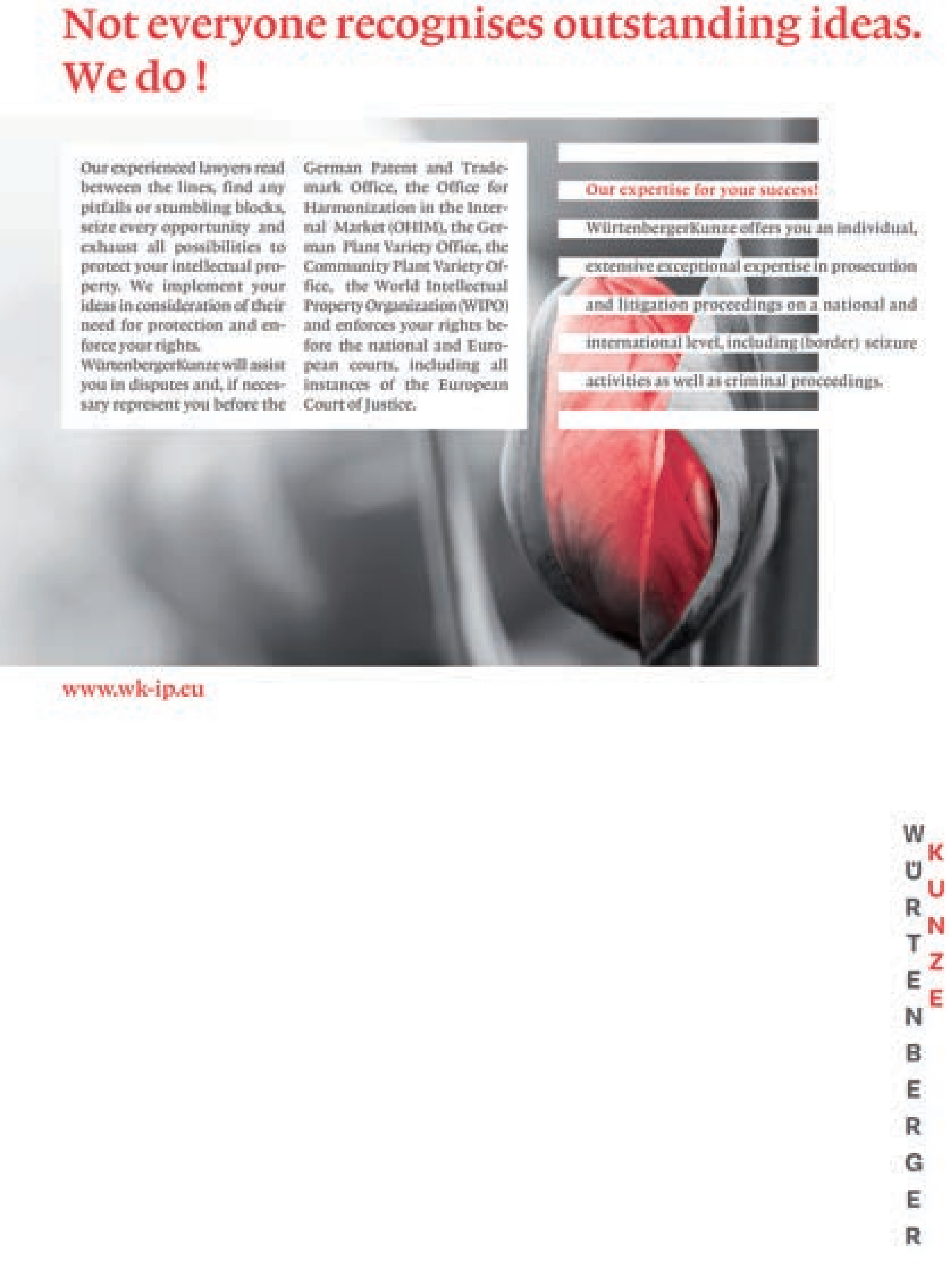

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